

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 15:35:06 ; Search time 18 Seconds
(without alignments)
38.571 Million cell updates/sec

Title: US-09-830-839-1

Perfect score: 79

Sequence: 1 MTEQWNFAGIEAAA 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications AA_New:
1: /SIDSS5/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /SIDSS5/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /SIDSS5/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
4: /SIDSS5/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
5: /SIDSS5/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	100.0	15	11	US-11-041-893-216
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3	79	100.0	20	11	US-11-041-893-237
4	79	100.0	20	11	US-11-156-365-26
5	79	100.0	95	11	US-11-041-893-214
6	79	100.0	97	9	US-10-909-957-4
7	79	100.0	249	9	US-10-909-957-2
8	69	87.3	13	11	US-11-041-893-42
9	69	87.3	13	11	US-11-041-893-48
10	59	74.7	15	11	US-11-041-893-217
11	58	73.4	10	11	US-11-041-893-245
12	54	68.4	10	11	US-11-041-893-246
13	50	63.3	9	11	US-11-041-893-43
14	40	50.6	295	9	US-10-454-437-16
15	40	50.6	694	11	US-11-074-176-340
16	40	50.6	697	11	US-11-074-176-150
17	39	49.4	243	11	US-11-137-465-39
18	39	49.4	382	11	US-11-096-568A-21702
19	38	48.1	324	11	US-11-096-568A-6972
20	38	48.1	380	11	US-11-096-568A-6971
21	38	48.1	396	11	US-11-096-568A-6970

38	48.1	454	11	US-11-087-099-8366	Sequence 8366, Ap
38	48.1	650	11	US-11-072-512-3636	Sequence 3636, Ap
37	46.8	15	11	US-11-156-365-8	Sequence 8, Appli
25	46.8	251	9	US-10-467-657-2306	Sequence 2306, Ap
26	46.8	256	11	US-11-045-004-1043	Sequence 1043, Ap
27	46.8	294	11	US-11-188-298-2826	Sequence 2826, Ap
28	46.8	325	11	US-11-239-674-4	Sequence 4, Appli
29	46.8	326	11	US-11-087-099-1226	Sequence 1226, Ap
30	46.8	368	9	US-10-858-730-217	Sequence 217, App
31	46.8	445	11	US-11-087-099-10405	Sequence 10405, A
32	46.8	445	11	US-11-087-099-12374	Sequence 12374, A
33	46.8	445	11	US-11-188-298-11360	Sequence 11360, A
34	46.8	585	9	US-10-467-657-3160	Sequence 3160, Ap
35	45.6	188	11	US-11-036-797-37	Sequence 37, Appl
36	45.6	239	11	US-11-096-568A-19957	Sequence 19957, A
37	45.6	255	11	US-11-096-568A-19956	Sequence 19956, A
38	45.6	288	11	US-11-096-568A-31370	Sequence 31370, A
39	45.6	326	11	US-11-087-099-1968	Sequence 1968, Ap
40	45.6	326	11	US-11-087-099-8338	Sequence 8338, Ap
41	45.6	326	11	US-11-087-099-9948	Sequence 9948, Ap
42	45.6	406	11	US-11-087-099-1278	Sequence 1278, Ap
43	45.6	420	11	US-11-096-568A-11992	Sequence 11992, A
44	45.6	444	11	US-11-087-099-4027	Sequence 4027, Ap
45	45.6	448	11	US-11-087-099-3085	Sequence 3085, Ap
46	45.6	448	11	US-11-096-568A-11991	Sequence 11991, A
47	45.6	470	11	US-11-087-099-11164	Sequence 11164, A
48	45.6	475	11	US-11-188-298-6764	Sequence 6764, Ap
49	45.6	511	11	US-11-135-667-35	Sequence 35, Appl
50	45.6	513	11	US-11-135-667-54	Sequence 54, Appl
51	45.6	532	11	US-11-096-568A-25921	Sequence 25921, A
52	45.6	535	11	US-11-096-568A-25920	Sequence 25920, A
53	45.6	565	11	US-11-096-568A-25919	Sequence 25919, A
54	45.6	642	11	US-11-079-463-8302	Sequence 8302, Ap
55	45.6	649	11	US-11-079-463-10379	Sequence 10379, A
56	45.6	743	11	US-11-045-004-2016	Sequence 2016, Ap
57	45.6	966	11	US-11-054-281-71	Sequence 71, Appl
58	45.6	974	11	US-11-054-281-73	Sequence 73, Appl
59	45.6	1487	9	US-10-511-989-24	Sequence 24, Appl
60	45.6	1866	8	US-10-511-937-2968	Sequence 2968, Ap
61	45.6	1866	9	US-10-511-989-186	Sequence 186, App
62	45.6	2107	9	US-10-995-561-827	Sequence 827, App
63	45.6	2480	9	US-10-995-561-825	Sequence 825, App
64	45.6	3116	9	US-10-995-561-826	Sequence 826, App
65	44.3	41	9	US-10-057-813-5	Sequence 5, Appli
66	44.3	153	11	US-11-294-997-9	Sequence 9, Appli
67	44.3	210	11	US-11-098-686-11205	Sequence 11205, A
68	44.3	232	11	US-11-156-516-39	Sequence 39, Appl
69	44.3	243	11	US-11-087-099-6529	Sequence 6529, Ap
70	44.3	301	9	US-10-131-826A-176	Sequence 176, App
71	44.3	301	9	US-10-973-115B-176	Sequence 176, App
72	44.3	301	9	US-10-137-873A-176	Sequence 176, App
73	44.3	301	9	US-10-152-370-176	Sequence 176, App
74	44.3	301	11	US-11-290-153-176	Sequence 176, App
75	44.3	306	11	US-11-087-099-6817	Sequence 6817, Ap
76	44.3	349	11	US-11-087-099-523	Sequence 523, App
77	44.3	360	11	US-11-294-997-11	Sequence 11, Appl
78	44.3	404	11	US-11-052-554A-344	Sequence 344, App
79	44.3	410	11	US-11-087-099-1216	Sequence 1216, Ap
80	44.3	417	11	US-11-087-099-1146	Sequence 1146, Ap
81	44.3	427	11	US-11-188-298-7493	Sequence 7493, Ap
82	44.3	440	11	US-11-087-099-10394	Sequence 10394, A
83	44.3	440	11	US-11-087-099-11247	Sequence 11247, A
84	44.3	451	11	US-11-087-099-10164	Sequence 10164, A
85	44.3	452	11	US-11-087-099-11368	Sequence 11368, A
86	44.3	459	11	US-11-087-099-11321	Sequence 11321, A
87	44.3	603	9	US-10-161-408-17	Sequence 17, Appl
88	44.3	603	11	US-11-082-154A-106	Sequence 106, App
89	44.3	608	11	US-11-085-864-2	Sequence 2, Appli
90	44.3	608	11	US-11-127-004-2	Sequence 2, Appli
91	44.3	608	11	US-11-190-408-2	Sequence 34196, A
92	44.3	643	11	US-11-096-568A-34196	Sequence 34196, A
93	44.3	656	11	US-11-096-568A-34195	Sequence 34195, A
94	44.3	665	11	US-11-096-568A-34194	Sequence 34194, A

95	35	44.3	764	11	US-11-087-099-5574	Sequence 5574, Ap	168	33	41.8	486	11	US-11-087-099-6341	Sequence 6341, Ap
96	35	44.3	764	11	US-11-188-298-5089	Sequence 5089, Ap	169	33	41.8	486	11	US-11-079-463-10041	Sequence 10041, A
97	35	44.3	791	11	US-11-096-568A-31251	Sequence 31251, A	170	33	41.8	488	11	US-11-188-298-585	Sequence 585, App
98	35	44.3	840	11	US-11-079-463-9322	Sequence 9322, Ap	171	33	41.8	501	11	US-11-055-822-52	Sequence 52, App
99	34	43.0	147	11	US-11-072-512-2557	Sequence 2557, Ap	172	33	41.8	501	11	US-11-239-674-50	Sequence 50, Appl
100	34	43.0	165	11	US-11-088-686-10343	Sequence 10343, Ap	173	33	41.8	505	9	US-10-506-454-913	Sequence 913, App
101	34	43.0	249	11	US-11-088-298-7615	Sequence 7615, Ap	174	33	41.8	521	11	US-11-188-298-21440	Sequence 21440, A
102	34	43.0	359	11	US-11-188-298-7615	Sequence 7615, Ap	175	33	41.8	521	11	US-11-135-603-2	Sequence 2, Appl
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104	34	43.0	433	11	US-11-182-016-51	Sequence 51, Appl	177	33	41.8	556	11	US-11-188-298-6539	Sequence 6539, A
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106	34	43.0	456	11	US-11-087-099-8799	Sequence 8799, Ap	179	33	41.8	583	11	US-11-188-298-713	Sequence 713, App
107	34	43.0	464	11	US-11-087-099-1003	Sequence 1003, Ap	180	33	41.8	591	11	US-11-188-298-713	Sequence 713, App
108	34	43.0	474	11	US-11-087-099-10672	Sequence 10672, A	181	33	41.8	591	11	US-11-188-298-8505	Sequence 8505, Ap
109	34	43.0	478	11	US-11-087-099-7019	Sequence 7019, Ap	182	33	41.8	591	11	US-11-188-298-10639	Sequence 10639, A
110	34	43.0	502	11	US-11-188-298-5646	Sequence 5646, Ap	183	33	41.8	591	11	US-11-188-298-13585	Sequence 13585, A
111	34	43.0	526	9	US-10-467-657-6754	Sequence 6754, Ap	184	33	41.8	591	11	US-11-188-298-20215	Sequence 20215, A
112	34	43.0	635	11	US-11-079-463-6686	Sequence 6686, Ap	185	33	41.8	621	9	US-10-632-150-56	Sequence 56, Appl
113	34	43.0	1530	11	US-11-045-004-34	Sequence 34, Appl	186	33	41.8	621	10	US-11-106-014-56	Sequence 56, Appl
114	33.5	42.4	268	9	US-10-883-512-78	Sequence 78, Appl	187	33	41.8	621	11	US-11-073-457-56	Sequence 56, Appl
115	33.5	42.4	1354	9	US-10-204-639-34	Sequence 34, Appl	188	33	41.8	621	11	US-11-073-460-56	Sequence 56, Appl
116	33	41.8	41	11	US-10-057-813-4	Sequence 4, Appl	189	33	41.8	639	11	US-11-188-298-5375	Sequence 5375, Ap
117	33	41.8	54	11	US-11-188-298-5056	Sequence 5056, Ap	190	33	41.8	643	11	US-11-188-298-7431	Sequence 7431, Ap
118	33	41.8	79	9	US-10-770-726-58	Sequence 58, Appl	191	33	41.8	681	11	US-11-188-298-3515	Sequence 3515, Ap
119	33	41.8	158	11	US-11-087-099-11941	Sequence 11941, A	192	33	41.8	681	11	US-11-188-298-5448	Sequence 5448, Ap
120	33	41.8	159	11	US-11-087-099-6366	Sequence 6366, Ap	193	33	41.8	796	11	US-11-188-298-7476	Sequence 7476, Ap
121	33	41.8	159	11	US-11-045-004-1072	Sequence 1072, Ap	194	33	41.8	796	11	US-11-188-298-20219	Sequence 20219, A
122	33	41.8	196	9	US-10-793-626-2088	Sequence 2088, Ap	195	33	41.8	797	11	US-11-188-298-3104	Sequence 3104, Ap
123	33	41.8	196	11	US-11-135-603-10	Sequence 10, Appl	196	33	41.8	797	11	US-11-188-298-3389	Sequence 3389, Ap
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129	33	41.8	302	11	US-11-087-099-240	Sequence 240, App	202	33	41.8	797	11	US-11-188-298-17369	Sequence 17369, A
130	33	41.8	310	11	US-11-188-298-10711	Sequence 10711, A	203	33	41.8	869	11	US-11-072-512-2532	Sequence 2532, Ap
131	33	41.8	320	11	US-11-087-099-7319	Sequence 7319, Ap	204	33	41.8	1119	11	US-11-079-463-7747	Sequence 7747, Ap
132	33	41.8	320	11	US-11-087-099-7772	Sequence 7772, Ap	205	33	41.8	1552	11	US-11-108-459-2	Sequence 2, Appl
133	33	41.8	326	11	US-11-188-298-8219	Sequence 8219, Ap	206	33	41.8	1558	9	US-10-329-258-14	Sequence 14, Appl
134	33	41.8	336	11	US-11-087-099-3799	Sequence 3799, Ap	207	33	41.8	1597	11	US-11-210-471-13	Sequence 13, Appl
135	33	41.8	341	11	US-11-188-298-18488	Sequence 18488, A	208	33	41.8	1607	11	US-11-108-459-4	Sequence 4, Appl
136	33	41.8	374	11	US-11-096-568A-23460	Sequence 23460, A	209	33	41.8	2031	11	US-11-045-004-456	Sequence 456, App
137	33	41.8	376	11	US-11-096-568A-23459	Sequence 23459, A	210	33	41.8	2712	11	US-11-004-399-1736	Sequence 1736, Ap
138	33	41.8	399	11	US-11-188-298-19862	Sequence 19862, A	211	33	41.8	3482	11	US-11-087-099-2068	Sequence 2068, Ap
139	33	41.8	410	11	US-11-172-740-1749	Sequence 1749, Ap	212	33	41.8	3488	11	US-11-087-099-9005	Sequence 9005, Ap
140	33	41.8	412	11	US-11-096-568A-23458	Sequence 23458, Ap	213	32.5	41.1	73	11	US-11-087-099-3517	Sequence 37, Appl
141	33	41.8	426	11	US-11-087-099-6894	Sequence 6894, Ap	214	32.5	41.1	2326	11	US-11-126-313-37	Sequence 37, Appl
142	33	41.8	433	9	US-10-131-826A-6	Sequence 6, Appl	215	32	40.5	51	11	US-11-188-298-8145	Sequence 8145, Ap
143	33	41.8	433	9	US-10-973-115B-6	Sequence 6, Appl	216	32	40.5	52	11	US-11-188-298-3419	Sequence 3419, Ap
144	33	41.8	433	9	US-10-137-873A-6	Sequence 6, Appl	217	32	40.5	52	11	US-11-188-298-17612	Sequence 17612, A
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146	33	41.8	433	11	US-11-290-153-6	Sequence 6, Appl	219	32	40.5	86	11	US-11-188-298-11032	Sequence 11032, A
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148	33	41.8	457	11	US-11-098-686-11046	Sequence 11046, A	221	32	40.5	105	9	US-10-453-372-1178	Sequence 1178, Ap
149	33	41.8	467	11	US-11-087-099-2054	Sequence 2054, Ap	222	32	40.5	105	11	US-11-024-959-405	Sequence 405, App
150	33	41.8	468	11	US-11-087-099-3324	Sequence 3324, Ap	223	32	40.5	105	11	US-11-024-959-406	Sequence 406, App
151	33	41.8	468	11	US-11-087-099-3450	Sequence 3450, Ap	224	32	40.5	106	11	US-11-072-512-2828	Sequence 2828, Ap
152	33	41.8	468	11	US-11-087-099-9301	Sequence 9301, Ap	225	32	40.5	144	11	US-11-188-298-2169	Sequence 2169, Ap
153	33	41.8	468	11	US-11-087-099-10159	Sequence 10159, A	226	32	40.5	144	11	US-11-188-298-12190	Sequence 12190, A
154	33	41.8	468	11	US-11-087-099-12285	Sequence 12285, A	227	32	40.5	148	11	US-11-188-298-16214	Sequence 16214, A
155	33	41.8	470	11	US-11-087-099-7728	Sequence 7728, Ap	228	32	40.5	151	11	US-11-072-512-2866	Sequence 2866, Ap
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157	33	41.8	472	11	US-11-087-099-12291	Sequence 12291, A	230	32	40.5	169	11	US-11-188-298-816	Sequence 816, App
158	33	41.8	473	9	US-10-793-626-60	Sequence 60, Appl	231	32	40.5	180	9	US-10-986-405-247	Sequence 247, App
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160	33	41.8	475	11	US-11-087-099-1870	Sequence 1870, Ap	233	32	40.5	180	9	US-10-986-405-276	Sequence 276, App
161	33	41.8	475	11	US-11-087-099-7571	Sequence 7571, Ap	234	32	40.5	180	9	US-10-986-405-277	Sequence 277, App
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163	33	41.8	481	11	US-11-087-099-6066	Sequence 6066, Ap	236	32	40.5	180	9	US-10-467-358B-2	Sequence 2, Appl
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165	33	41.8	483	11	US-11-087-099-4117	Sequence 4117, Ap	238	32	40.5	185	11	US-11-087-099-3423	Sequence 3423, Ap
166	33	41.8	485	11	US-11-087-099-3604	Sequence 3604, Ap	239	32	40.5	196	11	US-11-188-298-10614	Sequence 10614, A
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242	32	40.5	212	11	US-11-096-568A-25821	Sequence 25821, A	315	32	40.5	759	9	US-10-467-657-2722	Sequence 2722, App
243	32	40.5	229	9	US-10-986-405-296	Sequence 296, App	316	32	40.5	762	11	US-11-116-939-13	Sequence 13, Appl
244	32	40.5	232	11	US-11-188-298-13750	Sequence 13750, A	317	32	40.5	763	11	US-11-188-298-15673	Sequence 15673, A
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246	32	40.5	253	9	US-10-509-691-2	Sequence 2, Appl	319	32	40.5	766	9	US-10-501-035-234	Sequence 234, App
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248	32	40.5	256	11	US-11-087-099-8333	Sequence 8333, App	321	32	40.5	770	11	US-11-087-099-7757	Sequence 7757, App
249	32	40.5	260	11	US-11-096-568A-21906	Sequence 21906, A	322	32	40.5	770	11	US-11-188-298-18193	Sequence 18193, A
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252	32	40.5	291	11	US-11-087-099-3559	Sequence 3559, App	325	32	40.5	900	11	US-11-045-004-890	Sequence 890, App
253	32	40.5	308	11	US-11-194-246-286	Sequence 286, App	326	32	40.5	901	9	US-10-793-626-342	Sequence 342, App
254	32	40.5	313	9	US-10-723-207-4	Sequence 4, Appl	327	32	40.5	908	11	US-11-077-619-90	Sequence 90, Appl
255	32	40.5	318	11	US-11-000-463-432	Sequence 432, App	328	32	40.5	909	11	US-11-077-619-90	Sequence 8, Appl
256	32	40.5	318	11	US-11-000-463-904	Sequence 904, App	329	32	40.5	914	9	US-10-506-454-1422	Sequence 1422, App
257	32	40.5	320	11	US-11-096-568A-1218	Sequence 1218, App	330	32	40.5	914	9	US-11-132-285-40	Sequence 40, Appl
258	32	40.5	321	9	US-10-501-841-21	Sequence 21, Appl	331	32	40.5	1001	11	US-10-131-826A-38	Sequence 38, Appl
259	32	40.5	322	11	US-11-079-463-7139	Sequence 7139, App	332	32	40.5	1013	9	US-10-973-1158-38	Sequence 38, Appl
260	32	40.5	331	11	US-11-096-568A-25820	Sequence 25820, A	333	32	40.5	1013	9	US-10-137-873A-38	Sequence 38, Appl
261	32	40.5	335	11	US-11-087-099-2180	Sequence 2180, App	334	32	40.5	1013	9	US-10-152-370-38	Sequence 38, Appl
262	32	40.5	336	9	US-10-793-626-2278	Sequence 2278, App	335	32	40.5	1013	11	US-11-290-153-38	Sequence 38, Appl
263	32	40.5	340	11	US-11-087-099-1699	Sequence 1699, App	336	32	40.5	1196	11	US-11-188-298-15911	Sequence 15911, A
264	32	40.5	347	11	US-11-052-554A-307	Sequence 307, App	337	32	40.5	1207	9	US-10-755-092-7	Sequence 7, Appl
265	32	40.5	373	11	US-11-087-099-2679	Sequence 2679, App	338	32	40.5	1244	9	US-10-453-372-1186	Sequence 1186, App
266	32	40.5	386	11	US-11-072-512-3211	Sequence 3211, App	339	32	40.5	1566	9	US-10-453-372-1190	Sequence 1190, App
267	32	40.5	389	11	US-11-108-528-68	Sequence 68, Appl	340	32	40.5	1566	9	US-10-453-372-1190	Sequence 21, Appl
268	32	40.5	389	11	US-11-108-528-70	Sequence 70, Appl	341	32	40.5	2026	8	US-10-505-928-831	Sequence 831, App
269	32	40.5	392	11	US-11-096-568A-1217	Sequence 1217, App	342	32	40.5	2053	9	US-10-453-372-1174	Sequence 1174, App
270	32	40.5	394	11	US-11-224-260-5	Sequence 5, Appl	343	32	40.5	2143	9	US-10-453-372-1188	Sequence 1188, App
271	32	40.5	406	9	US-10-131-826A-502	Sequence 502, App	344	32	40.5	140	11	US-11-045-004-96	Sequence 96, Appl
272	32	40.5	406	9	US-10-973-1158-502	Sequence 502, App	345	31.5	39.9	457	9	US-10-451-375-6	Sequence 6, Appl
273	32	40.5	406	9	US-10-137-873A-502	Sequence 502, App	346	31.5	39.9	632	11	US-11-188-298-4759	Sequence 4759, App
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277	32	40.5	433	11	US-11-096-568A-25854	Sequence 25854, A	350	31.5	39.9	1021	11	US-11-188-298-12108	Sequence 12108, A
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279	32	40.5	436	11	US-11-087-099-7235	Sequence 7235, App	352	31	39.2	12	11	US-11-254-419-128	Sequence 128, App
280	32	40.5	437	11	US-11-087-099-871	Sequence 871, App	353	31	39.2	15	11	US-11-041-893-218	Sequence 218, App
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282	32	40.5	439	11	US-11-087-099-3160	Sequence 3160, App	355	31	39.2	41	9	US-10-057-813-3	Sequence 6, Appl
283	32	40.5	439	11	US-11-087-099-3928	Sequence 3928, App	356	31	39.2	79	8	US-10-504-487-2	Sequence 2, Appl
284	32	40.5	439	11	US-11-087-099-6119	Sequence 6119, App	357	31	39.2	129	9	US-10-821-234-1014	Sequence 1014, App
285	32	40.5	439	11	US-11-087-099-8125	Sequence 8125, App	358	31	39.2	157	11	US-11-188-298-5383	Sequence 5383, App
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288	32	40.5	439	11	US-11-087-099-11138	Sequence 11138, A	361	31	39.2	170	9	US-10-467-657-8078	Sequence 8078, App
289	32	40.5	439	11	US-11-096-568A-1216	Sequence 1216, App	362	31	39.2	171	11	US-11-087-099-5332	Sequence 5332, App
290	32	40.5	440	11	US-11-087-099-5856	Sequence 5856, App	363	31	39.2	173	11	US-11-188-298-2582	Sequence 2582, App
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294	32	40.5	475	11	US-11-087-099-7087	Sequence 7087, App	367	31	39.2	209	9	US-10-501-035-328	Sequence 328, App
295	32	40.5	475	11	US-11-087-099-1356	Sequence 1356, App	368	31	39.2	218	11	US-11-072-512-3815	Sequence 3815, App
296	32	40.5	476	11	US-11-087-099-3599	Sequence 3599, App	369	31	39.2	220	11	US-11-096-568A-18867	Sequence 18867, A
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303	32	40.5	513	11	US-11-135-667-48	Sequence 48, Appl	376	31	39.2	237	11	US-11-087-099-5785	Sequence 5785, App
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389	31	39.2	267	11	US-11-096-568A-32695	Sequence 32695, A	462
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395	31	39.2	295	11	US-11-096-568A-21704	Sequence 21704, A	468
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413	31	39.2	350	11	US-11-087-099-7435	Sequence 7435, Ap	486
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416	31	39.2	350	11	US-11-106-270-25	Sequence 25, Appl	489
417	31	39.2	350	11	US-11-106-270-26	Sequence 26, Appl	490
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419	31	39.2	352	11	US-11-106-270-16	Sequence 16, Appl	492
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433	31	39.2	388	11	US-11-087-099-9369	Sequence 9369, Ap	506
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438	31	39.2	393	11	US-11-194-246-309	Sequence 309, App	511
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449	31	39.2	424	11	US-11-087-099-5962	Sequence 5962, Ap	522
450	31	39.2	424	11	US-11-079-463-9298	Sequence 9298, Ap	523
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31	39.2	765	11	US-11-087-099-8430	Sequence 8430, Ap
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31	39.2	767	9	US-10-467-657-6630	Sequence 6630, Ap
31	39.2	773	9	US-10-538-343-2	Sequence 2, Appl
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31	39.2	822	9	US-10-510-716-8	Sequence 8, Appl
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31	39.2	849	11	US-11-079-463-9844	Sequence 9844, Ap
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683	30	38.0	435	9	US-10-506-454-797	Sequence 797, App	756	527	11	US-11-096-568A-10607	Sequence 10607, A
684	30	38.0	439	11	US-11-188-298-1078	Sequence 1078, App	757	527	11	US-11-096-568A-25624	Sequence 25624, A
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698	30	38.0	445	11	US-11-172-740-469	Sequence 469, App	771	557	9	US-11-096-568A-25748	Sequence 25748, A
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865	29.5	37.3	2339	11	US-11-096-281-11	Sequence 11, Appl	938	189	11	US-11-087-099-8246	Sequence 6991, Ap
866	29.5	37.3	3568	9	US-10-453-372-194	Sequence 194, App	939	189	11	US-11-096-568A-6991	Sequence 18233, A
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878	29	36.7	79	11	US-11-188-298-1514	Sequence 1514, Ap	951	208	9	US-10-793-626-1084	Sequence 25, Appl
879	29	36.7	79	11	US-11-188-298-4089	Sequence 4089, Ap	952	210	11	US-11-038-284-25	Sequence 25, Appl
880	29	36.7	84	11	US-11-188-298-1716	Sequence 1716, Ap	953	210	11	US-11-045-004-1950	Sequence 1950, Ap
881	29	36.7	84	11	US-11-188-298-9464	Sequence 9464, Ap	954	221	11	US-11-188-298-18421	Sequence 18421, A
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883	29	36.7	84	11	US-11-188-298-13890	Sequence 13890, A	956	221	11	US-11-188-298-13669	Sequence 13669, A
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885	29	36.7	84	11	US-11-188-298-16232	Sequence 16232, A	958	229	11	US-11-098-686-10556	Sequence 10556, A
886	29	36.7	84	11	US-11-188-298-17430	Sequence 17430, A	959	231	11	US-11-182-408-67	Sequence 67, Appl
887	29	36.7	84	11	US-11-188-298-18022	Sequence 18022, A	960	231	11	US-11-182-408-67	Sequence 417, App
888	29	36.7	84	11	US-11-188-298-18577	Sequence 18577, A	961	233	7	US-09-978-360A-417	Sequence 4557, Ap
889	29	36.7	87	11	US-11-079-463-10265	Sequence 10265, A	962	236	11	US-11-096-568A-4557	Sequence 10738, A
890	29	36.7	88	11	US-11-024-959-285	Sequence 285, App	963	237	11	US-11-098-686-10728	Sequence 9682, Ap
891	29	36.7	91	11	US-11-096-568A-14056	Sequence 14056, A	964	243	11	US-11-188-298-20194	Sequence 20194, A
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897	29	36.7	111	9	US-10-793-626-2744	Sequence 2744, Ap	970	252	11	US-11-096-568A-28500	Sequence 28500, A

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973 29 36.7 254 11 US-11-037-099-526 Sequence 526, App
974 29 36.7 254 11 US-11-188-298-9422 Ap Sequence 9422, Ap
975 29 36.7 255 9 US-10-508-454-1577 Sequence 1677, Ap
976 29 36.7 255 11 US-11-087-099-517 Sequence 517, App
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989 29 36.7 286 11 US-11-137-465-48 Sequence 48, App
990 29 36.7 294 11 US-11-188-298-18075 Sequence 18075, A
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992 29 36.7 301 11 US-11-079-463-8334 Sequence 8334, Ap
993 29 36.7 305 11 US-11-036-568A-3615 Sequence 3615, Ap
994 29 36.7 305 11 US-11-036-568A-15953 Sequence 15953, A
995 29 36.7 305 11 US-11-182-480-28 Sequence 28, Appl
996 29 36.7 305 11 US-11-182-408-28 Sequence 28, Appl
997 29 36.7 306 11 US-11-036-568A-15557 Sequence 15557, A
998 29 36.7 306 11 US-11-188-298-16349 Sequence 16349, A
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ALIGNMENTS

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RESULT 1
US-11-041-893-216
; Sequence 216, Application US/11041893
; Publication No. US2006002941A1
; GENERAL INFORMATION:
; APPLICANT: Mahairas, Gregory G.
; TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
; FILE REFERENCE: 100123.401
; CURRENT FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/616,855
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/538,713
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 216
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mycobacteria tuberculosis
US-11-041-893-216
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Db 1 MTEQQWNPAGIEAAA 15
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RESULT 2
US-11-041-893-41
; Sequence 41, Application US/11041893
; Publication No. US2006002941A1
; GENERAL INFORMATION:
; APPLICANT: Mahairas, Gregory G.
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; TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
; TITLE OF INVENTION: ALTERING AGENTS AND METHODS OF USE
; FILE REFERENCE: 100123.401
; CURRENT APPLICATION NUMBER: US/11/041.893
; CURRENT FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/616,855
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/538,713
; PRIOR FILING DATE: 2004-01-23
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-11-041-893-41
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MTEQQWNPAGIEAAA 15
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US-11-041-893-237
; Sequence 237, Application US/11041893
; Publication No. US2006002941A1
; GENERAL INFORMATION:
; APPLICANT: Mahairas, Gregory G.
; TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
; FILE REFERENCE: 100123.401
; CURRENT APPLICATION NUMBER: US/11/041.893
; CURRENT FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/616,855
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/538,713
; PRIOR FILING DATE: 2004-01-23
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 237
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mycobacteria tuberculosis
US-11-041-893-237
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US-11-156-365-26
; Sequence 26, Application US/11156365
; Publication No. US20060040332A1
; GENERAL INFORMATION:
; APPLICANT: BECKMAN COULTER, INC.
; APPLICANT: MAEUREN, Markus
; TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS EPITOPES AND METHODS OF USE THEREOF
; FILE REFERENCE: BECK1160-2
; CURRENT APPLICATION NUMBER: US/11/156,365
; CURRENT FILING DATE: 2005-06-16
; PRIOR APPLICATION NUMBER: US 60/622,505
; PRIOR FILING DATE: 2004-10-27
; PRIOR APPLICATION NUMBER: US 60/580,559
; PRIOR FILING DATE: 2004-06-17
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; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
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; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-11-156-365-26

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DB 1 MTEQWNFAGIEAAA 15
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RESULT 5
US-11-041-893-214
; Sequence 214, Application US/11041893
; Publication No. US2006002941A1
; GENERAL INFORMATION:

; APPLICANT: Mahairas, Gregory G.
; TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
; TITLE OF INVENTION: ALTERING AGENTS AND METHODS OF USE
; FILE REFERENCE: 100123.401

; CURRENT APPLICATION NUMBER: US/11/041,893
; CURRENT FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/616,855
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/538,713
; PRIOR FILING DATE: 2004-01-23
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 214
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Mycobacteria tuberculosis
US-11-041-893-214

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Best Local Similarity 100.0%; Pred. No. 1.5e-06;
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DB 1 MTEQWNFAGIEAAA 15
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RESULT 6
US-10-909-957-4
; Sequence 4, Application US/10909957
; Publication No. US20060024332A1
; GENERAL INFORMATION:

; APPLICANT: Waters, Wade R
; APPLICANT: Palmer, Mitchell V
; APPLICANT: Minion, Frank C
; TITLE OF INVENTION: Recombinant ESAT-6:CFP-10 Fusion Protein Useful for
; TITLE OF INVENTION: Specific Diagnosis of Tuberculosis
; FILE REFERENCE: 0072.04 - Waters et al.
; CURRENT APPLICATION NUMBER: US/10/909,957
; CURRENT FILING DATE: 2004-08-02

; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Mycobacterium bovis
US-10-909-957-4

Query Match 100.0%; Score 79; DB 9; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
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DB 3 MTEQWNFAGIEAAA 17
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RESULT 7

US-10-909-957-2
; Sequence 2, Application US/10909957
; Publication No. US20060024332A1
; GENERAL INFORMATION:

; APPLICANT: Waters, Wade R
; APPLICANT: Palmer, Mitchell V
; APPLICANT: Minion, Frank C
; TITLE OF INVENTION: Recombinant ESAT-6:CFP-10 Fusion Protein Useful for
; TITLE OF INVENTION: Specific Diagnosis of Tuberculosis
; FILE REFERENCE: 0072.04 - Waters et al.
; CURRENT APPLICATION NUMBER: US/10/909,957
; CURRENT FILING DATE: 2004-08-02

; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Mycobacterium bovis
US-10-909-957-2

Query Match 100.0%; Score 79; DB 9; Length 249;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQWNFAGIEAAA 15
|||||

DB 34 MTEQWNFAGIEAAA 48
|||||

RESULT 8

US-11-041-893-42
; Sequence 42, Application US/11041893
; Publication No. US2006002941A1
; GENERAL INFORMATION:

; APPLICANT: Mahairas, Gregory G.
; TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
; TITLE OF INVENTION: ALTERING AGENTS AND METHODS OF USE
; FILE REFERENCE: 100123.401

; CURRENT APPLICATION NUMBER: US/11/041,893
; CURRENT FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/616,855
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/538,713
; PRIOR FILING DATE: 2004-01-23
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-11-041-893-42

Query Match 87.3%; Score 69; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EQQWNFAGIEAAA 15
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DB 1 EQQWNFAGIEAAA 13
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RESULT 9

US-11-041-893-48
; Sequence 48, Application US/11041893
; Publication No. US2006002941A1
; GENERAL INFORMATION:

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; APPLICANT: Mahairas, Gregory G.
; TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
; FILE REFERENCE: 100123.401
; CURRENT APPLICATION NUMBER: US/11/041,893
; PRIOR FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/616,855
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/538,713
; PRIOR FILING DATE: 2004-01-23
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-11-041-893-48

Query Match      87.3%; Score 69; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 EQMNFAGIEAAA 15
DB      1 EQMNFAGIEAAA 13

RESULT 10
US-11-041-893-217
; Sequence 217, Application US/11041893
; Publication No. US20060002941A1
; GENERAL INFORMATION:
; APPLICANT: Mahairas, Gregory G.
; TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
; FILE REFERENCE: 100123.401
; CURRENT APPLICATION NUMBER: US/11/041,893
; PRIOR FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/616,855
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/538,713
; PRIOR FILING DATE: 2004-01-23
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 217
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-11-041-893-217

Query Match      74.7%; Score 59; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00086;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 QMNFAGIEAAA 15
DB      1 QMNFAGIEAAA 11

RESULT 11
US-11-041-893-245
; Sequence 245, Application US/11041893
; Publication No. US20060002941A1
; GENERAL INFORMATION:
; APPLICANT: Mahairas, Gregory G.
; TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
; FILE REFERENCE: 100123.401
; CURRENT APPLICATION NUMBER: US/11/041,893
; PRIOR FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/616,855
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/538,713
```

```
; PRIOR FILING DATE: 2004-01-23
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 245
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-11-041-893-245

Query Match      73.4%; Score 58; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MTEQQWNPAG 10
DB      1 MTEQQWNPAG 10

RESULT 12
US-11-041-893-246
; Sequence 246, Application US/11041893
; Publication No. US20060002941A1
; GENERAL INFORMATION:
; APPLICANT: Mahairas, Gregory G.
; TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
; FILE REFERENCE: 100123.401
; CURRENT APPLICATION NUMBER: US/11/041,893
; CURRENT FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/616,855
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/538,713
; PRIOR FILING DATE: 2004-01-23
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 246
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-11-041-893-246

Query Match      68.4%; Score 54; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 WNFAGIEAAA 15
DB      1 WNFAGIEAAA 10

RESULT 13
US-11-041-893-43
; Sequence 43, Application US/11041893
; Publication No. US20060002941A1
; GENERAL INFORMATION:
; APPLICANT: Mahairas, Gregory G.
; TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
; FILE REFERENCE: 100123.401
; CURRENT APPLICATION NUMBER: US/11/041,893
; CURRENT FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/616,855
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/538,713
; PRIOR FILING DATE: 2004-01-23
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-11-041-893-43
```

Query Match 63.3%; Score 50; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WNPAGIEAA 14
DB 1 WNPAGIEAA 9

RESULT 14

US-10-454-437-416
; Sequence 416, Application US/10454437
; Publication No. US2005027115A1
; GENERAL INFORMATION:
; APPLICANT: Pompeius, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
; FILE REFERENCE: BGI-128CPCN
; CURRENT APPLICATION NUMBER: US/10/454,437
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931636.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932126.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932127.2
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932129.9
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: DE 19932226.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932920.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932922.2
; PRIOR FILING DATE: 1999-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 442
; SEQ ID NO 416
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum

US-10-454-437-416

Query Match 50.6%; Score 40; DB 9; Length 295;
Best Local Similarity 55.6%; Pred. No. 20;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQOWNFA 9
DB 50 LTEEWNYA 58

RESULT 15

US-11-074-176-340
; Sequence 340, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klaenhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAuliffe, Olivia
; APPLICANT: Perill, Andrea Ascarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore

; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 340
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Lactobacillus acidophilus
US-11-074-176-340

Query Match 50.6%; Score 40; DB 11; Length 694;
Best Local Similarity 85.7%; Pred. No. 46;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 QQWNPAG 10
DB 359 QQWNPAG 365

RESULT 16

US-11-074-176-150
; Sequence 150, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klaenhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAuliffe, Olivia
; APPLICANT: Perill, Andrea Ascarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 150
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Lactobacillus acidophilus
US-11-074-176-150

Query Match 50.6%; Score 40; DB 11; Length 697;
Best Local Similarity 85.7%; Pred. No. 46;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 QQWNPAG 10
DB 362 QQWNPAG 368

RESULT 17

US-11-137-465-39
; Sequence 39, Application US/11137465
; Publication No. US2005025558A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdock, Paul R.
; APPLICANT: Rizvi, Safia, K.
; APPLICANT: Smith, Randall, P.
; APPLICANT: Xiang, Zhaoying
; APPLICANT: Kabnick, Karen
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50018
; CURRENT APPLICATION NUMBER: US/11/137,465
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US/10/239,663
; PRIOR FILING DATE: 2002-09-24

; PRIOR APPLICATION NUMBER: PCT/US01/09226
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/192,158
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,668
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: 60/200,166
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-137-465-39

Query Match 49.4%; Score 39; DB 11; Length 243;
Best Local Similarity 75.0%; Pred. No. 25;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTEQWNF 8
|||: |||
Db 1 MTEKWNF 8

RESULT 18
US-11-096-568A-21702
; Sequence 21702, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 21702
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(382)
; OTHER INFORMATION: Ceres Seq. ID no. 12405761
US-11-096-568A-21702

Query Match 49.4%; Score 39; DB 11; Length 382;
Best Local Similarity 66.7%; Pred. No. 39;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTEQWNFA 9
|||: |||
Db 322 MEEKWNFS 330

RESULT 19
US-11-096-568A-6972
; Sequence 6972, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 6972
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:

; NAME/KEY: misc feature
; LOCATION: (1)..(324)
; OTHER INFORMATION: Ceres Seq. ID no. 15169353
US-11-096-568A-6972
Query Match 48.1%; Score 38; DB 11; Length 324;
Best Local Similarity 70.0%; Pred. No. 49;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 WNFAGIEAAA 15
||||: |||
Db 36 WNFAFVAAAA 45

RESULT 20
US-11-096-568A-6971
; Sequence 6971, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 6971
; LENGTH: 380
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(380)
; OTHER INFORMATION: Ceres Seq. ID no. 15169352
US-11-096-568A-6971

Query Match 48.1%; Score 38; DB 11; Length 380;
Best Local Similarity 70.0%; Pred. No. 57;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 WNFAGIEAAA 15
||||: |||
Db 92 WNFAFVAAAA 101

RESULT 21
US-11-096-568A-6970
; Sequence 6970, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 6970
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(396)
; OTHER INFORMATION: Ceres Seq. ID no. 15169351
US-11-096-568A-6970

Query Match 48.1%; Score 38; DB 11; Length 396;
Best Local Similarity 70.0%; Pred. No. 59;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 WNFAGIEAAA 15
||||: |||

RESULT 26
US-11-045-004-1043
; Sequence 1043, Application US/11045004
; Publication No. US20060078901A1


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Db      176 TSKAWNTAGLKCA 188

RESULT 29
US-11-087-099-1226
; Sequence 1226, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 1226
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Escherichia coli
US-11-087-099-1226

Query Match      46.8%; Score 37; DB 11; Length 326;
Best Local Similarity 50.0%; Pred. No. 73;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      6 WNFAGIEAAA 15
      |:| |:| |:|
Db      202 WFIGVESAS 211

RESULT 30
US-10-858-730-217
; Sequence 217, Application US/10858730
; Publication No. US2005025566A1
; GENERAL INFORMATION:
; APPLICANT: Bailey, Richard B.
; APPLICANT: Blomquist, Paul
; APPLICANT: Doten, Reed
; APPLICANT: Driggers, Edward M.
; APPLICANT: Madden, Kevin T.
; APPLICANT: O'Leary, Jessica
; APPLICANT: O'Toole, George
; APPLICANT: Trueheart, Joshua
; APPLICANT: Walbridge, Michael J.
; APPLICANT: Yorgey, Peter S.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
; TITLE OF INVENTION: PRODUCTION
; FILE REFERENCE: 14184-030001
; CURRENT APPLICATION NUMBER: US/10/858,730
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/475,000
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US 60/551,860
; PRIOR FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 217
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-858-730-217

Query Match      46.8%; Score 37; DB 9; Length 368;
Best Local Similarity 46.2%; Pred. No. 82;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      2 TEQOWNFAGIEAA 14
      |:| |:| |:|
Db      219 TSKAWNTAGLKCA 231

RESULT 31
US-11-087-099-10405
; Sequence 10405, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 10405
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Salmonella enterica subsp. enterica serovar Typhi
US-11-087-099-10405

Query Match      46.8%; Score 37; DB 11; Length 445;
Best Local Similarity 50.0%; Pred. No. 98;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      6 WNFAGIEAAA 15
      |:| |:| |:|
Db      202 WFIGVESAS 211

RESULT 32
US-11-087-099-12374
; Sequence 12374, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 12374
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Escherichia coli O157:H7 EDL933
US-11-087-099-12374

Query Match      46.8%; Score 37; DB 11; Length 445;
Best Local Similarity 50.0%; Pred. No. 98;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      6 WNFAGIEAAA 15
      |:| |:| |:|
Db      202 WFIGVESAS 211

RESULT 33
US-11-188-298-11360
; Sequence 11360, Application US/11188298
; Publication No. US2006007552A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 11360
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Escherichia coli O157:H7 EDL933
US-11-188-298-11360

Query Match      46.8%; Score 37; DB 11; Length 445;
Best Local Similarity 50.0%; Pred. No. 98;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      6 WNFAGIEAAA 15
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Db          202 WSFIGVESAS 211      |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~
RESULT 34
US-10-467-657-3160
; Sequence 3160, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 3160
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3160

Query Match           46.8%; Score 37; DB 9; Length 585;
Best Local Similarity 70.0%; Pred.No.1.3e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY       2 TEOWNPAGI 11
        |||||
Db        298 TEQLWAFEGI 307

RESULT 35
US-11-036-797-37
; Sequence 37, Application US/11036797
; Publication No. US20050276817A1
; GENERAL INFORMATION:
; APPLICANT: Hondalus, Mary
; TITLE OF INVENTION: Rhodococcus Equi Mutatnts and Vaccines Comprising Same
; FILE REFERENCE: 12687/2012
; CURRENT APPLICATION NUMBER: US/11/036,797
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: PCT/US2003/022101
; PRIOR FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: 60/396,195
; PRIOR FILING DATE: 2002-07-16
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Rhodococcus equi
US-11-036-797-37

Query Match           45.6%; Score 36; DB 11; Length 188;
Best Local Similarity 46.2%; Pred.No.64;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY       3 EQOWNFAGIEAAA 15
        :|||:|:|
Db        78 QOQWTVGVLASA 90

RESULT 36
US-11-096-468A-19957
; Sequence 19957, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:

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;
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(288)
; OTHER INFORMATION: Ceres Seq. ID no. 13579815
US-11-096-568A-31370

Query Match 45.6%; Score 36; DB 11; Length 288;
Best Local Similarity 54.5%; Pred. No. 96;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 MTEQOWNFAGIEA 12
Db 13 TEQOWSLADPE 23

RESULT 39
US-11-087-099-1968
; Sequence 1968, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:

; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 1968
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Rickettsia conorii
US-11-087-099-1968

Query Match 45.6%; Score 36; DB 11; Length 326;
Best Local Similarity 42.9%; Pred. No. 1.1e+02;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 MTEQOWNFAGIEAA 14
Db 257 VVEGWWFFAGVGAS 270

RESULT 40
US-11-087-099-8338
; Sequence 8338, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:

; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 8338
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Rickettsia prowazekii
US-11-087-099-8338

Query Match 45.6%; Score 36; DB 11; Length 326;
Best Local Similarity 42.9%; Pred. No. 1.1e+02;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 MTEQOWNFAGIEAA 14
Db 257 IVEGWWFFAGVGAS 270

RESULT 41
US-11-087-099-9948
; Sequence 9948, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.

;
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 9948
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Rickettsia sibirica
US-11-087-099-9948

Query Match 45.6%; Score 36; DB 11; Length 326;
Best Local Similarity 42.9%; Pred. No. 1.1e+02;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 MTEQOWNFAGIEAA 14
Db 257 VVEGWWFFAGVGAS 270

RESULT 42
US-11-087-099-1278
; Sequence 1278, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:

; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 1278
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Shewanella oneidensis MR-1
US-11-087-099-1278

Query Match 45.6%; Score 36; DB 11; Length 406;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 WNPAGIEA 13
Db 180 WSFLGIEA 187

RESULT 43
US-11-096-568A-11992
; Sequence 11992, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:

; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 11992
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(420)
; OTHER INFORMATION: Ceres Seq. ID no. 15220013
US-11-096-568A-11992

Query Match 45.6%; Score 36; DB 11; Length 420;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 QWNPAGIEA 13

Db 213 QWSFEGINA 221
||:|||||
NAME/KEY: misc feature
LOCATION: (1)_(448)
OTHER INFORMATION: Ceres Seq. ID no. 15220012
US-11-096-568A-11991

Query Match 45.6%; Score 36; DB 11; Length 448;
Best Local Similarity 56.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 QWNFAGIEA 13
||:|||||
Db 241 QWSFEGINA 249

RESULT 47
US-11-087-099-11164
; Sequence 11164, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 11164
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Pasteurella multocida
US-11-087-099-11164

Query Match 45.6%; Score 36; DB 11; Length 470;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 6 WNFAGIEAAA 15
||:|||||
Db 210 WNFAGIEAAA 219

RESULT 48
US-11-188-298-6764
; Sequence 6764, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 6764
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Lactobacillus sakei
US-11-188-298-6764

Query Match 45.6%; Score 36; DB 11; Length 475;
Best Local Similarity 46.7%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MTEQOWNFAGIEAAA 15
||:|||||
Db 207 MVMVMVWVFGIEGAS 221

RESULT 49
US-11-135-667-35
; Sequence 35, Application US/11135667
; Publication No. US20060034817A1
; GENERAL INFORMATION:

Tue May 9 09:08:48 2006

; APPLICANT: ROBERTS, JOSEPH
; APPLICANT: SETHURAMAN, NATARAJAN
; APPLICANT: MACALLISTER, THOMAS
; TITLE OF INVENTION: CLONING, OVEREXPRESSION AND THERAPEUTIC USE OF
; FILE REFERENCE: 078728/0106
; CURRENT APPLICATION NUMBER: US/11/135,667
; CURRENT FILING DATE: 2005-05-24
; PRIOR APPLICATION NUMBER: US/09/833,745
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/197,770
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 511
; TYPE: PRT
; ORGANISM: Rhizobium meliloti
US-11-135-667-35

Query Match 45.6%; Score 36; DB 11; Length 511;
Best Local Similarity 53.3%; Pred. No. 1.7e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MTEQOWNFAGIEAAA 15
||| : : |||||
Db 430 MTENLFSIIIGIEALA 444

RESULT 50

US-11-135-667-54
; Sequence 54, Application US/11/135667
; Publication No. US20060034817A1
; GENERAL INFORMATION:
; APPLICANT: ROBERTS, JOSEPH
; APPLICANT: SETHURAMAN, NATARAJAN
; APPLICANT: MACALLISTER, THOMAS
; TITLE OF INVENTION: CLONING, OVEREXPRESSION AND THERAPEUTIC USE OF
; FILE REFERENCE: 078728/0106
; CURRENT APPLICATION NUMBER: US/11/135,667
; CURRENT FILING DATE: 2005-05-24
; PRIOR APPLICATION NUMBER: US/09/833,745
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/197,770
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Rhizobium meliloti
US-11-135-667-54

Query Match 45.6%; Score 36; DB 11; Length 513;
Best Local Similarity 53.3%; Pred. No. 1.7e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MTEQOWNFAGIEAAA 15
||| : : |||||
Db 436 MTENLFSIIIGIEALA 450

Search completed: May 4, 2006, 15:39:36
Job time : 24 secs

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OM protein - protein search, using sw model

Run on: May 4, 2006, 15:33:46 ; Search time 124 Seconds
(without alignments)
50.544 Million cell updates/sec

Title: US-09-830-839-1

Perfect score: 79

Sequence: 1 MTEQQWNFAGIEAAA 15

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Total number of hits satisfying chosen parameters: 1867569

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications AA_Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	79	100.0	15	4	US-10-345-000-1
3	79	100.0	15	5	US-10-520-084-1
4	79	100.0	51	3	US-09-886-349A-33
5	79	100.0	51	4	US-10-193-002-99
6	79	100.0	51	4	US-10-084-843-104
7	79	100.0	51	4	US-10-098-732A-33
8	79	100.0	51	6	US-11-028-898-104
9	79	100.0	51	6	US-11-082-005-99
10	79	100.0	95	3	US-09-805-427A-1
11	79	100.0	95	3	US-09-872-505-1
12	79	100.0	95	4	US-10-689-921-18
13	79	100.0	95	4	US-10-332-512A-12
14	79	100.0	95	5	US-10-520-084-36
15	79	100.0	95	5	US-10-510-021-65
16	79	100.0	403	3	US-09-791-171-173
17	79	100.0	403	3	US-09-805-427A-4
18	79	100.0	403	3	US-09-804-980-173
19	79	100.0	403	3	US-09-872-505-4
20	79	100.0	403	4	US-10-620-246-173
21	79	100.0	404	3	US-09-791-171-172
22	79	100.0	404	3	US-09-805-427A-3
23	79	100.0	404	3	US-09-804-980-172
24	79	100.0	404	3	US-09-872-505-3
25	79	100.0	404	4	US-10-620-246-172
26	59	74.7	20	3	US-09-813-333-60
27	59	74.7	20	4	US-10-044-703-60

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30	54	68.4	15	4	US-10-345-000-2	Sequence 2, Appl
31	54	68.4	15	5	US-10-520-084-2	Sequence 2, Appl
32	48	60.8	893	4	US-10-282-122A-69721	Sequence 69721, A
33	43	54.4	13	3	US-09-813-333-59	Sequence 59, Appl
34	43	54.4	13	4	US-10-044-703-59	Sequence 59, Appl
35	43	54.4	13	4	US-10-239-103-59	Sequence 59, Appl
36	43	54.4	16	5	US-10-505-929-21	Sequence 21, Appl
37	43	54.4	20	3	US-09-813-333-61	Sequence 61, Appl
38	43	54.4	20	4	US-10-044-703-61	Sequence 61, Appl
39	43	54.4	20	4	US-10-239-103-61	Sequence 61, Appl
40	43	54.4	911	4	US-10-282-122A-51365	Sequence 51365, A
41	42	53.2	409	4	US-10-289-762-554	Sequence 554, App
42	42	53.2	539	4	US-10-369-493-16773	Sequence 16773, A
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44	41	51.9	176	4	US-10-339-278-3	Sequence 3, Appl
45	41	51.9	249	4	US-10-425-115-346310	Sequence 346310, A
46	41	51.9	445	4	US-10-282-122A-76999	Sequence 76999, A
47	40	50.6	74	4	US-10-425-115-193261	Sequence 193261, A
48	40	50.6	295	3	US-09-738-626-4782	Sequence 4782, App
49	40	50.6	295	5	US-10-721-922A-456	Sequence 456, App
50	40	50.6	295	5	US-10-721-922A-458	Sequence 458, App
51	40	50.6	317	5	US-10-450-763-33703	Sequence 33703, A
52	40	50.6	939	4	US-10-282-122A-68011	Sequence 68011, A
53	39	49.4	101	4	US-10-767-701-42935	Sequence 42935, A
54	39	49.4	108	4	US-10-425-115-272799	Sequence 272799, A
55	39	49.4	243	4	US-10-239-663-39	Sequence 39, Appl
56	39	49.4	284	4	US-10-425-115-241609	Sequence 241609, A
57	39	49.4	288	4	US-10-369-493-8029	Sequence 8029, App
58	39	49.4	496	4	US-10-425-114-62705	Sequence 62705, A
59	39	49.4	916	3	US-09-815-243-12006	Sequence 12006, A
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62	38	48.1	112	4	US-10-425-115-195668	Sequence 195668, A
63	38	48.1	118	6	US-11-040-661-41	Sequence 41, Appl
64	38	48.1	160	4	US-10-425-114-57412	Sequence 57412, A
65	38	48.1	230	4	US-10-424-599-259017	Sequence 259017, A
66	38	48.1	301	3	US-09-738-626-6880	Sequence 6880, App
67	38	48.1	301	5	US-10-721-922A-454	Sequence 454, App
68	38	48.1	314	3	US-09-769-734-44	Sequence 44, Appl
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71	38	48.1	400	4	US-10-369-493-21850	Sequence 21850, A
72	38	48.1	410	3	US-09-847-081B-4	Sequence 4, Appl
73	38	48.1	425	4	US-10-282-122A-73102	Sequence 73102, A
74	38	48.1	438	4	US-10-198-070-38	Sequence 38, Appl
75	38	48.1	438	4	US-10-788-792-171	Sequence 171, App
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77	38	48.1	443	4	US-10-282-122A-75789	Sequence 75789, A
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79	38	48.1	444	4	US-10-282-122A-59813	Sequence 59813, A
80	38	48.1	451	4	US-10-425-115-201653	Sequence 201653, A
81	38	48.1	451	4	US-10-425-115-305515	Sequence 305515, A
82	38	48.1	455	4	US-10-108-260A-4328	Sequence 4328, App
83	38	48.1	508	4	US-10-041-018-285	Sequence 285, App
84	38	48.1	552	5	US-10-732-923-19657	Sequence 19657, A
85	38	48.1	593	4	US-10-437-963-134922	Sequence 134922, A
86	38	48.1	593	4	US-10-424-599-195397	Sequence 195397, A
87	38	48.1	633	4	US-10-437-963-122654	Sequence 122654, A
88	38	48.1	650	4	US-10-741-849-7205	Sequence 7205, App
89	38	48.1	909	4	US-10-104-047-3636	Sequence 3636, App
90	38	48.1	909	4	US-10-437-963-110771	Sequence 110771, A
91	38	48.1	1997	4	US-10-408-765A-1013	Sequence 1013, App
92	38	48.1	2559	5	US-10-756-149-4730	Sequence 4730, App
93	37.5	47.5	131	4	US-10-425-115-279431	Sequence 279431, A
94	37.5	47.5	247	4	US-10-425-115-350271	Sequence 350271, A
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96	37	46.8	48	4	US-10-424-599-207400	Sequence 207400, A
97	37	46.8	50	5	US-10-450-763-44730	Sequence 44730, A
98	37	46.8	98	4	US-10-425-115-210092	Sequence 210092, A
99	37	46.8	105	4	US-10-425-115-229021	Sequence 229021, A
100	37	46.8	113	4	US-10-425-115-346419	Sequence 346419, A

101	37	46.8	129	4	US-10-425-115-217483	Sequence 217483, A	174	36	45.6	430	4	US-10-424-599-277805	Sequence 277805,
102	37	46.8	154	4	US-10-767-701-49975	Sequence 49975, A	175	36	45.6	459	3	US-09-949-029-60	Sequence 60, Appl
103	37	46.8	166	4	US-10-767-701-56955	Sequence 56955, A	176	36	45.6	459	3	US-11-097-143-14730	Sequence 14730, A
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105	37	46.8	227	4	US-10-425-115-321419	Sequence 321419, A	178	36	45.6	489	4	US-10-369-493-2512	Sequence 2512, Ap
106	37	46.8	229	3	US-09-815-242-12391	Sequence 12391, A	179	36	45.6	496	3	US-09-976-782-122	Sequence 122, App
107	37	46.8	229	4	US-10-282-122A-44014	Sequence 44014, A	180	36	45.6	496	3	US-09-976-782-123	Sequence 123, App
108	37	46.8	240	4	US-10-369-493-9868	Sequence 9868, Ap	181	36	45.6	496	3	US-10-437-963-121987	Sequence 121987,
109	37	46.8	295	4	US-10-225-066A-1062	Sequence 1062, Ap	182	36	45.6	496	3	US-09-933-745-35	Sequence 35, Appl
110	37	46.8	295	4	US-10-225-066A-1062	Sequence 1062, Ap	183	36	45.6	511	3	US-09-933-745-35	Sequence 35, Appl
111	37	46.8	295	4	US-10-374-780A-2788	Sequence 2788, Ap	184	36	45.6	511	3	US-09-933-745-35	Sequence 35, Appl
112	37	46.8	295	4	US-10-225-066A-1062	Sequence 1062, Ap	185	36	45.6	511	3	US-09-933-745-35	Sequence 35, Appl
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114	37	46.8	303	4	US-10-369-493-16148	Sequence 16148, A	187	36	45.6	565	4	US-10-425-115-250662	Sequence 250662,
115	37	46.8	304	4	US-10-369-493-15396	Sequence 15396, A	188	36	45.6	565	4	US-10-425-115-250662	Sequence 250662,
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117	37	46.8	312	5	US-10-200-545-71	Sequence 71, Appl	190	36	45.6	602	4	US-10-364-648-2	Sequence 2, Appli
118	37	46.8	312	6	US-11-097-143-2538	Sequence 2538, Ap	191	36	45.6	602	4	US-10-364-648-2	Sequence 2, Appli
119	37	46.8	325	3	US-09-738-626-6035	Sequence 6035, Ap	192	36	45.6	602	4	US-10-364-648-2	Sequence 2, Appli
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121	37	46.8	325	3	US-10-721-922A-220	Sequence 220, App	194	36	45.6	602	4	US-10-364-648-2	Sequence 2, Appli
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133	37	46.8	993	4	US-10-489-229-2	Sequence 2, Appli	206	36	45.6	612	5	US-10-364-648-2	Sequence 2, Appli
134	36.5	46.2	289	5	US-10-775-678-72	Sequence 72, Appl	207	36	45.6	612	5	US-10-364-648-2	Sequence 2, Appli
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136	36.5	46.2	847	5	US-10-775-678-72	Sequence 72, Appl	209	36	45.6	612	5	US-10-364-648-2	Sequence 2, Appli
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139	36	45.6	75	4	US-10-424-599-250734	Sequence 250734, A	212	36	45.6	612	5	US-10-364-648-2	Sequence 2, Appli
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690	35	44.3	301	4	US-10-141-701-176	Sequence 176, App	763	35	44.3	515	3	US-09-823-356-3	Sequence 3, Appl
691	35	44.3	301	4	US-10-141-754-176	Sequence 176, App	764	35	44.3	515	3	US-09-823-356-3	Sequence 3, Appl
692	35	44.3	301	4	US-10-141-760-176	Sequence 176, App	765	35	44.3	542	6	US-11-017-143-27324	Sequence 27324, A
693	35	44.3	301	4	US-10-142-425-176	Sequence 176, App	766	35	44.3	551	6	US-11-017-143-391-4	Sequence 4, Appl
694	35	44.3	301	4	US-10-142-430-176	Sequence 176, App	767	35	44.3	579	4	US-10-369-493-3250	Sequence 3250, App
695	35	44.3	301	4	US-10-143-113-176	Sequence 176, App	768	35	44.3	602	4	US-10-195-518-5	Sequence 5, Appl
696	35	44.3	301	4	US-10-146-730-176	Sequence 176, App	769	35	44.3	603	4	US-10-161-403-106	Sequence 106, App
697	35	44.3	301	4	US-10-146-792-176	Sequence 176, App	770	35	44.3	603	4	US-10-120-145-6	Sequence 6, Appl
698	35	44.3	301	4	US-10-156-843-176	Sequence 176, App	771	35	44.3	603	4	US-10-364-648-17	Sequence 17, Appl
699	35	44.3	301	4	US-10-156-843-176	Sequence 176, App	772	35	44.3	603	4	US-10-364-648-23	Sequence 23, Appl
700	35	44.3	301	4	US-10-152-405-176	Sequence 176, App	773	35	44.3	603	4	US-10-369-493-842	Sequence 842, App
701	35	44.3	301	4	US-10-147-528-176	Sequence 176, App	774	35	44.3	603	4	US-10-369-493-842	Sequence 17, Appl
702	35	44.3	301	4	US-10-147-528-176	Sequence 176, App	775	35	44.3	603	4	US-10-369-493-842	Sequence 22, Appl
703	35	44.3	301	4	US-10-128-692A-176	Sequence 176, App	776	35	44.3	604	3	US-11-006-076-106	Sequence 106, App
704	35	44.3	301	4	US-10-140-927-176	Sequence 176, App	777	35	44.3	604	4	US-09-893-525-37	Sequence 37, Appl
705	35	44.3	301	4	US-10-147-937-176	Sequence 176, App	778	35	44.3	607	4	US-10-763-380-37	Sequence 37, Appl
706	35	44.3	301	4	US-10-145-127-176	Sequence 176, App	779	35	44.3	610	4	US-10-369-493-15291	Sequence 15291, A
707	35	44.3	301	4	US-10-160-503-176	Sequence 176, App	780	35	44.3	610	5	US-10-138-195-2	Sequence 2, Appl
708	35	44.3	301	4	US-10-143-118-176	Sequence 176, App	781	35	44.3	618	4	US-10-723-860-2068	Sequence 2068, App
709	35	44.3	301	4	US-10-144-933-176	Sequence 176, App	782	35	44.3	618	4	US-10-356-088-28	Sequence 28, Appl
710	35	44.3	301	4	US-10-158-787-176	Sequence 176, App	783	35	44.3	621	4	US-10-799-326-28	Sequence 28, Appl
711	35	44.3	301	4	US-10-142-426-176	Sequence 176, App	784	35	44.3	621	4	US-10-369-493-15602	Sequence 15602, A
712	35	44.3	301	4	US-10-140-024-176	Sequence 176, App	785	35	44.3	634	6	US-10-369-493-15602	Sequence 30057, A
713	35	44.3	301	4	US-10-147-536-176	Sequence 176, App	786	35	44.3	639	6	US-11-097-143-30057	Sequence 40, Appl
714	35	44.3	301	4	US-10-152-372-176	Sequence 176, App	787	35	44.3	659	5	US-10-763-380-40	Sequence 40, Appl
715	35	44.3	301	4	US-10-125-795-176	Sequence 176, App	788	35	44.3	659	5	US-10-482-029-86	Sequence 86, Appl
716	35	44.3	301	4	US-10-145-825-176	Sequence 176, App	789	35	44.3	673	4	US-10-416-898-4	Sequence 4, Appl
717	35	44.3	301	4	US-10-145-819-176	Sequence 176, App	790	35	44.3	673	4	US-10-416-898-4	Sequence 1545, App
718	35	44.3	301	4	US-10-147-513-176	Sequence 176, App	791	35	44.3	711	4	US-10-338-411-23	Sequence 23, Appl
719	35	44.3	301	4	US-10-147-518-176	Sequence 176, App	792	35	44.3	711	4	US-10-338-411-23	Sequence 23, Appl
720	35	44.3	301	5	US-10-775-678-46	Sequence 46, Appl	793	35	44.3	730	4	US-10-369-493-599	Sequence 599, App
721	35	44.3	301	5	US-10-145-961-176	Sequence 176, App	794	35	44.3	736	4	US-11-097-143-16302	Sequence 16302, A
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723	35	44.3	301	5	US-10-147-531-176	Sequence 176, App	796	35	44.3	736	4	US-10-437-963-146503	Sequence 146503, A
724	35	44.3	301	5	US-10-931-886-176	Sequence 176, App	797	35	44.3	791	5	US-10-282-122A-48330	Sequence 48330, A
725	35	44.3	301	5	US-10-158-788-176	Sequence 176, App	798	35	44.3	832	4	US-10-282-122A-48330	Sequence 42, Appl
726	35	44.3	301	5	US-10-643-836-318	Sequence 318, App	799	35	44.3	832	4	US-10-437-963-146503	Sequence 33, Appl
727	35	44.3	301	5	US-10-955-952-176	Sequence 176, App	800	35	44.3	839	3	US-10-893-525-42	Sequence 398, App
728	35	44.3	301	5	US-10-472-533-578	Sequence 378, App	801	35	44.3	850	4	US-10-763-380-42	Sequence 12, Appl
729	35	44.3	301	5	US-10-974-440-5	Sequence 5, Appl	802	35	44.3	850	4	US-10-041-007-2	Sequence 2, Appl
730	35	44.3	301	5	US-09-894-018-105	Sequence 105, App	803	35	44.3	873	4	US-10-041-007-2	Sequence 33, Appl
731	35	44.3	308	3	US-09-894-018-107	Sequence 107, App	804	35	44.3	873	4	US-10-041-018-398	Sequence 398, App
732	35	44.3	308	3	US-10-775-678-48	Sequence 48, App	805	35	44.3	873	4	US-10-282-122A-63053	Sequence 63053, A
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736	35	44.3	328	4	US-10-425-114-72865	Sequence 72865, A	809	35	44.3	1082	6	US-10-369-493-22488	Sequence 223644, A
737	35	44.3	351	5	US-10-732-923-6390	Sequence 6390, App	810	35	44.3	1223	4	US-10-437-963-113781	Sequence 113781, A
738	35	44.3	351	5	US-10-024-828-9	Sequence 9, Appl	811	35	44.3	1379	4	US-10-437-963-113781	Sequence 22488, A
739	35	44.3	360	4	US-10-048-402-9	Sequence 9, Appl	812	34	43.0	33	4	US-10-425-115-238597	Sequence 238597, A
740	35	44.3	360	6	US-10-369-493-4046	Sequence 4046, App	813	34	43.0	44	4	US-10-425-115-238597	Sequence 157924, A
741	35	44.3	392	4	US-10-291-172-751	Sequence 751, App	814	34	43.0	51	4	US-10-424-599-157924	Sequence 148756, A
742	35	44.3	399	4	US-10-221-278-751	Sequence 751, App	815	34	43.0	54	4	US-09-864-088-364	Sequence 364, App
743	35	44.3	404	4	US-10-425-114-53828	Sequence 53828, A	816	34	43.0	55	3	US-10-424-599-281034	Sequence 281034, A
744	35	44.3	422	4	US-10-471-243-6	Sequence 6, Appl	817	34	43.0	68	4	US-10-424-599-159455	Sequence 159455, A
745	35	44.3	422	5	US-10-739-930-6551	Sequence 6551, App	818	34	43.0	73	4	US-10-424-599-159455	Sequence 166695, A
746	35	44.3	428	5	US-10-437-963-181993	Sequence 181993, A	819	34	43.0	79	4	US-10-425-115-204425	Sequence 204425, A
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755	35	44.3	472	4	US-10-504-582-142	Sequence 142, App	828	34	43.0	156	4	US-10-074-024-2357	Sequence 2357, App
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848	34	43.0	323	5	US-10-450-763-36859	Sequence 36859, A	921	34	43.0	620	4	US-10-282-122A-62670	Sequence 62670, A
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851	34	43.0	345	4	US-10-739-096-52	Sequence 52, Appl	924	34	43.0	639	4	US-10-282-122A-64611	Sequence 64611, A
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857	34	43.0	354	4	US-10-032-585-7733	Sequence 7733, Ap	929	34	43.0	811	4	US-10-425-114-71468	Sequence 71468, A
858	34	43.0	376	4	US-10-369-493-554	Sequence 554, App	930	34	43.0	813	4	US-10-282-122A-52335	Sequence 52335, A
859	34	43.0	378	5	US-10-732-923-18398	Sequence 18398, A	931	34	43.0	814	4	US-10-282-122A-46085	Sequence 46085, A
860	34	43.0	379	4	US-10-451-467A-300	Sequence 300, App	932	34	43.0	828	4	US-10-308-128-10	Sequence 10, Appl
861	34	43.0	380	4	US-10-369-493-2180	Sequence 2180, Ap	933	34	43.0	828	4	US-10-437-963-200157	Sequence 200157, A
862	34	43.0	387	4	US-10-408-692-2	Sequence 2, Appl	934	34	43.0	836	5	US-09-738-626-5805	Sequence 5805, Ap
863	34	43.0	387	4	US-10-741-387-136	Sequence 136, App	935	34	43.0	848	5	US-10-732-923-13574	Sequence 13574, A
864	34	43.0	398	6	US-11-097-143-19071	Sequence 19071, A	936	34	43.0	854	5	US-10-424-599-246646	Sequence 246646, A
865	34	43.0	400	4	US-10-437-963-128809	Sequence 128809, A	937	34	43.0	855	5	US-10-732-923-13575	Sequence 13575, A
866	34	43.0	409	4	US-10-788-792-129	Sequence 129, App	938	34	43.0	867	5	US-10-732-923-6789	Sequence 6789, Ap
867	34	43.0	410	5	US-10-732-923-7522	Sequence 7522, Ap	939	34	43.0	878	5	US-10-732-923-6973	Sequence 6973, Ap
868	34	43.0	410	5	US-10-732-923-7537	Sequence 7537, Ap	940	34	43.0	892	4	US-10-282-122A-45813	Sequence 45813, A
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872	34	43.0	433	3	US-10-807-856-18	Sequence 856, Ap	944	34	43.0	934	5	US-10-450-763-45257	Sequence 45257, A
873	34	43.0	438	4	US-10-425-114-47181	Sequence 47181, A	945	34	43.0	950	4	US-10-437-963-196072	Sequence 196072, A
874	34	43.0	440	4	US-10-328-714-3203	Sequence 3203, Ap	946	34	43.0	950	5	US-10-450-763-34699	Sequence 34699, A
875	34	43.0	444	4	US-10-369-493-16537	Sequence 16537, A	947	34	43.0	950	5	US-10-450-763-43058	Sequence 43058, A
876	34	43.0	466	4	US-10-282-122A-71914	Sequence 71914, A	948	34	43.0	991	6	US-11-097-143-1260	Sequence 1260, Ap
877	34	43.0	469	5	US-10-450-763-42854	Sequence 42854, A	949	34	43.0	1145	4	US-10-195-144-11	Sequence 11, Appl
878	34	43.0	474	4	US-10-282-122A-57928	Sequence 57928, A	950	34	43.0	1145	4	US-10-389-566-696	Sequence 696, App
879	34	43.0	474	4	US-10-282-122A-57680	Sequence 57680, A	951	34	43.0	1233	4	US-10-437-963-131235	Sequence 131235, A
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882	34	43.0	487	5	US-10-732-923-9845	Sequence 9845, Ap	954	34	43.0	1434	4	US-11-097-143-19734	Sequence 19734, A
883	34	43.0	487	5	US-09-976-782-121	Sequence 782, Ap	955	34	43.0	1520	6	US-10-156-761-14889	Sequence 14889, A
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885	34	43.0	488	4	US-10-126-962-2	Sequence 126, App	957	34	43.0	2012	5	US-10-450-763-32558	Sequence 32558, A
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887	34	43.0	491	4	US-10-781-014-366	Sequence 366, App	959	34	43.0	2500	5	US-10-369-493-5760	Sequence 5760, Ap
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892	34	43.0	515	4	US-10-424-599-246184	Sequence 246184, A	964	34	43.0	26926	5	US-10-656-873A-2	Sequence 2, Appl
893	34	43.0	525	5	US-10-450-763-36613	Sequence 36613, A	965	34	43.0	26926	5	US-10-756-149-4768	Sequence 4768, Ap
894	34	43.0	528	4	US-10-282-122A-50764	Sequence 50764, A	966	34	43.0	27118	5	US-10-805-684-110	Sequence 110, App
895	34	43.0	539	4	US-10-282-122A-59760	Sequence 59760, A	967	34	43.0	34350	5	US-10-745-237-394	Sequence 394, App
896	34	43.0	540	4	US-10-437-963-115233	Sequence 115233, A	968	34	43.0	36946	5	US-10-840-512-155	Sequence 155, App
897	34	43.0	549	4	US-10-282-122A-73087	Sequence 73087, A	969	34	43.0	79	4	US-10-424-599-270637	Sequence 270637, A
898	34	43.0	552	6	US-11-097-143-41271	Sequence 41271, A	970	33.5	42.4	141	5	US-10-629-953-18	Sequence 18, Appl
899	34	43.0	552	6	US-11-097-143-41277	Sequence 41277, A	971	33.5	42.4	163	4	US-10-424-599-147198	Sequence 147198, A
900	34	43.0	555	3	US-09-927-827-47	Sequence 47, Appl	972	33.5	42.4	196	4	US-10-425-114-38036	Sequence 38036, A
901	34	43.0	556	3	US-10-732-923-18348	Sequence 18348, A	973	33.5	42.4	215	3	US-09-738-626-5940	Sequence 5940, Ap
902	34	43.0	556	5	US-10-732-923-18394	Sequence 18394, A	974	33.5	42.4	268	4	US-10-421-138A-120	Sequence 120, App
903	34	43.0	556	5	US-10-732-923-18396	Sequence 18396, A	975	33.5	42.4	268	4	US-10-421-138A-124	Sequence 124, App
							976	33.5	42.4				

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977 33.5 42.4 268 5 US-10-230-415-120
978 33.5 42.4 268 5 US-10-230-415-124
979 33.5 42.4 268 5 US-10-732-223-18710
980 33.5 42.4 349 4 US-10-424-599-255516
981 33.5 42.4 628 4 US-10-425-114-42203
982 33.5 42.4 630 6 US-11-097-143-22287
983 33.5 42.4 835 4 US-10-425-115-261342
984 33.5 42.4 1105 6 US-10-840-060-180
985 33.5 42.4 1105 6 US-11-097-143-18384
986 33.5 42.4 1169 5 US-10-840-060-178
987 33.5 42.4 1169 5 US-10-840-060-178
988 33.5 42.4 1169 6 US-11-097-143-18372
989 33.5 42.4 1169 6 US-11-097-143-18393
990 33.5 42.4 1431 4 US-10-437-963-104186
991 33 41.8 25 4 US-10-416-249-546
992 33 41.8 37 3 US-09-864-761-39026
993 33 41.8 48 4 US-10-424-599-267913
994 33 41.8 49 4 US-10-437-963-180477
995 33 41.8 53 4 US-10-424-599-241954
996 33 41.8 56 4 US-10-425-115-369123
997 33 41.8 62 4 US-10-424-599-154787
998 33 41.8 64 4 US-10-424-599-253385
999 33 41.8 66 4 US-10-424-599-159902
1000 33 41.8 69 4 US-10-424-599-148089
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Sequence 120, App
Sequence 124, App
Sequence 18710, A
Sequence 255516, A
Sequence 22287, A
Sequence 261342, A
Sequence 180, App
Sequence 18384, A
Sequence 178, App
Sequence 18372, A
Sequence 18393, A
Sequence 104186, A
Sequence 546, App
Sequence 39026, A
Sequence 267913, A
Sequence 180477, A
Sequence 241954, A
Sequence 369123, A
Sequence 154787, A
Sequence 253385, A
Sequence 159902, A
Sequence 148089, A
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US-10-345-000-1
; Sequence 1, Application US/10345000
; Publication No. US20040018177A1
; GENERAL INFORMATION:
; APPLICANT: OXON PHARMACEUTICALS LIMITED
; TITLE OF INVENTION: VACCINATION METHOD
; FILE REFERENCE: 550-409
; CURRENT APPLICATION NUMBER: US/10/345,000
; CURRENT FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-345-000-1
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Query Match 100.0%; Score 79; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTEQWNNFAGIEAAA 15
DB 1 MTEQWNNFAGIEAAA 15
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ALIGNMENTS

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RESULT 1
; Sequence 79, Application US/10079167
; Publication No. US20030138454A1
; GENERAL INFORMATION:
; APPLICANT: Hill, Adrian V.S.
; APPLICANT: McShane, Helen
; APPLICANT: Gilbert, Sarah C.
; APPLICANT: Rees, William
; APPLICANT: Schneider, Joerg
; TITLE OF INVENTION: Vaccination Method
; FILE REFERENCE: 2907 1000-001
; CURRENT APPLICATION NUMBER: US/10/079,167
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/454,204
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: PCT/GB98/01681
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: GB 97 11957.2
; PRIOR FILING DATE: 1997-06-09
; PRIOR APPLICATION NUMBER: PCT/GB01/04116
; PRIOR FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: GB 00 23203.3
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 79
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: T cell epitope in ESAT6
US-10-079-167-79
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Query Match 100.0%; Score 79; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MTEQWNNFAGIEAAA 15
DB 1 MTEQWNNFAGIEAAA 15
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RESULT 2

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RESULT 3
US-10-520-084-1
; Sequence 1, Application US/10520084
; Publication No. US20050208594A1
; GENERAL INFORMATION:
; APPLICANT: Ajit Lalvani
; APPLICANT: Katie Ewer
; APPLICANT: Isis Innovation Limited
; TITLE OF INVENTION: DIAGNOSTICS METHOD
; FILE REFERENCE: 3772-22 / N.86130A JCI
; CURRENT APPLICATION NUMBER: US/10/520,084
; CURRENT FILING DATE: 2005-01-05
; PRIOR APPLICATION NUMBER: PCT/GB03/002936
; PRIOR FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: GB 0215710.5
; PRIOR FILING DATE: 2002-07-05
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-520-084-1
```

```
Query Match 100.0%; Score 79; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 MTEQWNNFAGIEAAA 15
DB 1 MTEQWNNFAGIEAAA 15
```

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RESULT 4
US-09-886-349A-33
; Sequence 33, Application US/09886349A
; Publication No. US20040086523A1
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir
; APPLICANT: Reed, Steven
; APPLICANT: Alderson, Mark
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
; FILE REFERENCE: 014058-009070US
; CURRENT APPLICATION NUMBER: US/09/886,349A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 09/597,796
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;; PRIOR FILING DATE: 2000-06-20
;; PRIOR APPLICATION NUMBER: US 60/265,737
;; PRIOR FILING DATE: 2001-02-01
;; NUMBER OF SEQ ID NOS: 50
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 33
;; TYPE: PRT
;; LENGTH: 51
;; ORGANISM: Mycobacterium tuberculosis
;; FEATURE:
;; OTHER INFORMATION: ESAT-6
US-09-886-349A-33

Query Match 100.0%; Score 79; DB 3; Length 51;
Best Local Similarity 100.0%; Pred. No. 4.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTEQOWNFAGIEAAA 15
Db 1 MTEQOWNFAGIEAAA 15

RESULT 5
US-10-193-002-99
; Sequence 99, Application US/10193002
; Publication No. US20030135026A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; Skeiky, Yasir A.W.
; Dillon, Davin C.
; Campos-Neto, Antonia
; Houghton, Raymond
; Vedwick, Thomas S.
; Twardzik, Daniel R.
; Lodes, Michael J.
; Hendrickson, Ronald C.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
; TUBERCULOSIS

NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-Jul-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9

TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 99:
US-10-193-002-99

Query Match 100.0%; Score 79; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 4.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTEQOWNFAGIEAAA 15
Db 1 MTEQOWNFAGIEAAA 15

RESULT 6
US-10-084-843-104
; Sequence 104, Application US/10084843
; Publication No. US20030143243A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; Skeiky, Yasir A.W.
; Dillon, Davin C.
; Campos-Neto, Antonio
; Houghton, Raymond
; Vedwick, Thomas S.
; Twardzik, Daniel R.
; Lodes, Michael J.
; Hendrickson, Ronald C.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
; AND DIAGNOSIS OF TUBERCULOSIS

NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9

TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 104:
US-10-084-843-104

Query Match 100.0%; Score 79; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 4.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTEQOWNFAGIEAAA 15
Db 1 MTEQOWNFAGIEAAA 15

RESULT 7
US-10-098-732A-33

;
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 99:
; US-11-082-005-99

Query Match 100.0%; Score 79; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 4.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQOWNFAGIEAAA 15
| | | | | | | | | | | | | | | | | |
Db 1 MTEQOWNFAGIEAAA 15

RESULT 10
US-09-805-427A-1

; Sequence 1, Application US/09805427A
; Patent No. US20020176867A1

; GENERAL INFORMATION:

; APPLICANT: Statens Serum Institut
; TITLE OF INVENTION: Hybrids of M. tuberculosis Antigens

; FILE REFERENCE: 670001-2002.5

; CURRENT APPLICATION NUMBER: US/09/805,427A

; CURRENT FILING DATE: 2001-03-13

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1

; LENGTH: 95

; TYPE: PRT

; ORGANISM: Mycobacterium tuberculosis

; US-09-805-427A-1

Query Match 100.0%; Score 79; DB 3; Length 95;
Best Local Similarity 100.0%; Pred. No. 8.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQOWNFAGIEAAA 15
| | | | | | | | | | | | | | | | | |
Db 1 MTEQOWNFAGIEAAA 15

RESULT 11
US-09-872-505-1

; Sequence 1, Application US/09872505
; Publication No. US20040013685A1

; GENERAL INFORMATION:

; APPLICANT: Statens Serum Institut

; TITLE OF INVENTION: Nucleic Acid Fragments Derived From M. Tuberculosis

; FILE REFERENCE: 670001-2002.6

; CURRENT APPLICATION NUMBER: US/09/872,505

; CURRENT FILING DATE: 2001-06-01

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1

; LENGTH: 95

; TYPE: PRT

; ORGANISM: Mycobacterium tuberculosis

; US-09-872-505-1

Query Match 100.0%; Score 79; DB 3; Length 95;
Best Local Similarity 100.0%; Pred. No. 8.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQOWNFAGIEAAA 15
| | | | | | | | | | | | | | | | | |
Db 1 MTEQOWNFAGIEAAA 15

RESULT 12
US-10-689-921-18

; Sequence 18, Application US/10689921
; Publication No. US20040146948A1

; GENERAL INFORMATION:

; APPLICANT: Britton, Warwick

; APPLICANT: Demangel, Caroline
; TITLE OF INVENTION: Compositions and Methods for Targeting
; TITLE OF INVENTION: Antigen-Presenting Cells With Antibody Single-Chain Variable
; TITLE OF INVENTION: Region Fragments
; FILE REFERENCE: 13311.1002U
; CURRENT APPLICATION NUMBER: US/10/689,921
; CURRENT FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
; US-10-689-921-18

Query Match 100.0%; Score 79; DB 4; Length 95;
Best Local Similarity 100.0%; Pred. No. 8.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQOWNFAGIEAAA 15
| | | | | | | | | | | | | | | | | |
Db 1 MTEQOWNFAGIEAAA 15

RESULT 13

US-10-332-512A-12

; Sequence 12, Application US/10332512A

; Publication No. US20040180056A1

; GENERAL INFORMATION:

; APPLICANT: ORME, Ian M.

; APPLICANT: BELISLE, John T.

; TITLE OF INVENTION: MID-LIFE VACCINE AND METHODS FOR BOOSTING ANTI-MYCOBACTERIAL IMM

; FILE REFERENCE: 38861-186292

; CURRENT APPLICATION NUMBER: US/10/332,512A

; CURRENT FILING DATE: 2003-01-10

; PRIOR APPLICATION NUMBER: PCT/US01/21717

; PRIOR FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: US 60/217,646

; PRIOR FILING DATE: 2000-07-10

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 12

; LENGTH: 95

; TYPE: PRT

; ORGANISM: Mycobacterium tuberculosis

; US-10-332-512A-12

Query Match 100.0%; Score 79; DB 4; Length 95;
Best Local Similarity 100.0%; Pred. No. 8.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQOWNFAGIEAAA 15
| | | | | | | | | | | | | | | | | |
Db 1 MTEQOWNFAGIEAAA 15

RESULT 14

US-10-520-084-36

; Sequence 36, Application US/10520084

; Publication No. US20050208594A1

; GENERAL INFORMATION:

; APPLICANT: Ajit LALVANI

; APPLICANT: Katie EWER

; APPLICANT: ISIS INNOVATION LIMITED

; TITLE OF INVENTION: DIAGNOSTICS METHOD

; FILE REFERENCE: 3772-22 / N.86130A JCT

; CURRENT APPLICATION NUMBER: US/10/520,084

; CURRENT FILING DATE: 2005-01-05

; PRIOR APPLICATION NUMBER: PCT/GB03/002936

; PRIOR FILING DATE: 2003-07-07

; PRIOR APPLICATION NUMBER: GB 0215710.5

; PRIOR FILING DATE: 2002-07-05

; NUMBER OF SEQ ID NOS: 37

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-520-084-36

Query Match      100.0%; Score 79; DB 5; Length 95;
Best Local Similarity 100.0%; Pred. No. 8.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MTEQQWNFAGIEAAA 15
        |||||
DB      1 MTEQQWNFAGIEAAA 15

RESULT 15
US-10-510-021-65
; Sequence 65, Application US/10510021
; Publication No. US20050220811A1
; GENERAL INFORMATION:
; APPLICANT: Cole, Stewart
; APPLICANT: Pym, Alexander S
; APPLICANT: Brosch, Roland
; APPLICANT: Brodin, Priscille
; APPLICANT: Majlessi, Ialeh
; APPLICANT: Demangel, Claudine
; APPLICANT: Leclerc, Claude
; TITLE OF INVENTION: Identification of virulence associated regions RD1 and
; TITLE OF INVENTION: RD5 leading to improve vaccine of M. bovis BCG and M.
; FILE OF INVENTION: microti
; FILE REFERENCE: D20217
; CURRENT APPLICATION NUMBER: US/10/510,021
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: PCT/IB03/01789
; PRIOR FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: EP 02/290864
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: Rv3875-Esat6 - 6 kDa early secretory antigenic
; OTHER INFORMATION: target Esat6 (Esat-6)
US-10-510-021-65

Query Match      100.0%; Score 79; DB 5; Length 95;
Best Local Similarity 100.0%; Pred. No. 8.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MTEQQWNFAGIEAAA 15
        |||||
DB      1 MTEQQWNFAGIEAAA 15

RESULT 16
US-09-791-171-173
; Sequence 173, Application US/09791171
; Patent No. US20020094336A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSEN, Peter
; APPLICANT: NIELSEN, Rikke
; APPLICANT: OETTINGER, Thomas
; APPLICANT: RASMUSSEN, Peter Birk
; APPLICANT: ROSENKRANDS, Ida
; APPLICANT: WELDINGH, Karin
; APPLICANT: FLORIO, Walter
; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
; TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
; FILE REFERENCE: 670001-2002.1
US-09-791-171-173
; Sequence 65, Application US/10510021
; Publication No. US20050220811A1
; GENERAL INFORMATION:
; APPLICANT: Cole, Stewart
; APPLICANT: Pym, Alexander S
; APPLICANT: Brosch, Roland
; APPLICANT: Brodin, Priscille
; APPLICANT: Majlessi, Ialeh
; APPLICANT: Demangel, Claudine
; APPLICANT: Leclerc, Claude
; TITLE OF INVENTION: Identification of virulence associated regions RD1 and
; TITLE OF INVENTION: RD5 leading to improve vaccine of M. bovis BCG and M.
; FILE OF INVENTION: microti
; FILE REFERENCE: D20217
; CURRENT APPLICATION NUMBER: US/10/510,021
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: PCT/IB03/01789
; PRIOR FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: EP 02/290864
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: Rv3875-Esat6 - 6 kDa early secretory antigenic
; OTHER INFORMATION: target Esat6 (Esat-6)
US-10-510-021-65

Query Match      100.0%; Score 79; DB 5; Length 95;
Best Local Similarity 100.0%; Pred. No. 8.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MTEQQWNFAGIEAAA 15
        |||||
DB      1 MTEQQWNFAGIEAAA 15

RESULT 17
US-09-805-427A-4
; Sequence 4, Application US/09805427A
; Patent No. US20020176867A1
; GENERAL INFORMATION:
; APPLICANT: Statens Serum Institut
; TITLE OF INVENTION: Hybrids of M. tuberculosis Antigens
; FILE REFERENCE: 670001-2002.5
; CURRENT APPLICATION NUMBER: US/09/805,427A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant Fusion protein ESAT-6-Ag85B
US-09-805-427A-4

Query Match      100.0%; Score 79; DB 3; Length 403;
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MTEQQWNFAGIEAAA 15
        |||||
DB      22 MTEQQWNFAGIEAAA 36

RESULT 18
US-09-804-980-173
; Sequence 173, Application US/09804980
; Publication No. US20030147897A1
; GENERAL INFORMATION:
; APPLICANT: Statens Serum Institut
; APPLICANT: Anderson, Peter
; TITLE OF INVENTION: M. Tuberculosis Antigens
; FILE REFERENCE: 670001-2002.4
; CURRENT APPLICATION NUMBER: US/09/804,980
; CURRENT FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 257
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 173
; LENGTH: 403
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;
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-804-980-173

Query Match 100.0%; Score 79; DB 3; Length 403;
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQQWNFAGIEAAA 15
|||||
Db 22 MTEQQWNFAGIEAAA 36

RESULT 19

US-09-872-505-4
; Sequence 4, Application US/09872505
; Publication No. US20040013685A1
; GENERAL INFORMATION:
; APPLICANT: Statens Serum Institut
; TITLE OF INVENTION: Nucleic Acid Fragments Derived From M. Tuberculosis
; FILE REFERENCE: 670001-2002.6
; CURRENT APPLICATION NUMBER: US/09/872,505
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant Fusion protein ESAT-6-Ag85B
US-09-872-505-4

Query Match 100.0%; Score 79; DB 3; Length 403;
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQQWNFAGIEAAA 15
|||||
Db 22 MTEQQWNFAGIEAAA 36

RESULT 20

US-10-620-246-173
; Sequence 173, Application US/10620246
; Publication No. US20040115211A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSEN, Peter
; APPLICANT: NIELSEN, Rikke
; APPLICANT: OETTINGER, Thomas
; APPLICANT: RASMUSSEN, Peter Birk
; APPLICANT: ROSENKRANDS, Ida
; APPLICANT: WELDLINGH, Karin
; APPLICANT: FLORIO, Walter
; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
; FILE REFERENCE: 670001-2002.1A
; CURRENT APPLICATION NUMBER: US/10/620,246
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 09/050,739
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 0376/97
; PRIOR FILING DATE: 1997-04-02
; PRIOR APPLICATION NUMBER: 1277/97
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/044,624
; PRIOR FILING DATE: 1997-04-18
; PRIOR APPLICATION NUMBER: 60/070,488
; PRIOR FILING DATE: 1998-01-05
; PRIOR APPLICATION NUMBER: 10/138,473
; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 09/791,171
; PRIOR FILING DATE: 2001-02-20

;
; PRIOR APPLICATION NUMBER: 09/415,884
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: 60/116,673
; PRIOR FILING DATE: 1999-01-21
; PRIOR APPLICATION NUMBER: 1281/98
; PRIOR FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 173
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-620-246-173

Query Match 100.0%; Score 79; DB 4; Length 403;
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQQWNFAGIEAAA 15
|||||
Db 22 MTEQQWNFAGIEAAA 36

RESULT 21

US-09-791-171-172
; Sequence 172, Application US/09791171
; Patent No. US20020094336A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSEN, Peter
; APPLICANT: NIELSEN, Rikke
; APPLICANT: OETTINGER, Thomas
; APPLICANT: RASMUSSEN, Peter Birk
; APPLICANT: ROSENKRANDS, Ida
; APPLICANT: WELDLINGH, Karin
; APPLICANT: FLORIO, Walter
; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
; FILE REFERENCE: 670001-2002.1
; CURRENT APPLICATION NUMBER: US/09/791,171
; CURRENT FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 09/050,739
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 0376/97
; PRIOR FILING DATE: 1997-04-02
; PRIOR APPLICATION NUMBER: 1277/97
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/044,624
; PRIOR FILING DATE: 1997-04-18
; PRIOR APPLICATION NUMBER: 60/070,488
; PRIOR FILING DATE: 1998-01-05
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 172
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-791-171-172

Query Match 100.0%; Score 79; DB 3; Length 404;
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQQWNFAGIEAAA 15
|||||
Db 310 MTEQQWNFAGIEAAA 324

RESULT 22

US-09-805-427A-3
; Sequence 3, Application US/09805427A
; Patent No. US20020176867A1
; GENERAL INFORMATION:
; APPLICANT: Statens Serum Institut

; TITLE OF INVENTION: Hybrids of M. tuberculosis Antigens

; FILE REFERENCE: 670001-2002.5

; CURRENT FILING DATE: 2001-03-13

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: Patentin version 3.0

; SEQ ID NO 3

; LENGTH: 404

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Recombinant Fusion protein Ag85B-ESAT-6

US-09-805-427A-3

Query Match 100.0%; Score 79; DB 3; Length 404;

Best Local Similarity 100.0%; Pred. No. 3.8e-05; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQOWNFAGIEAAA 15

|||||

Db 310 MTEQOWNFAGIEAAA 324

RESULT 23

US-09-804-980-172

; Sequence 172, Application US/09804980

; Publication No. US2003014789/A1

; GENERAL INFORMATION:

; APPLICANT: Statens Serum Institut

; APPLICANT: Anderson, Peter

; TITLE OF INVENTION: M. Tuberculosis Antigens

; FILE REFERENCE: 670001-2002.4

; CURRENT APPLICATION NUMBER: US/09/804,980

; CURRENT FILING DATE: 2001-03-12

; NUMBER OF SEQ ID NOS: 257

; SOFTWARE: Patentin version 3.0

; SEQ ID NO 172

; LENGTH: 404

; TYPE: PRT

; ORGANISM: Mycobacterium tuberculosis

US-09-804-980-172

Query Match 100.0%; Score 79; DB 3; Length 404;

Best Local Similarity 100.0%; Pred. No. 3.8e-05; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQOWNFAGIEAAA 15

|||||

Db 310 MTEQOWNFAGIEAAA 324

RESULT 24

US-09-872-505-3

; Sequence 3, Application US/09872505

; Publication No. US20040013685A1

; GENERAL INFORMATION:

; APPLICANT: Statens Serum Institut

; TITLE OF INVENTION: Nucleic Acid Fragments Derived From M. Tuberculosis

; FILE REFERENCE: 670001-2002.6

; CURRENT APPLICATION NUMBER: US/09/872,505

; CURRENT FILING DATE: 2001-06-01

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: Patentin version 3.0

; SEQ ID NO 3

; LENGTH: 404

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Recombinant Fusion protein Ag85B-ESAT-6

US-09-872-505-3

Query Match 100.0%; Score 79; DB 3; Length 404;

Best Local Similarity 100.0%; Pred. No. 3.8e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQOWNFAGIEAAA 15

|||||

Db 310 MTEQOWNFAGIEAAA 324

RESULT 25

US-10-620-246-172

; Sequence 172, Application US/10620246

; Publication No. US2004011521A1

; GENERAL INFORMATION:

; APPLICANT: ANDERSEN, Peter

; APPLICANT: OETLINGER, Thomas

; APPLICANT: RASMUSSEN, Peter Birk

; APPLICANT: ROSENKRANDS, Ida

; APPLICANT: WELDINGH, Karin

; APPLICANT: FLORIO, Walter

; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS

; FILE REFERENCE: 670001-2002.1A

; CURRENT APPLICATION NUMBER: US/10/620,246

; CURRENT FILING DATE: 2003-07-15

; PRIOR APPLICATION NUMBER: 09/050,739

; PRIOR FILING DATE: 1998-03-30

; PRIOR APPLICATION NUMBER: 0376/97

; PRIOR FILING DATE: 1997-04-02

; PRIOR APPLICATION NUMBER: 1277/97

; PRIOR FILING DATE: 1997-11-10

; PRIOR APPLICATION NUMBER: 60/044,624

; PRIOR FILING DATE: 1997-04-18

; PRIOR APPLICATION NUMBER: 60/070,488

; PRIOR FILING DATE: 1998-01-05

; PRIOR APPLICATION NUMBER: 10/138,473

; PRIOR FILING DATE: 2002-05-02

; PRIOR APPLICATION NUMBER: 09/791,171

; PRIOR FILING DATE: 2001-02-20

; PRIOR APPLICATION NUMBER: 09/415,884

; PRIOR FILING DATE: 1999-10-08

; PRIOR APPLICATION NUMBER: 60/116,673

; PRIOR FILING DATE: 1999-01-21

; PRIOR APPLICATION NUMBER: 1281/98

; PRIOR FILING DATE: 1998-10-08

; NUMBER OF SEQ ID NOS: 173

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 172

; LENGTH: 404

; TYPE: PRT

; ORGANISM: Mycobacterium tuberculosis

US-10-620-246-172

Query Match 100.0%; Score 79; DB 4; Length 404;

Best Local Similarity 100.0%; Pred. No. 3.8e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQOWNFAGIEAAA 15

|||||

Db 310 MTEQOWNFAGIEAAA 324

RESULT 26

US-09-813-333-60

; Sequence 60, Application US/09813333

; Patent No. US20020119160A1

; GENERAL INFORMATION:

; APPLICANT: DeGroot, Anne S

; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters

; FILE REFERENCE: 17999-004 US

; CURRENT APPLICATION NUMBER: US/09/813,333

; CURRENT FILING DATE: 2001-03-20

; PRIOR APPLICATION NUMBER: 60/190,834

; PRIOR FILING DATE: 2000-03-20

```
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-813-333-60

Query Match      74.7%; Score 59; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 QWNFAGIEAAA 15
Db      1 QWNFAGIEAAA 11
|||||

RESULT 27
US-10-044-703-60
; Sequence 60, Application US/10044703
; Publication No. US20020192233A1
; GENERAL INFORMATION:
; APPLICANT: Degroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004 US
; CURRENT APPLICATION NUMBER: US/10/044,703
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-044-703-60

Query Match      74.7%; Score 59; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 QWNFAGIEAAA 15
Db      1 QWNFAGIEAAA 11
|||||

RESULT 28
US-10-239-103-60
; Sequence 60, Application US/10239103
; Publication No. US20040057961A1
; GENERAL INFORMATION:
; APPLICANT: Brown University Research Foundation
; APPLICANT: Degroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004-061
; CURRENT APPLICATION NUMBER: US/10/239,103
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 09/813,333
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-239-103-60

Query Match      74.7%; Score 59; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      5 QWNFAGIEAAA 15
Db      1 QWNFAGIEAAA 11
|||||

RESULT 29
US-10-079-167-80
; Sequence 80, Application US/10079167
; Publication No. US20030138454A1
; GENERAL INFORMATION:
; APPLICANT: Hill, Adrian V.S.
; APPLICANT: McShane, Helen
; APPLICANT: Gilbert, Sarah C.
; APPLICANT: Reece, William
; APPLICANT: Schneider, Joerg
; TITLE OF INVENTION: Vaccination Method
; FILE REFERENCE: 2907.1000-001
; CURRENT APPLICATION NUMBER: US/10/079,167
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/454,204
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: PCT/GB98/01681
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: GB 97 11957.2
; PRIOR FILING DATE: 1997-06-09
; PRIOR APPLICATION NUMBER: PCT/GB01/04116
; PRIOR FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: GB 00 23203.3
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: T cell epitope in ESAT6
US-10-079-167-80

Query Match      68.4%; Score 54; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 WNFAGIEAAA 15
Db      1 WNFAGIEAAA 10
|||||

RESULT 30
US-10-345-000-2
; Sequence 2, Application US/10345000
; Publication No. US20040018177A1
; GENERAL INFORMATION:
; APPLICANT: OXON PHARMACEUTICALS LIMITED
; TITLE OF INVENTION: VACCINATION METHOD
; FILE REFERENCE: 550-409
; CURRENT APPLICATION NUMBER: US/10/345,000
; CURRENT FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-345-000-2

Query Match      68.4%; Score 54; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 WNFAGIEAAA 15
Db      1 WNFAGIEAAA 10
|||||
```

```
RESULT 31
US-10-520-084-2
; Sequence 2, Application US/10520084
; Publication No. US20050208594A1
; GENERAL INFORMATION:
; APPLICANT: AJIT LALVANI
; APPLICANT: KATIE EWER
; APPLICANT: ISIS INNOVATION LIMITED
; TITLE OF INVENTION: DIAGNOSTICS METHOD
; FILE REFERENCE: 3772-22 / N.86130A JCI
; CURRENT APPLICATION NUMBER: US/10/520,084
; CURRENT FILING DATE: 2005-01-05
; PRIOR APPLICATION NUMBER: PCT/GB03/002936
; PRIOR FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: GB 0215710.5
; PRIOR FILING DATE: 2002-07-05
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-520-084-2
Query Match 68.4%; Score 54; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.027; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WNPAGIEAAA 15
| | | | | | | |
DB 1 WNPAGIEAAA 10

RESULT 32
US-10-282-122A-69721
; Sequence 69721, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Frawick, John
; APPLICANT: Carl, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636

US-10-520-084-2
Query Match 68.4%; Score 54; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.027; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WNPAGIEAAA 15
| | | | | | | |
DB 1 WNPAGIEAAA 10

RESULT 33
US-10-282-122A-69721
; Sequence 69721, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Frawick, John
; APPLICANT: Carl, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636

US-10-520-084-2
Query Match 68.4%; Score 54; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.027; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WNPAGIEAAA 15
| | | | | | | |
DB 1 WNPAGIEAAA 10

RESULT 34
US-10-044-703-59
; Sequence 59, Application US/10044703
; Publication No. US20020192233A1
; GENERAL INFORMATION:
; APPLICANT: Degroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004 US/10/044,703
; CURRENT APPLICATION NUMBER: US/10/044,703
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-044-703-59
Query Match 54.4%; Score 43; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NPAIEAAA 15
| | | | | | | |
DB 1 NPAIEAAA 9

RESULT 35
US-10-044-703-59
; Sequence 59, Application US/10044703
; Publication No. US20020192233A1
; GENERAL INFORMATION:
; APPLICANT: Degroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004 US/10/044,703
; CURRENT APPLICATION NUMBER: US/10/044,703
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-044-703-59
Query Match 54.4%; Score 43; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 7 NFAGIEAAA 15
| | | | | | | |
Db 1 NFAGIEAAA 9

RESULT 35
US-10-239-103-59
; Sequence 59, Application US/10239103
; Publication No. US20040057961A1
; GENERAL INFORMATION:
; APPLICANT: Brown University Research Foundation
; APPLICANT: DeGroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004-061
; CURRENT APPLICATION NUMBER: US/10/239,103
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 09/813,333
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-239-103-59

Query Match 54.4%; Score 43; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NFAGIEAAA 15
| | | | | | | |
Db 1 NFAGIEAAA 9

RESULT 36
US-10-505-929-21
; Sequence 21, Application US/10505929
; Publication No. US20050221381A1
; GENERAL INFORMATION:
; APPLICANT: KLADE, CHRISTOF
; APPLICANT: SCHALICH, JULIANE
; APPLICANT: VITVITSKA, ORESTA
; APPLICANT: AICHSINGER, GERALD
; APPLICANT: OTAVA, ALEXANDER
; APPLICANT: MATTNER, FRANK
; TITLE OF INVENTION: METHOD FOR ISOLATING LIGANDS
; FILE REFERENCE: SONN.055US
; CURRENT APPLICATION NUMBER: US/10/505,929
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: PCT/EP03/02005
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: A 316/2002
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: A 1376/2002
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 584
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Cytomegalovirus
US-10-505-929-21

Query Match 54.4%; Score 43; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NFAGIEAAA 15
| | | | | | | |

Db 1 NFAGIEAAA 9

RESULT 37
US-09-813-333-61
; Sequence 61, Application US/09813333
; Patent No. US20020119160A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004 US
; CURRENT APPLICATION NUMBER: US/09/813,333
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-813-333-61

Query Match 54.4%; Score 43; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NFAGIEAAA 15
| | | | | | | |
Db 1 NFAGIEAAA 9

RESULT 38
US-10-044-703-61
; Sequence 61, Application US/10044703
; Publication No. US20020192233A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004 US
; CURRENT APPLICATION NUMBER: US/10/044,703
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-044-703-61

Query Match 54.4%; Score 43; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NFAGIEAAA 15
| | | | | | | |
Db 1 NFAGIEAAA 9

RESULT 39
US-10-239-103-61
; Sequence 61, Application US/10239103
; Publication No. US20040057961A1
; GENERAL INFORMATION:
; APPLICANT: Brown University Research Foundation
; APPLICANT: DeGroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004-061
; CURRENT APPLICATION NUMBER: US/10/239,103
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 09/813,333

; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-239-103-61

Query Match 54.4%; Score 43; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NFAGIEAAA 15
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DB 1 NFAGIEAAA 9

RESULT 40
US-10-282-122A-51365
; Sequence 51365, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Maione, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Orlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51365
; LENGTH: 911
; TYPE: PRT
; ORGANISM: Bordetella pertussis
US-10-282-122A-51365

Query Match 54.4%; Score 43; DB 4; Length 911;
Best Local Similarity 58.3%; Pred. No. 1.4e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 EQOWNFAGIEAA 14
||| : |||
DB 705 EQOWDVAGLEKA 716

RESULT 41
US-10-289-762-554
; Sequence 554, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffois, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 554
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-554

Query Match 53.2%; Score 42; DB 4; Length 409;
Best Local Similarity 77.8%; Pred. No. 94;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 WNFAGIEAA 14
||| : |||||
DB 345 WNVLGIEAA 353

RESULT 42
US-10-369-493-16773
; Sequence 16773, Application US/10369493
; Publication No. US20030235675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 16773
; LENGTH: 539
; TYPE: PRT
; ORGANISM: Caulobacter crescentus
US-10-369-493-16773

Query Match 53.2%; Score 42; DB 4; Length 539;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTEQOWNFAGIEAA 14
||| : |||
DB 48 LSKQAWDEAGLEAA 61

RESULT 43
US-10-425-115-185330
; Sequence 185330, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 185330
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Zea mays
; NAME/KEY: unsure
; LOCATION: (1)-(117)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_100609C.1.pep
US-10-425-115-185330

Query Match 51.9%; Score 41; DB 4; Length 117;
Best Local Similarity 50.0%; Pred. No. 39;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 TEOQWNPAGIEAAA 15
| | | | | | | | | | | | | | | |
Db 51 TPQHWRFAGVRCNA 64

RESULT 44
US-10-339-278-3
; Sequence 3, Application US/10339278
; Publication No. US20030124676A1
; GENERAL INFORMATION:
; APPLICANT: Quax, Wilhelmus J.
; APPLICANT: Caldwell, Robert M.
; TITLE OF INVENTION: Increasing Production of Proteins in Gram-Positive
; TITLE OF INVENTION: Microorganisms
; FILE REFERENCE: GC383-US
; CURRENT APPLICATION NUMBER: US/10/339,278
; CURRENT FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: PCT/US98/14704
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: EP 97305288.9
; PRIOR FILING DATE: 1997-07-15
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-339-278-3

Query Match 51.9%; Score 41; DB 4; Length 176;
Best Local Similarity 60.0%; Pred. No. 59;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 EQQWNPAGIE 12
| | | | | | | | | | | | | | | |
Db 132 ERQWDFLGLE 141

RESULT 45
US-10-425-115-346310
; Sequence 346310, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 346310
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Zea mays
; NAME/KEY: unsure
; LOCATION: (1)-(249)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_789C.1.pep
US-10-425-115-346310

Query Match 51.9%; Score 41; DB 4; Length 249;
Best Local Similarity 46.2%; Pred. No. 85;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MTEQWNPAGIEA 13
| | | | | | | | | | | | | | | |
Db 32 LQESRWNFIGISS 44

RESULT 46
US-10-282-122A-76999
; Sequence 76999, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,948
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 76999
; LENGTH: 445
; TYPE: PRT

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; ORGANISM: Vibrio cholerae
US-10-282-122A-76999

Query Match      51.8%; Score 41; DB 4; Length 445;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      6 WNFAGIEAAA 15
DB      199 WSFVGVESAA 208

RESULT 47
US-10-425-115-193261
; Sequence 193261, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 193261
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_107839C.1.pep
US-10-425-115-193261

Query Match      50.6%; Score 40; DB 4; Length 74;
Best Local Similarity 45.5%; Pred. No. 36;
Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY      2 TEQOWNFAGIE 12
DB      54 TDRKNWFSQAQ 64

RESULT 48
US-09-738-626-4782
; Sequence 4782, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKOYO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: Patent in ver. 3.0
; SEQ ID NO 4782
; LENGTH: 295

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; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4782

Query Match      50.6%; Score 40; DB 3; Length 295;
Best Local Similarity 55.6%; Pred. No. 1.5e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 MTEQQWNFA 9
DB      50 LTEEWNFA 58

RESULT 49
US-10-721-922A-456
; Sequence 456, Application US/10721922A
; Publication No. US20050191732A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberkauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; INVOLVED IN HOMEOSTASIS AND ADAPTATION
; FILE REFERENCE: BGI-132CPCN
; CURRENT APPLICATION NUMBER: US/10/721,922A
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: 09/602777
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 09/603124
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143694
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: US 60/151778
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932124.8
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932126.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932127.2
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932133.7
; PRIOR FILING DATE: 1999-07-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 480
; SEQ ID NO 456
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-721-922A-456

Query Match      50.6%; Score 40; DB 5; Length 295;
Best Local Similarity 55.6%; Pred. No. 1.5e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 MTEQQWNFA 9
DB      50 LTEEWNFA 58

RESULT 50
US-10-721-922A-458
; Sequence 458, Application US/10721922A
; Publication No. US20050191732A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig

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Tue May 9 09:08:48 2006

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; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
; FILE REFERENCE: BGI-132CPCN
; CURRENT APPLICATION NUMBER: US/10/721,922A
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: 09/6027777
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 09/603124
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143694
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: US 60/151778
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932124.8
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932126.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932127.2
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932133.7
; PRIOR FILING DATE: 1999-07-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 480
; SEQ ID NO 458
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-721-922A-458

Query Match      50.6%; Score 40; DB 5; Length 295;
Best Local Similarity 55.6%; Pred. No. 1.5e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MTEQQWNPA 9
Db      50 LTEEWNYA 58
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Search completed: May 4, 2006, 15:39:08
Job time : 141 secs

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OM protein - protein search, using sw model

Run on: May 4, 2006, 15:18:01 ; Search time 33 Seconds
(without alignments)
37.580 Million cell updates/sec

Title: US-09-830-839-1

Perfect score: 79

Sequence: 1 MTEQQWNFAGIEAAA 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/iaa/5 COMB.pep.*
- 2: /cgn2_6/prodata/1/iaa/6 COMB.pep.*
- 3: /cgn2_6/prodata/1/iaa/H COMB.pep.*
- 4: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep.*
- 5: /cgn2_6/prodata/1/iaa/RE COMB.pep.*
- 6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	79	100.0	51	2	US-08-818-111-99
3	79	100.0	51	2	US-09-056-556-104
4	79	100.0	51	2	US-09-072-596-99
5	79	100.0	51	2	US-09-072-967-104
6	79	100.0	51	2	US-10-193-002-99
7	79	100.0	51	2	US-10-084-843-104
8	79	100.0	95	1	US-08-465-640-2
9	79	100.0	403	2	US-09-050-739-173
10	79	100.0	404	2	US-09-050-739-172
11	52	65.8	10	2	US-09-001-984C-77
12	52	65.8	10	2	US-09-396-347F-77
13	42	53.2	409	2	US-09-198-452A-554
14	42	53.2	413	1	US-08-579-667-4
15	42	53.2	413	2	US-09-438-185A-515
16	42	53.2	578	2	US-09-949-016-9799
17	41	51.9	176	2	US-09-462-842-3
18	41	51.9	176	2	US-09-393-171-3
19	40	50.6	295	2	US-09-602-777A-416
20	39	49.4	538	2	US-09-252-991A-18026
21	39	49.4	928	2	US-09-352-991A-24200
22	38	48.1	118	2	US-09-830-807-41
23	38	48.1	155	2	US-08-585-808-3
24	38	48.1	155	2	US-08-505-860C-3
25	38	48.1	349	2	US-09-489-039A-13578
26	38	48.1	410	1	US-08-579-667-2
27	38	48.1	410	1	US-08-579-667-6

28	38	48.1	410	1	US-08-579-667-8	Sequence 8, Appli
29	38	48.1	650	2	US-10-104-047-3636	Sequence 3636, Ap
30	38	48.1	795	2	US-09-252-991A-30635	Sequence 30635, A
31	38	48.1	2293	2	US-09-368-590-2	Sequence 2, Appli
32	38	48.1	2600	2	US-09-949-016-7309	Sequence 7309, Ap
33	37	46.8	331	2	US-09-489-039A-9639	Sequence 9639, Ap
34	37	46.8	435	2	US-09-252-991A-23220	Sequence 23220, A
35	37	46.8	493	2	US-09-540-236-2120	Sequence 2120, Ap
36	37	46.8	668	2	US-09-538-092-599	Sequence 599, App
37	37	46.8	820	2	US-09-134-000C-6437	Sequence 6437, Ap
38	36.5	46.2	934	1	US-08-215-805A-80	Sequence 80, Appli
39	36	45.6	88	2	US-09-270-767-33601	Sequence 33601, A
40	36	45.6	88	2	US-09-270-767-48818	Sequence 48818, A
41	36	45.6	149	2	US-09-634-238-265	Sequence 265, App
42	36	45.6	149	2	US-09-489-039A-8963	Sequence 8963, Ap
43	36	45.6	221	2	US-09-904-615-155	Sequence 155, App
44	36	45.6	221	2	US-10-054-988-155	Sequence 155, App
45	36	45.6	282	2	US-09-724-623-113	Sequence 113, App
46	36	45.6	376	2	US-09-270-957-4	Sequence 4, Appli
47	36	45.6	376	2	US-09-270-957-19	Sequence 19, Appli
48	36	45.6	470	2	US-09-902-540-9896	Sequence 9896, Ap
49	36	45.6	511	2	US-09-833-745-35	Sequence 35, Appli
50	36	45.6	513	2	US-09-833-745-54	Sequence 54, Appli
51	36	45.6	602	2	US-09-149-727-2	Sequence 2, Appli
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53	36	45.6	602	2	US-09-270-957-8	Sequence 8, Appli
54	36	45.6	602	2	US-09-270-957-15	Sequence 15, Appli
55	36	45.6	607	2	US-09-149-727-8	Sequence 8, Appli
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57	36	45.6	608	2	US-08-637-670-36	Sequence 36, Appli
58	36	45.6	615	2	US-09-270-957-28	Sequence 28, Appli
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60	36	45.6	702	2	US-09-107-532A-5645	Sequence 5645, Ap
61	36	45.6	2123	2	US-09-949-016-7517	Sequence 7517, Ap
62	36	45.6	3070	2	US-09-961-403-7	Sequence 7, Appli
63	36	45.6	3084	2	US-09-562-702A-12	Sequence 12, Appli
64	36	45.6	3088	2	US-09-562-702A-8	Sequence 8, Appli
65	36	45.6	3089	2	US-09-562-702A-4	Sequence 4, Appli
66	36	45.6	3106	2	US-09-562-702A-10	Sequence 10, Appli
67	36	45.6	3110	2	US-09-562-702A-2	Sequence 2, Appli
68	36	45.6	3110	2	US-09-562-702A-6	Sequence 6, Appli
69	36	45.6	3110	2	US-09-561-709B-7	Sequence 7, Appli
70	36	45.6	3110	2	US-09-917-254-86	Sequence 86, Appli
71	36	45.6	3110	2	US-09-949-016-5937	Sequence 5937, Ap
72	36	45.6	3111	1	US-08-460-309-4	Sequence 4, Appli
73	36	45.6	3111	1	US-08-125-077-4	Sequence 4, Appli
74	35.5	44.9	593	1	US-08-202-389-12	Sequence 12, Appli
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76	35.5	44.9	593	1	US-08-448-250-5	Sequence 5, Appli
77	35.5	44.9	593	2	US-09-282-257-5	Sequence 5, Appli
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83	35	44.3	205	2	US-09-252-991A-23460	Sequence 23460, A
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85	35	44.3	265	2	US-09-902-540-13026	Sequence 13026, A
86	35	44.3	360	2	US-09-509-902A-9	Sequence 9, Appli
87	35	44.3	360	2	US-10-024-828-9	Sequence 9, Appli
88	35	44.3	360	2	US-09-909-474D-11	Sequence 11, Appli
89	35	44.3	384	2	US-09-270-767-45349	Sequence 45349, A
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91	35	44.3	410	2	US-09-252-991A-31174	Sequence 31174, A
92	35	44.3	415	2	US-09-328-352-4649	Sequence 4649, Ap
93	35	44.3	448	2	US-09-543-681A-7245	Sequence 7245, Ap
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95	35	44.3	478	2	US-09-134-000C-5543	Sequence 5543, Ap
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102	35	44.3	602	1	US-09-151-957-5	Sequence 5, Appli	175	34	43.0	981	2	US-09-902-540-9848	Sequence 9848, Ap
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110	35	44.3	832	2	US-08-630-820-7	Sequence 7, Appli	183	33	41.8	102	1	US-09-205-658-258	Sequence 258, App
111	35	44.3	832	2	US-09-273-453-7	Sequence 7, Appli	184	33	41.8	110	2	US-09-949-016-9743	Sequence 9743, Ap
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116	35	44.3	1010	1	US-09-118-276-12	Sequence 12, Appli	189	33	41.8	173	2	US-09-852-991A-27731	Sequence 27731, A
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122	34.5	43.7	561	1	US-08-167-035-37	Sequence 37, Appl	195	33	41.8	202	2	US-09-949-016-10231	Sequence 10231, A
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124	34	43.0	67	1	US-08-208-887A-37	Sequence 37, Appl	197	33	41.8	245	2	US-08-989-140C-12	Sequence 12, Appl
125	34	43.0	67	1	US-08-538-005-37	Sequence 57, Appl	198	33	41.8	245	2	US-09-543-681A-5597	Sequence 42449, A
126	34	43.0	67	1	US-09-280-538-57	Sequence 57, Appl	199	33	41.8	274	2	US-09-270-767-42449	Sequence 8219, Ap
127	34	43.0	118	2	US-09-270-767-57365	Sequence 57365, A	200	33	41.8	278	2	US-09-328-352-8219	Sequence 331, App
128	34	43.0	118	2	US-09-270-767-52582	Sequence 52582, A	201	33	41.8	302	2	US-08-311-731A-331	Sequence 692, App
129	34	43.0	147	2	US-09-488-270A-2	Sequence 22, Appl	202	33	41.8	326	2	US-09-830-230A-692	Sequence 58, Appl
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132	34	43.0	189	2	US-09-270-767-47558	Sequence 47558, A	205	33	41.8	359	2	US-09-489-039A-13753	Sequence 13753, A
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134	34	43.0	201	2	US-09-335-411-6	Sequence 6, Appli	207	33	41.8	376	2	US-09-491-577-60	Sequence 60, Appl
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136	34	43.0	314	2	US-09-252-991A-27617	Sequence 27617, A	209	33	41.8	408	2	US-09-902-540-15301	Sequence 15301, A
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139	34	43.0	353	2	US-09-252-991A-17672	Sequence 17672, A	212	33	41.8	435	2	US-09-138-452A-216	Sequence 216, App
140	34	43.0	367	2	US-09-248-796A-15401	Sequence 2, Appli	213	33	41.8	448	2	US-09-328-352-5694	Sequence 5694, Ap
141	34	43.0	387	2	US-09-563-269-2	Sequence 2, Appli	214	33	41.8	451	2	US-09-543-681A-6572	Sequence 6572, Ap
142	34	43.0	387	2	US-09-643-596B-136	Sequence 136, App	215	33	41.8	457	2	US-09-438-185A-199	Sequence 199, App
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145	34	43.0	409	1	US-08-961-716-3	Sequence 3, Appli	218	33	41.8	484	2	US-09-581-831-2	Sequence 2, Appli
146	34	43.0	409	2	US-08-477-346-51	Sequence 51, Appl	219	33	41.8	484	2	US-09-252-991A-32881	Sequence 32881, A
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149	34	43.0	409	2	US-08-487-072A-51	Sequence 51, Appl	222	33	41.8	489	2	US-09-252-991A-24949	Sequence 24949, A
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155	34	43.0	470	2	US-09-328-352-6673	Sequence 6673, Ap	228	33	41.8	513	2	US-09-252-991A-22551	Sequence 22551, A
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164	34	43.0	624	1	US-08-392-826C-2	Sequence 5, Appli	237	33	41.8	591	2	US-09-433-4563	Sequence 4363, Ap
165	34	43.0	654	1	US-08-320-945-2	Sequence 2, Appli	238	33	41.8	596	2	US-09-107-833-4563	Sequence 20, Appl
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167	34	43.0	741	2	US-09-362-842-67	Sequence 67, Appl	240	33	41.8	612	2	US-09-583-110-2911	Sequence 583, Appl
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172	34	43.0	968	2	US-08-816-346-2	Sequence 2, Appli	245	33	41.8	703	2	US-09-489-039A-8335	Sequence 8335, Ap
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253	33	41.8	874	1	US-08-456-647B-6	Sequence 6, Appli	326	32	40.5	226	2	US-09-694-094-1	Sequence 1, Appli
254	33	41.8	874	1	US-08-237-401A-6	Sequence 6, Appli	327	32	40.5	226	2	US-10-308-373-1	Sequence 1, Appli
255	33	41.8	877	2	US-09-328-352-8162	Sequence 8162, Ap	328	32	40.5	249	2	US-09-710-279-954	Sequence 954, App
256	33	41.8	880	1	US-08-445-640-10	Sequence 10, Appl	329	32	40.5	253	2	US-09-710-279-2428	Sequence 2428, App
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261	33	41.8	890	1	US-08-445-640-2	Sequence 2, Appli	334	32	40.5	276	1	US-08-847-900-1	Sequence 1, Appli
262	33	41.8	890	1	US-08-472-934-8	Sequence 8, Appli	335	32	40.5	278	2	US-08-633-993A-13	Sequence 13, Appl
263	33	41.8	890	1	US-08-323-460A-8	Sequence 8, Appli	336	32	40.5	278	2	US-08-844-188-13	Sequence 13, Appl
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266	33	41.8	890	2	US-08-461-145C-8	Sequence 8, Appli	339	32	40.5	278	2	US-09-548-334A-13	Sequence 13, Appl
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270	33	41.8	890	2	US-09-223-490-2	Sequence 2, Appli	343	32	40.5	278	2	US-10-412-203-13	Sequence 13, Appl
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272	33	41.8	911	1	US-08-441-104A-1	Sequence 1, Appli	345	32	40.5	284	2	US-09-134-001C-3445	Sequence 3445, Ap
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282	33	41.8	1247	1	US-08-461-146C-10	Sequence 10, Appl	355	32	40.5	321	2	US-08-469-649-2	Sequence 2, Appli
283	33	41.8	1247	1	US-08-461-145C-10	Sequence 10, Appl	356	32	40.5	332	1	US-09-347-878-60	Sequence 60, Appl
284	33	41.8	1287	2	US-09-949-016-7826	Sequence 7826, Ap	357	32	40.5	332	2	US-09-710-279-2278	Sequence 2278, Ap
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290	33	41.8	3519	2	US-09-428-517-4	Sequence 4, Appli	363	32	40.5	349	2	US-09-643-596B-126	Sequence 126, App
291	33	41.8	3816	2	US-09-428-517-3	Sequence 3, Appli	364	32	40.5	354	2	US-09-378-088A-58	Sequence 58, Appl
292	33	41.8	4150	2	US-09-428-517-2	Sequence 2, Appli	365	32	40.5	354	2	US-10-099-278-126	Sequence 126, App
293	32.5	41.1	175	2	US-09-270-767-31720	Sequence 31720, A	366	32	40.5	355	1	US-08-666-367B-6	Sequence 6, Appli
294	32.5	41.1	232	2	US-09-328-352-5918	Sequence 5918, Ap	367	32	40.5	355	2	US-09-143-438-6	Sequence 6, Appli
295	32.5	41.1	529	2	US-09-134-000C-6759	Sequence 6759, Ap	368	32	40.5	355	2	US-09-336-536-43	Sequence 43, Appl
296	32.5	41.1	2516	2	US-08-374-077C-2	Sequence 2, Appli	369	32	40.5	355	2	US-09-148-545-197	Sequence 197, App
297	32.5	41.1	2516	2	US-08-895-590-2	Sequence 2, Appli	370	32	40.5	355	2	US-09-621-011-197	Sequence 197, App
298	32.5	41.1	2516	2	US-09-539-879A-2	Sequence 2, Appli	371	32	40.5	367	2	US-09-378-088A-156	Sequence 156, App
299	32	40.5	85	2	US-09-774-639-142	Sequence 142, App	372	32	40.5	367	2	US-09-643-596B-58	Sequence 58, Appl
300	32	40.5	89	2	US-09-583-110-4570	Sequence 4570, App	373	32	40.5	367	2	US-09-643-596B-126	Sequence 126, App
301	32	40.5	106	2	US-10-104-047-2828	Sequence 2828, Ap	374	32	40.5	367	2	US-10-099-278-58	Sequence 58, Appl
302	32	40.5	115	1	US-08-485-449-4	Sequence 4, Appli	375	32	40.5	367	2	US-10-099-278-126	Sequence 126, App
303	32	40.5	125	2	US-09-107-532A-7210	Sequence 7210, Ap	376	32	40.5	367	2	US-10-099-278-126	Sequence 126, App
304	32	40.5	129	2	US-09-270-767-31736	Sequence 31736, A	377	32	40.5	371	2	US-09-378-088A-86	Sequence 86, Appl
305	32	40.5	142	2	US-09-270-767-46853	Sequence 46853, A	378	32	40.5	371	2	US-09-643-596B-86	Sequence 86, Appl
306	32	40.5	151	2	US-10-104-047-2666	Sequence 2666, Ap	379	32	40.5	371	2	US-10-099-278-86	Sequence 86, Appl
307	32	40.5	156	2	US-09-622-166A-20	Sequence 20, Appl	380	32	40.5	376	1	US-08-485-443-5	Sequence 5, Appli
308	32	40.5	156	2	US-10-423-007-20	Sequence 20, Appl	381	32	40.5	383	2	US-08-844-188-43	Sequence 43, Appl
309	32	40.5	166	1	US-08-365-103B-14	Sequence 14, Appl	382	32	40.5	383	2	US-09-378-088A-43	Sequence 43, Appl
310	32	40.5	167	1	US-08-365-103B-12	Sequence 12, Appl	383	32	40.5	383	2	US-09-548-334A-43	Sequence 43, Appl
311	32	40.5	170	2	US-09-489-039A-10687	Sequence 10687, A	384	32	40.5	383	2	US-09-547-621-43	Sequence 43, Appl
312	32	40.5	174	2	US-09-270-767-47776	Sequence 47776, A	385	32	40.5	383	2	US-09-643-596B-43	Sequence 43, Appl
313	32	40.5	177	2	US-09-252-991A-27635	Sequence 27635, A	386	32	40.5	383	2	US-09-643-596B-148	Sequence 148, App
314	32	40.5	180	1	US-08-624-650-1	Sequence 1, Appli	387	32	40.5	383	2	US-10-412-203-43	Sequence 43, Appl
315	32	40.5	180	2	US-09-818-648-1	Sequence 1, Appli	388	32	40.5	383	2	US-10-099-278-43	Sequence 43, Appl
316	32	40.5	180	2	US-09-355-925-5	Sequence 5, Appli	389	32	40.5	385	2	US-09-336-536-18	Sequence 18, Appl
317	32	40.5	180	2	US-09-452-991A-32278	Sequence 32278, A	390	32	40.5	385	2	US-09-336-536-24	Sequence 24, Appl
318	32	40.5	180	2	US-09-787-375-2	Sequence 2, Appli	391	32	40.5	385	2	US-09-538-092-333	Sequence 333, App
319	32	40.5	180	2	US-09-622-166A-3	Sequence 3, Appli	392	32	40.5	385	2		

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540	31.5	39.9	977	2	US-09-383-912-8	Sequence 8, Appli	613	31	39.2	237	2	US-09-270-767-35857	Sequence 35857, A
541	31.5	39.9	1069	1	US-07-777-715-9	Sequence 9, Appli	614	31	39.2	237	2	US-09-270-767-51074	Sequence 51074, A
542	31.5	39.9	1069	1	US-08-170-126-4	Sequence 4, Appli	615	31	39.2	240	2	US-09-489-039A-7742	Sequence 7742, Ap
543	31.5	39.9	1069	1	US-08-954-418-4	Sequence 4, Appli	616	31	39.2	241	2	US-08-178-257-19	Sequence 19, Appl
544	31.5	39.9	1098	1	US-07-777-715-7	Sequence 7, Appli	617	31	39.2	243	2	US-09-978-248A-9	Sequence 9, Appli
545	31.5	39.9	1098	1	US-08-170-126-2	Sequence 2, Appli	618	31	39.2	249	1	US-08-157-005-4	Sequence 4, Appli
546	31.5	39.9	1098	1	US-08-954-418-2	Sequence 2, Appli	619	31	39.2	249	1	US-08-799-464A-16	Sequence 16, Appl
547	31	39.2	12	1	US-08-764-640-128	Sequence 128, App	620	31	39.2	249	2	US-08-478-316-15	Sequence 15, Appl
548	31	39.2	12	1	US-08-973-225-128	Sequence 128, App	621	31	39.2	249	2	US-08-478-316-15	Sequence 15, Appl
549	31	39.2	12	2	US-09-244-298A-128	Sequence 128, App	622	31	39.2	249	2	US-09-565-864-4	Sequence 4, Appli
550	31	39.2	12	2	US-09-516-704-128	Sequence 128, App	623	31	39.2	249	2	US-08-301-435-73	Sequence 73, Appl
551	31	39.2	12	2	US-09-549-090-128	Sequence 128, App	624	31	39.2	249	2	US-09-601-326-15	Sequence 15, Appl
552	31	39.2	12	2	US-09-832-230A-128	Sequence 128, App	625	31	39.2	249	2	US-10-226-065-4	Sequence 4, Appli
553	31	39.2	12	2	US-09-428-082B-50	Sequence 50, Appl	626	31	39.2	249	2	US-10-226-065-4	Sequence 13, Appl
554	31	39.2	20	1	US-08-484-530-38	Sequence 38, Appl	627	31	39.2	249	2	US-09-701-868-13	Sequence 16, Appl
555	31	39.2	20	1	US-08-827-618A-38	Sequence 38, Appl	628	31	39.2	249	4	PCT-US95-09927-16	Sequence 16, Appl
556	31	39.2	20	2	US-08-483-552A-38	Sequence 38, Appl	629	31	39.2	249	4	PCT-US95-10904-73	Sequence 73, Appl
557	31	39.2	20	2	US-08-476-501-38	Sequence 38, Appl	630	31	39.2	250	1	US-08-872-961A-1	Sequence 1, Appli
558	31	39.2	47	2	US-09-902-540-15443	Sequence 15443, A	631	31	39.2	250	1	US-09-231-258-1	Sequence 1, Appli
559	31	39.2	48	2	US-09-205-658-282	Sequence 282, App	632	31	39.2	254	2	US-09-252-991A-20270	Sequence 20270, A
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561	31	39.2	70	2	US-09-270-767-39679	Sequence 39679, A	634	31	39.2	273	2	US-08-235-836C-104	Sequence 104, App
562	31	39.2	70	2	US-09-270-767-54896	Sequence 54896, A	635	31	39.2	273	6	5512669-4	Patent No. 5512669
563	31	39.2	79	2	US-09-917-254-63	Sequence 63, Appl	636	31	39.2	274	2	US-09-543-681A-4828	Sequence 4828, Ap
564	31	39.2	79	2	US-09-538-092-1063	Sequence 1063, Ap	637	31	39.2	276	2	US-09-902-540-10488	Sequence 10488, A
565	31	39.2	80	2	US-09-621-976-4160	Sequence 4160, Ap	638	31	39.2	279	2	US-09-252-991A-18598	Sequence 18598, A
566	31	39.2	82	2	US-09-949-016-9105	Sequence 9105, Ap	639	31	39.2	281	1	US-07-941-523-23	Sequence 23, Appl
567	31	39.2	93	2	US-09-543-681A-6152	Sequence 6152, Ap	640	31	39.2	283	2	US-09-902-540-13326	Sequence 13326, A
568	31	39.2	96	2	US-09-148-545-195	Sequence 195, App	641	31	39.2	286	2	US-09-949-016-6939	Sequence 6939, Ap
569	31	39.2	96	2	US-09-148-545-249	Sequence 249, App	642	31	39.2	289	2	US-09-949-016-11194	Sequence 11194, A
570	31	39.2	96	2	US-09-640-211A-1011	Sequence 1011, Ap	643	31	39.2	291	2	US-09-270-767-33107	Sequence 33107, A
571	31	39.2	96	2	US-09-621-011-195	Sequence 195, App	644	31	39.2	291	2	US-09-270-767-48324	Sequence 48324, A
572	31	39.2	96	2	US-09-621-011-249	Sequence 249, App	645	31	39.2	296	1	US-08-320-161-11	Sequence 11, Appl
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574	31	39.2	116	2	US-09-902-540-13488	Sequence 13488, A	647	31	39.2	296	2	US-08-479-017-3	Sequence 3, Appli
575	31	39.2	136	2	US-09-270-767-32376	Sequence 32376, A	648	31	39.2	296	2	US-08-455-829-11	Sequence 11, Appl
576	31	39.2	136	2	US-09-270-767-47593	Sequence 47593, A	649	31	39.2	296	2	US-08-235-836C-22	Sequence 22, Appl
577	31	39.2	149	2	US-09-543-681A-8072	Sequence 8072, Ap	650	31	39.2	296	2	US-08-455-973-11	Sequence 11, Appl
578	31	39.2	150	2	US-09-538-092-37	Sequence 37, Appl	651	31	39.2	298	2	US-09-434-354-49	Sequence 49, Appl
579	31	39.2	164	2	US-09-270-767-40861	Sequence 40861, A	652	31	39.2	298	2	US-09-709-785-49	Sequence 49, Appl
580	31	39.2	164	2	US-09-270-767-56077	Sequence 56077, A	653	31	39.2	298	2	US-09-811-132-33	Sequence 33, Appl
581	31	39.2	169	2	US-09-489-039A-9006	Sequence 9006, Ap	654	31	39.2	298	2	US-09-811-094-33	Sequence 33, Appl
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583	31	39.2	178	2	US-09-270-767-34739	Sequence 34739, A	656	31	39.2	298	2	US-09-809-827-33	Sequence 33, Appl
584	31	39.2	178	2	US-09-270-767-50016	Sequence 50016, A	657	31	39.2	298	2	US-09-809-889-33	Sequence 33, Appl
585	31	39.2	183	2	US-09-489-039A-13227	Sequence 13227, A	658	31	39.2	303	2	US-09-328-352-8214	Sequence 8214, Ap
586	31	39.2	183	2	US-09-902-540-11456	Sequence 11456, A	659	31	39.2	314	2	US-09-489-039A-9520	Sequence 9520, Ap
587	31	39.2	191	2	US-09-949-016-7105	Sequence 7105, Ap	660	31	39.2	321	2	US-09-252-991A-23121	Sequence 23121, A
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589	31	39.2	192	2	US-09-540-236-3508	Sequence 3508, Ap	662	31	39.2	331	2	US-09-489-847-309	Sequence 309, App
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591	31	39.2	198	2	US-08-962-560C-6	Sequence 6, Appli	664	31	39.2	339	2	US-09-171-461-36	Sequence 36, Appl
592	31	39.2	198	2	US-09-902-540-14281	Sequence 14281, A	665	31	39.2	339	2	US-09-970-711-36	Sequence 36, Appl
593	31	39.2	200	2	US-09-543-681A-6084	Sequence 6084, Ap	666	31	39.2	339	2	US-09-949-016-7998	Sequence 7998, Ap
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595	31	39.2	202	2	US-09-270-767-34939	Sequence 34939, A	668	31	39.2	344	2	US-09-415-277C-5	Sequence 5, Appli
596	31	39.2	203	2	US-09-270-767-50156	Sequence 50156, A	669	31	39.2	345	2	US-09-252-991A-21042	Sequence 21042, A
597	31	39.2	205	1	US-08-531-525-31	Sequence 31, Appl	670	31	39.2	367	2	US-09-378-088A-54	Sequence 54, Appl
598	31	39.2	205	1	US-08-718-270A-31	Sequence 31, Appl	671	31	39.2	367	2	US-09-643-596B-54	Sequence 54, Appl
599	31	39.2	206	2	US-09-078-317-15	Sequence 15, Appl	672	31	39.2	368	2	US-10-099-278-54	Sequence 54, Appl
600	31	39.2	206	2	US-09-454-818-15	Sequence 15, Appl	673	31	39.2	368	2	US-09-252-991A-19552	Sequence 19552, A
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605	31	39.2	207	1	US-09-489-039A-11637	Sequence 11637, A	678	31	39.2	385	2	US-08-633-993A-11	Sequence 11, Appl
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686	31	39.2	385	2	Sequence 11, Appl	759	31	39.2	585	2	US-09-043-930-3	Sequence 3, Appli
687	31	39.2	385	2	Sequence 68, Appl	760	31	39.2	585	2	US-09-043-930-4	Sequence 4, Appli
688	31	39.2	385	2	Sequence 116, Appl	761	31	39.2	585	2	US-09-043-930-5	Sequence 5, Appli
689	31	39.2	385	2	Sequence 11, Appl	762	31	39.2	585	2	US-09-043-930-6	Sequence 6, Appli
690	31	39.2	385	2	Sequence 11, Appl	763	31	39.2	585	2	US-09-043-930-7	Sequence 7, Appli
691	31	39.2	385	2	Sequence 68, Appl	764	31	39.2	585	2	US-09-043-930-8	Sequence 8, Appli
692	31	39.2	385	2	Sequence 116, Appl	765	31	39.2	585	2	US-08-476-501-57	Sequence 57, Appl
693	31	39.2	386	2	Sequence 28, Appl	766	31	39.2	585	2	US-08-476-501-59	Sequence 59, Appl
694	31	39.2	386	2	Sequence 28, Appl	767	31	39.2	585	2	US-03-015-399-6	Sequence 6, Appli
695	31	39.2	386	2	Sequence 28, Appl	768	31	39.2	585	6	5475086-6	Patent No. 5475086
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697	31	39.2	386	2	Sequence 28, Appl	770	31	39.2	601	2	US-09-252-991A-21813	Sequence 21813, A
698	31	39.2	386	2	Sequence 28, Appl	771	31	39.2	607	2	US-09-349-016-7623	Sequence 7823, Ap
699	31	39.2	386	2	Sequence 28, Appl	772	31	39.2	608	2	US-09-134-000C-4810	Sequence 4810, Ap
700	31	39.2	386	2	Sequence 28, Appl	773	31	39.2	614	2	US-10-104-047-3692	Sequence 3892, Ap
701	31	39.2	392	2	Sequence 90, Appl	774	31	39.2	621	1	US-08-969-714-1	Sequence 1, Appli
702	31	39.2	392	2	Sequence 90, Appl	775	31	39.2	638	2	US-08-969-714-1	Sequence 2, Appli
703	31	39.2	392	2	Sequence 90, Appl	776	31	39.2	639	2	US-08-376-856-2	Sequence 2, Appli
704	31	39.2	392	2	Sequence 114, App	777	31	39.2	639	2	US-08-376-856-2	Sequence 347, App
705	31	39.2	394	2	Sequence 9514, Ap	778	31	39.2	639	2	US-10-012-231A-347	Sequence 347, App
706	31	39.2	402	2	Sequence 2235, Ap	779	31	39.2	639	2	US-10-015-389A-347	Sequence 347, App
707	31	39.2	428	2	Sequence 19535, A	780	31	39.2	639	2	US-10-006-768A-347	Sequence 347, App
708	31	39.2	428	2	Sequence 3817, Ap	781	31	39.2	639	2	US-10-015-671A-347	Sequence 347, App
709	31	39.2	429	2	Sequence 14642, A	782	31	39.2	639	2	US-10-015-393A-347	Sequence 347, App
710	31	39.2	430	2	Sequence 5244, Ap	783	31	39.2	639	2	US-10-011-833A-347	Sequence 347, App
711	31	39.2	434	2	Sequence 5244, Ap	784	31	39.2	639	2	US-10-006-041A-347	Sequence 347, App
712	31	39.2	435	2	Sequence 25043, A	785	31	39.2	639	2	US-10-012-064A-347	Sequence 347, App
713	31	39.2	437	2	Sequence 7245, Ap	786	31	39.2	645	1	US-08-969-714-3	Sequence 3, Appli
714	31	39.2	437	2	Sequence 7245, Ap	787	31	39.2	647	1	US-08-218-943-1	Sequence 1, Appli
715	31	39.2	441	2	Sequence 1207, Ap	788	31	39.2	652	1	US-08-313-185-53	Sequence 53, Appl
716	31	39.2	443	2	Sequence 120, App	789	31	39.2	652	1	US-08-459-499-17	Sequence 17, Appl
717	31	39.2	443	2	Sequence 10582, A	790	31	39.2	652	2	US-09-082-614A-53	Sequence 53, Appl
718	31	39.2	448	2	Sequence 24264, A	791	31	39.2	658	1	US-08-409-995-5	Sequence 5, Appli
719	31	39.2	453	2	Sequence 5359, Ap	792	31	39.2	658	2	US-08-685-467-5	Sequence 5, Appli
720	31	39.2	454	2	Sequence 116, App	793	31	39.2	658	2	US-08-913-942-5	Sequence 5, Appli
721	31	39.2	458	2	Sequence 13954, A	794	31	39.2	663	2	US-08-684-707-5	Sequence 2, Appli
722	31	39.2	460	2	Sequence 2784, Ap	795	31	39.2	693	2	US-09-382-106-2	Sequence 16667, A
723	31	39.2	463	2	Sequence 29935, A	796	31	39.2	695	2	US-09-248-796A-16667	Sequence 18020, A
724	31	39.2	466	2	Sequence 15709, A	797	31	39.2	716	2	US-09-248-796A-18020	Sequence 21345, A
725	31	39.2	466	2	Sequence 107, App	798	31	39.2	724	2	US-09-252-991A-21345	Sequence 2, Appli
726	31	39.2	466	2	Sequence 110, App	799	31	39.2	730	1	US-09-701-868-11	Sequence 11, Appl
727	31	39.2	485	2	Sequence 9, Appli	800	31	39.2	731	1	US-08-696-944-2	Sequence 20, Appl
728	31	39.2	485	2	Sequence 9, Appli	801	31	39.2	731	1	US-08-696-944-20	Sequence 20, Appl
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ALIGNMENTS

RESULT 1
US-08-818-112-104
; Sequence 104, Application US/08818112
; Patent No. 6290969
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
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; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Twardzik, Daniel R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
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; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/818,112
; FILING DATE: 13-MAR-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
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; REFERENCE/DOCKET NUMBER: 210121.411C6
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; TELEPHONE: (206) 682-4800
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; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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Query Match 100.0%; Score 79; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. NO. 6.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MTEQQWNFAGIEAAA 15
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US-08-818-111-99
; Sequence 99, Application US/08818111
; Patent No. 6338852
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Houghton, Raymond
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Twardzik, Daniel R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
; TUBERCULOSIS
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESS: SEED and BERRY LLP
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; SOFTWARE: Patent In Release #1.0, Version #1.30
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; FILING DATE: 13-MAR-1997
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; ATTORNEY/AGENT INFORMATION:
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; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-818-111-99
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Best Local Similarity 100.0%; Pred. NO. 6.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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US-09-056-556-104
; Sequence 104, Application US/09056556
; Patent No. 6350456
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND
NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
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COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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FILING DATE: 07-APR-1998
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ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
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INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-056-556-104
Query Match 100.0%; Score 79; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 6.4e-07;
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Patent No. 6458366
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
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APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998

TREATM
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-072-596-99
Query Match 100.0%; Score 79; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 6.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTEQOWNFAGIEAAA 15
Db 1 MTEQOWNFAGIEAAA 15
RESULT 5
US-09-072-967-104
Sequence 104, Application US/09072967
Patent No. 6592877
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-072-967-104

Query Match 100.0%; Score 79; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 6.4e-07; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQWNPAGIEAAA 15
|||||
DB 1 MTEQWNPAGIEAAA 15

RESULT 6
US-10-193-002-99
; Sequence 99, Application US/10193002
; Patent No. 6949246

GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
TUBERCULOSIS

NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-Jul-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998

ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9

TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 99:
US-10-193-002-99

Query Match 100.0%; Score 79; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 6.4e-07; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQWNPAGIEAAA 15
|||||
DB 1 MTEQWNPAGIEAAA 15

RESULT 7
US-10-084-843-104
; Sequence 104, Application US/10084843

Patent No. 6962710
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS

NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998

ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9

TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 104:
US-10-084-843-104

Query Match 100.0%; Score 79; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 6.4e-07; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQWNPAGIEAAA 15
|||||
DB 1 MTEQWNPAGIEAAA 15

RESULT 8
US-08-465-640-2
; Sequence 2, Application US/08465640
; Patent No. 5955077

GENERAL INFORMATION:
APPLICANT: ANDERSEN, Peter
APPLICANT: ANDERSEN, Ase Bengaard
APPLICANT: HASLOV, Kaare
APPLICANT: SORENSEN, Anne Lund

TITLE OF INVENTION: TUBERCULOSIS VACCINE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brody and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington

```
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20004
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/465,640
/ FILING DATE: 05-JUN-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/123,182
/ FILING DATE: 20-SEP-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/DK94/00273
/ FILING DATE: 01-JUL-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: COOPER, IVER P
/ REGISTRATION NUMBER: 28,005
/ REFERENCE/DOCKET NUMBER: ANDERSEN=3A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-628-5197
/ TELEFAX: 202-737-3528
/ TELEX: 248633
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 95 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-465-640-2

Query Match 100.0%; Score 79; DB 1; Length 95;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQOWNFAGIEAAA 15
Db 1 MTEQOWNFAGIEAAA 15

RESULT 9
US-09-050-739-173
; Sequence 173, Application US/09050739
; Patent No. 6641814
; GENERAL INFORMATION:
; APPLICANT: ANDERSEN, Peter
; APPLICANT: NIELSEN, Rikke
; APPLICANT: OETTINGER, Thomas
; APPLICANT: RASMUSSEN, Peter Birk
; APPLICANT: ROSENKRANDS, Ida
; APPLICANT: WELDINGH, Karin
; APPLICANT: FLORIO, Walter
; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
; FILE REFERENCE: 670001-2002.1
; CURRENT APPLICATION NUMBER: US/09/050,739
; CURRENT FILING DATE: 1998-03-30
; EARLIER APPLICATION NUMBER: 0376/97
; EARLIER FILING DATE: 1997-04-02
; EARLIER APPLICATION NUMBER: 1277/97
; EARLIER FILING DATE: 1997-11-10
; EARLIER APPLICATION NUMBER: 60/044,624
; EARLIER FILING DATE: 1997-04-18
; EARLIER APPLICATION NUMBER: 60/070,488
; EARLIER FILING DATE: 1998-01-05
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 173
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis

US-09-050-739-173
Query Match 100.0%; Score 79; DB 2; Length 404;
Best Local Similarity 100.0%; Pred. No. 6.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQOWNFAGIEAAA 15
Db 310 MTEQOWNFAGIEAAA 324

RESULT 11
US-09-001-984C-77
; Sequence 77, Application US/09001984C
; Patent No. 6245331
; GENERAL INFORMATION:
; APPLICANT: Laal, Suman
; APPLICANT: Zolla-Pazner, Susan
; APPLICANT: Bellisle, John T
; TITLE OF INVENTION: EARLY DETECTION OF MYCOBACTERIAL DISEASE
; FILE REFERENCE: NYU-011
; CURRENT APPLICATION NUMBER: US/09/001,984C
; CURRENT FILING DATE: 1997-12-31
; PRIOR APPLICATION NUMBER: 60/034,003
; PRIOR FILING DATE: 1996-12-31
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 77
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis strain H37Rv
```

US-09-001-984C-77

Query Match 65.8%; Score 52; DB 2; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0057; 0; Indels 0;
Matches 9; Conservative 1; Mismatches 0; Gaps 0;

QY 2 TEQOWNFAGI 11
||||:||||
DB 1 TEQOWDFAGI 10

RESULT 12

US-09-396-347F-77
; Sequence 77, Application US/09396347F
; Patent No. 6506384
; GENERAL INFORMATION:
; APPLICANT: Laal, Suman
; APPLICANT: Zolla-Pazner, Susan
; APPLICANT: Bellisle, John T
; TITLE OF INVENTION: EARLY DETECTION OF MYCOBACTERIAL DISEASE
; FILE REFERENCE: 32004-169276
; CURRENT APPLICATION NUMBER: US/09/396,347F
; CURRENT FILING DATE: 1999-09-14
; PRIOR APPLICATION NUMBER: 09/001,984
; PRIOR FILING DATE: 1997-12-31
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 77
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis strain H37Rv
US-09-396-347F-77

Query Match 65.8%; Score 52; DB 2; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0057;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TEQOWNFAGI 11
||||:||||
DB 1 TEQOWDFAGI 10

RESULT 13

US-09-198-452A-554
; Sequence 554, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 554
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-554

Query Match 53.2%; Score 42; DB 2; Length 409;
Best Local Similarity 77.8%; Pred. No. 24;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 WNFAGIEAA 14
||:|||||
DB 345 WNYLGIEAA 353

RESULT 14

US-08-579-667-4
; Sequence 4, Application US/08579667

; Patent No. 5705624
; GENERAL INFORMATION:
; APPLICANT: Fitzmaurice, Wayne P.
; APPLICANT: Hellmann, Gary M.
; APPLICANT: Grill, Laurence K.
; APPLICANT: Kumasai, Monto H.
; APPLICANT: Della-Cioppa, Guy R.
; TITLE OF INVENTION: DNA SEQUENCES ENCODING ENZYMES USEFUL IN
; TITLE OF INVENTION: PHYTOENE BIOSYNTHESIS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Virginia C. Bennett
; STREET: 1211 East Morehead Street, PO Drawer 34009
; CITY: Charlotte
; STATE: No. 5705624th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/579,667
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Virginia C.
; REGISTRATION NUMBER: 37,092
; REFERENCE/DOCKET NUMBER: 627-196
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 413 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-579-667-4

Query Match 53.2%; Score 42; DB 1; Length 413;
Best Local Similarity 50.0%; Pred. No. 24;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 EQOWNFAGIEAA 14
||||:||||
DB 50 EQOWNFGSVKSA 61

RESULT 15

US-09-438-185A-515
; Sequence 515, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kalman, Sue
; APPLICANT: Davis, Ronald
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: PastSeq for Windows Version 3.0
; SEQ ID NO 515
; LENGTH: 413
; TYPE: PRT

; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: CPN0513
US-09-438-185A-515

Query Match 53.2%; Score 42; DB 2; Length 413;
Best Local Similarity 77.8%; Pred. No. 24;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 WNPAGIEAA 14
||: |||||
Db 349 WNYLGIEAA 357

RESULT 16

US-09-949-016-9799
; Sequence 9799, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 9799
; LENGTH: 578
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9799

Query Match 53.2%; Score 42; DB 2; Length 578;
Best Local Similarity 50.0%; Pred. No. 36;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 TEQOWNPAGIEAAA 15
:: ||: |||||
Db 26 SDQWDSAGVEVAA 39

RESULT 17

US-09-462-842-3
; Sequence 3, Application US/09462842
; Patent No. 6521421
; GENERAL INFORMATION:
; APPLICANT: Quax, Wilhelmus J.
; APPLICANT: Caldwell, Robert M.
; TITLE OF INVENTION: Increasing Production of Proteins in Gram-Positive
; TITLE OF INVENTION: Microorganisms
; FILE REFERENCE: GC383-US
; CURRENT APPLICATION NUMBER: US/09/462,842
; CURRENT FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: PCT/US98/14704
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: EP 97305288.9
; PRIOR FILING DATE: 1997-07-15
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-09-462-842-3

Query Match 51.9%; Score 41; DB 2; Length 176;

Best Local Similarity 60.0%; Pred. No. 14;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 EOQWNPAGIE 12
|: ||: ||: |
Db 132 ERQWDFLGIE 141

RESULT 18

US-09-393-171-3
; Sequence 3, Application US/09393171
; Patent No. 6673569
; GENERAL INFORMATION:
; APPLICANT: KUROKAWA, Yoichi
; APPLICANT: YANAGI, Hideki
; APPLICANT: YURA, Takashi
; TITLE OF INVENTION: Dsba/Dsbb/Dsbc/Dsdb expression plasmid
; FILE REFERENCE: 1422-391P
; CURRENT APPLICATION NUMBER: US/09/393,171
; CURRENT FILING DATE: 1999-09-09
; EARLIER APPLICATION NUMBER: JP 10/255702
; EARLIER FILING DATE: 1998-09-09
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 3
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-393-171-3

Query Match 51.9%; Score 41; DB 2; Length 176;
Best Local Similarity 60.0%; Pred. No. 14;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 EOQWNPAGIE 12
|: ||: ||: |
Db 132 ERQWDFLGIE 141

RESULT 19

US-09-602-777A-416
; Sequence 416, Application US/09602777A
; Patent No. 6831165
; GENERAL INFORMATION:
; APPLICANT: Pompeius, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Habermann, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; INVOLVED IN HOMEOSTASIS AND ADAPTATION
; FILE REFERENCE: BGI-128CP
; CURRENT APPLICATION NUMBER: US/09/602,777A
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931636.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932126.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932127.2
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932129.9
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: DE 19932226.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932920.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932922.2
; PRIOR FILING DATE: 1999-07-14

; PRIOR APPLICATION NUMBER: DE 19932924.9
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932928.1
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932930.3
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932933.8
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932935.4
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932973.7
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933002.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933003.4
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933005.0
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933006.9
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19941378.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941390.8
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941391.6
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19942088.2
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 442
; SEQ ID NO 416
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-602-777A-416

Query Match 50.6%; Score 40; DB 2; Length 295;
Best Local Similarity 55.6%; Pred. No. 37;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQQNFA 9
:|:|:|:|
DB 50 LTEEWNFA 58

RESULT 20
US-09-252-991A-18026
; Sequence 18026, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18026
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18026

Query Match 49.4%; Score 39; DB 2; Length 538;
Best Local Similarity 63.6%; Pred. No. 1.1e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 EQQWFAIEA 13

Db 375 EQQWFAIEA 385
||||:|:|
RESULT 21
US-09-252-991A-24200
; Sequence 24200, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24200
; LENGTH: 928
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24200

Query Match 49.4%; Score 39; DB 2; Length 928;
Best Local Similarity 54.5%; Pred. No. 2.1e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 QQWFAIEAA 14
:|:|:|:|
DB 711 EQWDIEGLEAA 721

RESULT 22
US-09-830-807-41
; Sequence 41, Application US/09830807
; Patent No. 6846667
; GENERAL INFORMATION:
; APPLICANT: Crooke, Helen R.
; APPLICANT: Clarke, Enda E.
; APPLICANT: Everest, Paul H.
; APPLICANT: Dougan, Gordon
; APPLICANT: Holden, David W.
; APPLICANT: Shea, Jacqueline E.
; APPLICANT: Feldman, Robert G.
; TITLE OF INVENTION: VIRULENCE GENES AND PROTEINS, AND THEIR USE
; FILE REFERENCE: CJE-65
; CURRENT APPLICATION NUMBER: US/09/830,807
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 41
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-830-807-41

Query Match 48.1%; Score 38; DB 2; Length 118;
Best Local Similarity 54.5%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 TEQQWFAIE 12
:|:|:|:|
DB 64 THSSWNLAGIQ 74

RESULT 23
US-08-685-808-3
; Sequence 3, Application US/08685808
; Patent No. 6048715
; GENERAL INFORMATION:

APPLICANT: HAYNES, CHARLES A., et al
TITLE OF INVENTION: SEPARATION AND CONCENTRATION SYSTEMS BASED
ON SOLUBLE OLIGOSACCHARIDE BINDING DOMAINS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VENTER LAW GROUP
STREET: 260 Sheridan Ave., Ste. 440
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/685,808
FILING DATE: 24-JULY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/505,860
FILING DATE: 24-JULY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Rae-Venter, Barbara
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CBDT.017.01US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
TELEFAX: (650) 328-4477
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 155 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: no
US-08-685-808-3

Query Match 48.1%; Score 38; DB 2; Length 155;
Best Local Similarity 60.0%; Pred. No. 40;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 QOWNFAGIEA 13
||||| :||
Db 91 QOWNFLEQA 100

RESULT 24
US-08-505-860C-3
Sequence 3, Application US/08505860C
Patent No. 6174700
GENERAL INFORMATION:
APPLICANT: HAYNES, CHARLES A., et al
TITLE OF INVENTION: SEPARATION AND CONCENTRATION SYSTEMS BASED
ON SOLUBLE OLIGOSACCHARIDE BINDING DOMAINS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VENTER LAW GROUP
STREET: 260 Sheridan Ave., Ste. 440
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/505,860C
FILING DATE: 24-JULY-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Rae-Venter, Barbara
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CBDT.017.00US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
TELEFAX: (650) 328-4477
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 155 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: no
US-08-505-860C-3

Query Match 48.1%; Score 38; DB 2; Length 155;
Best Local Similarity 60.0%; Pred. No. 40;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 QOWNFAGIEA 13
||||| :||
Db 91 QOWNFLEQA 100

RESULT 25
US-09-489-039A-13578
Sequence 13578, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13578
LENGTH: 349
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13578

Query Match 48.1%; Score 38; DB 2; Length 349;
Best Local Similarity 60.0%; Pred. No. 1e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 WNPAGIEAAA 15
||||| :||
Db 243 WAPVGVESAA 252

RESULT 26
US-08-579-667-2
Sequence 2, Application US/08579667
Patent No. 5705624
GENERAL INFORMATION:
APPLICANT: Fitzmaurice, Wayne P.
APPLICANT: Hellmann, Gary M.
APPLICANT: Grill, Laurence K.
APPLICANT: Kumagai, Monto H.
APPLICANT: Della-Cioppa, Guy R.
TITLE OF INVENTION: DNA SEQUENCES ENCODING ENZYMES USEFUL IN
PHYTOENE BIOSYNTHESIS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Virginia C. Bennett
STREET: 1211 East Morehead Street, PO Drawer 34009
CITY: Charlotte
STATE: NO. 5705624th Carolina
COUNTRY: USA

; TITLE OF INVENTION: No. 6943241e1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3636
; LENGTH: 650
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3636

Query Match 48.1%; Score 38; DB 2; Length 650;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 QOWNFAGIEAAA 15
|||:|
Db 33 QOWNIAGVGGA 44

RESULT 30
US-09-252-991A-30635
; Sequence 30635, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30635
; LENGTH: 795
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30635

Query Match 48.1%; Score 38; DB 2; Length 795;
Best Local Similarity 50.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 EQOWNFAGIE 12
:|:|:|
Db 321 DQWRFLGVE 330

RESULT 31
US-09-368-590-2
; Sequence 2, Application US/09368590
; Patent No. 6187563
; GENERAL INFORMATION:
; APPLICANT: Solimena, Michele
; TITLE OF INVENTION: INTERACTING POLYPEPTIDES FOR
; TITLE OF INVENTION: AUTOANTIGENS OF AUTOIMMUNE DISEASES
; FILE REFERENCE: 101918-200 (CCR-941)
; CURRENT APPLICATION NUMBER: US/09/368,590
; CURRENT FILING DATE: 1999-08-04
; EARLIER APPLICATION NUMBER: 60/095,657
; EARLIER FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 2293
; TYPE: PRT
; ORGANISM: Human

US-09-368-590-2

Query Match 48.1%; Score 38; DB 2; Length 2293;
Best Local Similarity 60.0%; Pred. No. 8.8e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 QOWNFAGIEAAA 14
||:|:|
Db 719 QWRSLGLEAA 728

RESULT 32
US-09-949-016-7309
; Sequence 7309, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7309
; LENGTH: 2600
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7309

Query Match 48.1%; Score 38; DB 2; Length 2600;
Best Local Similarity 60.0%; Pred. No. 1e+03;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 QOWNFAGIEAA 14
||:|:|
Db 1057 QWRSLGLEAA 1066

RESULT 33
US-09-489-039A-9639
; Sequence 9639, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 9639
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9639

Query Match 46.8%; Score 37; DB 2; Length 331;
Best Local Similarity 54.5%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 QOWNFAGIEAA 14
||:|:|
Db 285 QLWTFKGLDAA 295

```
RESULT 34
US-09-252-991A-23220
; Sequence 23220, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23220
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23220

Query Match 46.8%; Score 37; DB 2; Length 435;
Best Local Similarity 50.0%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 6; Conservative 4; Mismatches 4;

QY 4 QOWNFAGIEAAX 15
Db 296 ERWSTAGIDATA 307

RESULT 35
US-09-540-236-2120
; Sequence 2120, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709 2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2120
; LENGTH: 493
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2120

Query Match 46.8%; Score 37; DB 2; Length 493;
Best Local Similarity 44.4%; Pred. No. 2.3e+02; 3; Indels 4; Gaps 1;
Matches 8; Conservative 3; Mismatches 3;

QY 1 MTEQOWN----FAGIEAA 14
Db 35 VTDQANLLALFVGVIAT 52

RESULT 36
US-09-538-092-599
; Sequence 599, Application US/09538092
; Patent No. 6753514
; GENERAL INFORMATION:
; APPLICANT: Manfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
```

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; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuratPatSeqFormatter Version 0.9
; SEQ ID NO 599
; LENGTH: 668
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number YML088W
US-09-538-092-599

Query Match 46.8%; Score 37; DB 2; Length 668;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 EQQWNFAG 10
Db 341 EQQWNFAG 348

RESULT 37
US-09-134-000C-6437
; Sequence 6437, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6437
; LENGTH: 820
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6437

Query Match 46.8%; Score 37; DB 2; Length 820;
Best Local Similarity 45.5%; Pred. No. 4.1e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MTEQQWNFAGI 11
Db 88 LSENWNNFNGI 98

RESULT 38
US-08-215-805A-80
; Sequence 80, Application US/08215805A
; Patent No. 5559008
; GENERAL INFORMATION:
; APPLICANT: Chang, Yung-Fu
; TITLE OF INVENTION: LEUKOTOXIN GENE FROM PASTEURELLA
; TITLE OF INVENTION: SUI5
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
```

```
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/215,805A
/ FILING DATE: 22-MAR-1994
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Timian, Susan J.
/ REGISTRATION NUMBER: 34,103
/ REFERENCE/DOCKET NUMBER: 19603/61 (D-1329A)
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (716) 263-1636
/ TELEFAX: (716) 263-1600
/ INFORMATION FOR SEQ ID NO: 80:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 934 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ ORIGINAL SOURCE:
/ ORGANISM: Pasteurella suis
/ STRAIN: 5943
/ IMMEDIATE SOURCE:
/ LIBRARY: P. suis DNA in Bacteriophage lambda-dash
/ CLONE: (Lambda)yfc33-37
/ US-08-215-805A-80

Query Match 46.2%; Score 36.5; DB 1; Length 934;
Best Local Similarity 50.0%; Pred. No. 5,8e+02;
Matches 8; Conservative 2; Mismatches 1; Indels 5; Gaps 1;

QY 1 MTEQQW-----NFAGI 11
Db 463 ITQQQWNNIGNLAGI 478

RESULT 39
US-09-270-767-33601
/ Sequence 33601, Application US/09270767
/ Patent No. 6703491
/ GENERAL INFORMATION:
/ APPLICANT: Homburger et al.
/ TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
/ FILE REFERENCE: File Reference: 7326-094
/ CURRENT APPLICATION NUMBER: US/09/270,767
/ CURRENT FILING DATE: 1999-03-17
/ NUMBER OF SEQ ID NOS: 62517
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 33601
/ LENGTH: 88
/ TYPE: PRT
/ ORGANISM: Drosophila melanogaster
US-09-270-767-33601

Query Match 45.6%; Score 36; DB 2; Length 88;
Best Local Similarity 50.0%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 6; Indels 6; Gaps 0;

QY 4 QQWNPAGIEAAA 15
Db 65 QQWNPFGSNKTA 76

RESULT 40
US-09-270-767-48818
/ Sequence 48818, Application US/09270767
/ Patent No. 6703491
/ GENERAL INFORMATION:
/ APPLICANT: Homburger et al.
/ TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
/ FILE REFERENCE: File Reference: 7326-094
/ CURRENT APPLICATION NUMBER: US/09/270,767
/ CURRENT FILING DATE: 1999-03-17
/ NUMBER OF SEQ ID NOS: 62517
```

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/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 48818
/ LENGTH: 88
/ TYPE: PRT
/ ORGANISM: Drosophila melanogaster
US-09-270-767-48818

Query Match 45.6%; Score 36; DB 2; Length 88;
Best Local Similarity 50.0%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 6; Indels 6; Gaps 0;

QY 4 QQWNPAGIEAAA 15
Db 65 QQWNPFGSNKTA 76

RESULT 41
US-09-634-238-265
/ Sequence 265, Application US/09634238
/ Patent No. 6544772
/ GENERAL INFORMATION:
/ APPLICANT: Glenn, Matthew
/ APPLICANT: Havukkala, Ilkka J.
/ APPLICANT: Bloksberg, Leonard, N.
/ APPLICANT: Lubbers, Mark W.
/ APPLICANT: Dekker, James
/ APPLICANT: Christenson, Anna C.
/ APPLICANT: Holland, Ross
/ APPLICANT: O'Toole, Paul W.
/ APPLICANT: Reid, Julian R.
/ APPLICANT: Coolbear, Timothy
/ TITLE OF INVENTION: Polynucleotides, materials incorporating
/ TITLE OF INVENTION: them and methods for using them.
/ FILE REFERENCE: 11000.1043U1
/ CURRENT APPLICATION NUMBER: US/09/634,238
/ CURRENT FILING DATE: 2000-08-08
/ NUMBER OF SEQ ID NOS: 422
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 265
/ LENGTH: 149
/ TYPE: PRT
/ ORGANISM: Lactobacillus rhamnosus
US-09-634-238-265

Query Match 45.6%; Score 36; DB 2; Length 149;
Best Local Similarity 77.8%; Pred. No. 86;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 NFAGIEAAA 15
Db 67 NIAGVEAAA 75

RESULT 42
US-09-489-039A-8963
/ Sequence 8963, Application US/09489039A
/ Patent No. 6610836
/ GENERAL INFORMATION:
/ APPLICANT: Gary Breton et. al
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
/ TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: 2709.2004001
/ CURRENT APPLICATION NUMBER: US/09/489,039A
/ CURRENT FILING DATE: 2000-01-27
/ PRIOR APPLICATION NUMBER: US 60/117,747
/ PRIOR FILING DATE: 1999-01-29
/ NUMBER OF SEQ ID NOS: 14342
/ SEQ ID NO 8963
/ LENGTH: 149
/ TYPE: PRT
/ ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8963
```

Query Match 45.6%; Score 36; DB 2; Length 149;
Best Local Similarity 53.8%; Pred. No. 86;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 MTEQWNFAGIEA 13
:|||||
Db 32 LTEQWRIVRIIA 44

RESULT 43
US-09-904-615-155
; Sequence 155, Application US/09904615
; Patent No. 6566325
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 49 Human Secreted Proteins
; FILE REFERENCE: PZ032P1
; CURRENT APPLICATION NUMBER: US/09/904,615
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/511,554
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/097,917
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: 60/098,634
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 155
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-615-155

Query Match 45.6%; Score 36; DB 2; Length 221;
Best Local Similarity 70.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 WNFAGIEAAA 15
|||
Db 132 WNLGDEAAA 141

RESULT 44
US-10-054-988-155
; Sequence 155, Application US/10054988
; Patent No. 6953667
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 49 Human Secreted Proteins
; FILE REFERENCE: PZ032P1
; CURRENT APPLICATION NUMBER: US/10/054,988
; CURRENT FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: 09/904,615
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/511,554
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/097,917
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: 60/098,634
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 155
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-054-988-155

Query Match 45.6%; Score 36; DB 2; Length 221;
Best Local Similarity 70.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 WNFAGIEAAA 15

Db 132 WNLGDEAAA 141
|||
|||

RESULT 45
US-09-724-623-113
; Sequence 113, Application US/09724623
; Patent No. 6476209
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Lubbers, Mark W
; APPLICANT: Dekker, James
; TITLE OF INVENTION: Polynucleotides, materials incorporating
; FILE REFERENCE: 104801
; CURRENT APPLICATION NUMBER: US/09/724,623
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Lactobacillus rhamnosus
US-09-724-623-113

Query Match 45.6%; Score 36; DB 2; Length 282;
Best Local Similarity 77.8%; Pred. No. 1.8e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 NFAGIEAAA 15
|||
Db 191 NIAGVEAAA 199

RESULT 46
US-09-270-957-4
; Sequence 4, Application US/09270957
; Patent No. 6641996
; GENERAL INFORMATION:
; APPLICANT: Richard A. Jefferson and Jorge E. Mayer
; TITLE OF INVENTION: MICROBIAL -GLUCURONIDASE GENES, GENE
; FILE REFERENCE: 190106.405C1
; CURRENT APPLICATION NUMBER: US/09/270,957
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Staphylococcus homini
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)-(376)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-270-957-4

Query Match 45.6%; Score 36; DB 2; Length 376;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 EQQWNPFA 9
|||
Db 319 EQAWNFA 325

RESULT 47
US-09-270-957-19
; Sequence 19, Application US/09270957
; Patent No. 6641996
; GENERAL INFORMATION:
; APPLICANT: Richard A. Jefferson and Jorge E. Mayer
; TITLE OF INVENTION: MICROBIAL -GLUCURONIDASE GENES, GENE

; TITLE OF INVENTION: PRODUCTS, AND USES THEREOF
; FILE REFERENCE: 190106.405C1
; CURRENT APPLICATION NUMBER: US/09/270,957
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Staphylococcus homini
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(376)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-270-957-19

Query Match 45.6%; Score 36; DB 2; Length 376;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 EQOWNFA 9
DB 319 EQOWNFA 325

RESULT 48

US-09-902-540-9896
; Sequence 9896, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 9896
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-9896

Query Match 45.6%; Score 36; DB 2; Length 470;
Best Local Similarity 46.7%; Pred. No. 3.2e+02;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 MTEQOWNFAGIEAAA 15
DB 162 VAEQOWNFVRTOARA 176

RESULT 49

US-09-833-745-35
; Sequence 35, Application US/09833745
; Patent No. 6939541
; GENERAL INFORMATION:
; APPLICANT: ROBERTS, JOSEPH
; APPLICANT: SETHURAMAN, NATARAJAN
; APPLICANT: MACALLISTER, THOMAS
; TITLE OF INVENTION: CLONING, OVEREXPRESSION AND THERAPEUTIC USE OF
; TITLE OF INVENTION: BIOACTIVE HISTIDINE AMMONIA LYASE
; FILE REFERENCE: 078728/0106
; CURRENT APPLICATION NUMBER: US/09/833,745
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/197,770
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 35
; LENGTH: 511
; TYPE: PRT
; ORGANISM: Rhizobium meliloti
US-09-833-745-35

Query Match 45.6%; Score 36; DB 2; Length 511;
Best Local Similarity 53.3%; Pred. No. 3.5e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MTEQOWNFAGIEAAA 15
DB 430 MTENLFSIIGIEALA 444

RESULT 50

US-09-833-745-54
; Sequence 54, Application US/09833745
; Patent No. 6939541
; GENERAL INFORMATION:
; APPLICANT: ROBERTS, JOSEPH
; APPLICANT: SETHURAMAN, NATARAJAN
; APPLICANT: MACALLISTER, THOMAS
; TITLE OF INVENTION: CLONING, OVEREXPRESSION AND THERAPEUTIC USE OF
; TITLE OF INVENTION: BIOACTIVE HISTIDINE AMMONIA LYASE
; FILE REFERENCE: 078728/0106
; CURRENT APPLICATION NUMBER: US/09/833,745
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/197,770
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Rhizobium meliloti
US-09-833-745-54

Query Match 45.6%; Score 36; DB 2; Length 513;
Best Local Similarity 53.3%; Pred. No. 3.6e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MTEQOWNFAGIEAAA 15
DB 436 MTENLFSIIGIEALA 450

Search completed: May 4, 2006, 15:19:33
Job time : 41 secs

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OM protein - protein search, using sw model

Run on: May 4, 2006, 15:00:31 ; Search time 155 Seconds
(without alignments)
68.277 Million cell updates/sec

Title: US-09-830-839-1

Perfect score: 79

Sequence: 1 MTEQQWNFAGIEAAA 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	100.0	95	2	Q540D8 MYCTU
2	74	93.7	94	1	ESXA MYCBO
3	74	93.7	94	1	ESXA MYCTU
4	71	89.9	56	2	Q5G541 MYCUL
5	71	89.9	56	2	Q5G545 MYCUL
6	66	83.5	72	2	Q4VQH8 9MYCO
7	48	60.8	913	2	Q87WZ3 PSES
8	46	58.2	284	2	Q4J587 AZOVI
9	46	58.2	2151	2	Q5CXT8 CRVPV
10	45	57.0	230	2	Q5Y972 PLEOS
11	45	57.0	476	1	NOEA RHIME
12	45	57.0	476	2	Q6PW80 RHIME
13	45	57.0	913	2	Q4ZNZ8 PSES
14	45	57.0	4331	2	Q41YL2 AZOVI
15	43	54.4	217	2	Q9KMV8 VIBCH
16	43	54.4	247	2	Q8X3F8 EC057
17	43	54.4	770	2	Q5NGF1 FRATT
18	43	54.4	785	2	Q8DJE8 SYNECHOC
19	43	54.4	911	2	Q7WFT1 BORER
20	43	54.4	911	2	Q7W4C3 BORPA
21	43	54.4	911	2	Q7VUR2 BORPE
22	42	53.2	262	2	Q4K3D7 PSEF5
23	42	53.2	369	2	Q9Z839 CHLNP
24	42	53.2	384	2	Q7VPE24 CHLNP
25	42	53.2	539	1	G6P1 CAUCR
26	42	53.2	723	2	Q9A279 CAUCR
27	41.5	52.5	418	2	Q8PQM3 XANAC
28	41	51.9	98	2	Q5QWV0 IDILO
29	41	51.9	176	1	DSBB ECO57
30	41	51.9	176	1	DSBB ECOLI
31	41	51.9	182	2	P95622 RHILE

32	41	51.9	213	1	TRMB PROMA
33	41	51.9	217	2	Q8KU04 RHILV
34	41	51.9	248	2	Q83LH0 SHIFL
35	41	51.9	319	2	Q6ABJ4 PROAC
36	41	51.9	377	2	Q8H746 PHYCI
37	41	51.9	440	2	Q9FAD1 MORJA
38	41	51.9	443	2	Q9AMK7 VIBVU
39	41	51.9	444	2	Q5E343 VIBF1
40	41	51.9	445	2	Q8DAX6 VIBCH
41	41	51.9	445	2	Q8KV76 VIBCH
42	41	51.9	447	2	Q75VK9 VIBPA
43	41	51.9	447	2	Q87KT5 VIBPA
44	41	51.9	452	2	Q7MIY1 VIBVY
45	41	51.9	471	2	Q28786 ARCFU
46	41	51.9	601	2	Q4L323 STAUF
47	41	51.9	719	2	Q7UWA6 RHOB
48	41	51.9	903	2	Q7NQ59 CHRVO
49	41	51.9	934	2	Q8XVJ6 RALSO
50	41	51.9	947	2	Q4HUJ5 GIBZE
51	41	51.9	1249	2	Q7S114 NEUCR
52	41	51.9	1424	2	Q4P656 USTMA
53	41	50.6	38	2	Q9KTC4 VIBCH
54	40	50.6	99	2	Q5C050 SCHJA
55	40	50.6	176	1	DSBB ECOL6
56	40	50.6	176	1	DSBB SHIFL
57	40	50.6	265	2	Q5KZF9 GEOKA
58	40	50.6	295	2	Q8NR92 CORGL
59	40	50.6	328	2	Q5PQAL XENLA
60	40	50.6	333	2	Q4J4Y5 AZOVI
61	40	50.6	387	2	Q7V6M7 PROMM
62	40	50.6	403	2	Q6F9M3 ACIAD
63	40	50.6	419	2	Q7QF89 GIALA
64	40	50.6	495	2	Q4WZC2 ASPFU
65	40	50.6	495	2	Q4TKF3 SPFH
66	40	50.6	530	2	Q6D6L4 ERWCT
67	40	50.6	694	2	Q5FIS9 LACAC
68	40	50.6	802	2	Q62MR9 BURMA
69	40	50.6	818	2	Q63YK4 BURPS
70	40	50.6	939	2	Q88N69 PSEPK
71	40	50.6	925	2	Q5FRP7 GLUOX
72	39.5	50.0	329	2	Q87FK8 VIBPA
73	39.5	50.0	814	2	Q5DTV6 MOUSE
74	39.5	50.0	826	2	Q8BZ42 MOUSE
75	39	49.4	81	2	Q981F7 RHILV
76	39	49.4	158	2	Q5GV13 XANOR
77	39	49.4	158	2	Q8PQUL XANAC
78	39	49.4	164	2	Q5XV85 ARATH
79	39	49.4	172	2	Q89R01 BRAJA
80	39	49.4	199	2	Q87PV4 VIBPA
81	39	49.4	199	2	Q4T901 TETNG
82	39	49.4	212	2	Q5XV86 ARATH
83	39	49.4	219	1	TRMB ANASP
84	39	49.4	225	2	Q61QT9 CAEBR
85	39	49.4	230	2	Q4J668 AZOVI
86	39	49.4	231	2	Q4JAP2 CORJK
87	39	49.4	260	2	Q8G610 BIFLO
88	39	49.4	264	2	Q6AG55 LEIXX
89	39	49.4	270	1	LGT1 BACC1
90	39	49.4	270	1	LGT BACAN
91	39	49.4	270	1	LGT BACCR
92	39	49.4	270	1	LGT BACCC
93	39	49.4	270	1	LGT BACHX
94	39	49.4	270	2	Q4MLY5 BACCE
95	39	49.4	282	2	Q8RQLO PASPI
96	39	49.4	296	2	Q62CE8 BURMA
97	39	49.4	320	2	Q5BPL5 ARATH
98	39	49.4	320	2	Q5XV84 ARATH
99	39	49.4	325	2	Q966M0 CAEBL
100	39	49.4	328	1	LGT BORBU
101	39	49.4	328	1	LGT BORGA
102	39	49.4	329	2	Q8PPI4 XANAC
103	39	49.4	352	2	Q89KM1 BRAJA
104	39	49.4	393	2	Q8YTF8 ANASP

Q7vdu8	prochloroco
Q8ku04	rhizobium l
Q83lh0	shigella fl
Q6abj4	proionibac
Q8h746	phytophthor
Q9fad1	moritella j
Q9amk7	vibrio vuln
Q5e343	vibrio fisc
Q8dax6	vibrio vuln
Q8kv76	vibrio chol
Q75vk9	vibrio para
Q87kt5	vibrio para
Q7miy1	vibrio vuln
Q28786	archaeoglob
Q4l323	staphylococ
Q7uwa6	rhodopirell
Q7nc59	chromobacte
Q8xvj6	ralstonia s
Q4hujs	gibberella
Q7s114	neurospora
Q4p656	ustilago ma
Q9krc4	vibrio chol
Q5c050	schistosoma
P59343	escherichia
Q54155	shigella fl
Q8nr92	geobacillus
Q5pqal	corynebacte
Q4j4y5	xenopus lae
Q7v6m7	azotobacter
Q6f9m3	prochloroco
Q7qf89	giardia lam
Q4wzc2	aspergillus
Q4tkf3	erythrobact
Q6d6l4	erwinia car
Q5f1s9	lactobacill
Q62mr9	burkholderi
Q63yk4	burkholderi
Q88n69	pseudomonas
Q5frp7	gluconobact
Q87fk8	vibrio para
Q5dtv6	mus musculu
Q8bz42	mus musculu
Q981f7	rhizobium l
Q5gv13	xanthomonas
Q8pqul	xanthomonas
Q5xv85	arabidopsis
Q89r01	bradyrhizob
Q87pv4	vibrio para
Q4t901	tetradodon n
Q5xv86	arabidopsis
Q8yvx4	anabaena sp
Q61qt9	caenorhabdi
Q4j668	azotobacter
Q4jap2	corynebacte
Q8g610	bifidobacte
Q6ag55	leifsonia x
Q72xv7	bacillus ce
Q81x52	bacillus an
Q81517	bacillus ce
Q631j1	bacillus ce
Q6hbc7	bacillus th
Q4mbc7	bacillus ce
Q8rgl0	pasteurella
Q62ce8	burkholderi
Q5bpl5	arabidopsis
Q5xv84	arabidopsis
Q966m0	caenorhabdi
Q51337	borrelia bu
Q661q7	borrelia ga
Q89kml	bradyrhizob
Q8ytf8	anabaena sp

105	39	49.4	418	1	PGK_PORGI	Q7mu77 porphyron	178	38	48.1	443	2	Q8ZN34_SALTY	Q8zn34 salmonella
106	39	49.4	428	2	Q4LS94_9BURK	Q4ls94 burkholderi	179	38	48.1	444	1	CADB_ECOLI	P23891 escherichia
107	39	49.4	444	2	Q6F223_MESFL	Q6f223 mesophilasma	180	38	48.1	444	2	Q7BA92_ECOLI	P23891 escherichia
108	39	49.4	447	2	Q4HN80_CAMLA	Q4hn80 campylobact	181	38	48.1	454	2	Q8H749_PHYCH	Q8h749 phytochlor
109	39	49.4	470	2	Q605J9_METCA	Q605j9 methylococc	182	38	48.1	454	2	Q83W84_ECOLI	Q83w84 escherichia
110	39	49.4	474	2	Q5E4B6_VIBFL	Q5e4b6 vibrio fisc	183	38	48.1	455	2	Q8N833_HUMAN	Q8n833 homo sapien
111	39	49.4	480	2	Q73J30_TREDE	Q73j30 treponema d	184	38	48.1	460	2	Q4P876_USTMA	Q4p876 ustilago ma
112	39	49.4	482	2	Q4KDE4_PSEFS	Q4kde4 pseudomonas	185	38	48.1	508	1	HMC52_PIG	Q02734 sus scrofa
113	39	49.4	557	2	Q4KDE4_PSEFS	Q4kde4 pseudomonas	186	38	48.1	524	2	Q4RTP5_TETNG	Q4rtf5 tetraodon n
114	39	49.4	598	2	Q8M0N2_STRAS	Q8m0n2 streptococc	187	38	48.1	525	2	Q5P8K4_AZOSE	Q5p8k4 azocarcus sp
115	39	49.4	599	2	Q8S6A6_STR3	Q8s6a6 streptococc	188	38	48.1	526	2	Q54P61_DICDI	Q54p61 dictyostell
116	39	49.4	667	2	Q4IM95_GIBZE	Q4im95 gibberella	189	38	48.1	535	2	Q5N2P5_SYNP6	Q5n2f5 synecchococ
117	39	49.4	714	2	Q9KSHI_LACLC	Q9kshi lactococcus	190	38	48.1	543	2	Q59TQ8_CANAL	Q59tq8 candida alb
118	39	49.4	714	2	Q9KSHI_LACLC	Q9kshi lactococcus	191	38	48.1	549	2	Q6CVA7_KLUJA	Q6cvx7 kluyveromyc
119	39	49.4	785	2	Q4I544_GIBZE	Q4i544 gibberella	192	38	48.1	568	2	Q759E1_ASHGO	Q759e1 ashbya goss
120	39	49.4	804	2	Q75RX8_9ACTO	Q75rx8 streptomyce	193	38	48.1	579	2	Q59TM6_ORYSA	Q59tm6 oryza sativ
121	39	49.4	834	2	Q58612_9IRYP	Q58612 trypanosoma	194	38	48.1	633	2	Q59TM6_CANAL	Q59tm6 candida alb
122	39	49.4	860	2	Q7UX43_RHOBA	Q7ux43 rhodospirell	195	38	48.1	643	2	Q4WCV2_ASPFU	Q4wcv2 aspergillus
123	39	49.4	861	2	Q7SLW6_NEUCR	Q7slw6 neurospora	196	38	48.1	650	2	Q8N9W4_HUMAN	Q8n9w4 homo sapien
124	39	49.4	909	2	Q8W866_NITEU	Q8w866 nitrosomona	197	38	48.1	651	1	DREB_CHICK	F18302 gallus gall
125	39	49.4	910	2	Q6ARD6_DESPS	Q6ard6 desulfotale	198	38	48.1	651	2	Q6BMH9_DEBHA	Q6bmh9 debaryomyce
126	39	49.4	916	2	Q9LCT3_PSEAE	Q9lct3 pseudomonas	199	38	48.1	691	2	Q5KYI6_GEOKA	Q5kyi6 geobacillus
127	39	49.4	957	2	Q4IYH5_AZOVI	Q4iyh5 azotobacter	200	38	48.1	718	2	Q8A6K3_BACTN	Q8a6k3 bacteroides
128	39	49.4	971	2	Q6G301_BARHE	Q6g301 bartonella	201	38	48.1	735	2	Q4HV00_GIBZE	Q4hv00 gibberella
129	39	49.4	971	2	Q6G301_BARHE	Q6g301 bartonella	202	38	48.1	806	2	Q9P478_AGABI	Q9p4t8 agarcus bi
130	38.5	48.7	372	2	Q98BQ8_RHILO	Q98bq8 rhizobium l	203	38	48.1	885	2	Q46002_CLOCE	Q46002 clostridium
131	38.5	48.7	392	2	Q9A560_CAUCR	Q9a560 caulobacter	204	38	48.1	886	2	Q65V86_MAMSM	Q65v86 manheimia
132	38.5	48.7	418	2	Q5GUK7_XANOR	Q5guk7 xanthomonas	205	38	48.1	907	2	Q5F705_AZOSE	Q5f705 azocarcus sp
133	38.5	48.7	418	2	Q4UZZ4_XANCP	Q4uzz4 xanthomonas	206	38	48.1	909	2	Q4XQF6_ORISA	Q4xqt6 oryza sativ
134	38.5	48.7	418	2	Q8PDQ2_XANCP	Q8pdq2 xanthomonas	207	38	48.1	913	2	Q4K7C1_PSEFS	Q4k7c1 pseudomonas
135	38.5	48.7	569	2	Q880E0_PSESM	Q880e0 pseudomonas	208	38	48.1	969	2	Q5ZEM7_MAGGR	Q5zem7 magnaporthe
136	38.5	48.7	905	2	Q4WAZ0_ASPFU	Q4waz0 aspergillus	209	38	48.1	996	2	Q6MKL4_DDEBA	Q6mk14 bdellovibri
137	38	48.1	82	2	Q74H51_GROSJ	Q74h51 geobacter s	210	38	48.1	1018	2	Q89CC0_BRAJA	Q89cc0 bradyrhizob
138	38	48.1	109	2	Q5P669_AZOSE	Q5p669 azocarcus sp	211	38	48.1	1201	2	Q5BH35_EMENI	Q5bh35 aspergillus
139	38	48.1	142	2	Q8FMW9_COREP	Q8fmw9 corynebacte	212	38	48.1	1962	2	Q4RQW3_TETNG	Q4rqw3 tetraodon n
140	38	48.1	147	2	Q8G8S5_ECOLI	Q8g8s5 escherichia	213	38	48.1	2002	2	Q71S06_HUMAN	Q71s06 homo sapien
141	38	48.1	192	1	RLJ_MOLSU	Q7m844 wolinnella s	214	38	48.1	2555	2	Q91ZB6_MOUSE	Q91ze6 mus musculu
142	38	48.1	219	2	Q525T4_LEGPH	Q52st4 legionella s	215	38	48.1	2561	2	Q8VIB5_MOUSE	Q8vte5 mus musculu
143	38	48.1	240	2	Q528B8_MAGGR	Q528b8 magnaporthe	216	38	48.1	2564	1	SPTN4_HUMAN	Q91te8 homo sapien
144	38	48.1	273	2	Q5WL32_EACSK	Q5wl32 bacillus cl	217	38	48.1	2644	2	Q6RK12_BOTCI	Q6rk12 botrytis ci
145	38	48.1	278	2	Q5LW71_SILPO	Q5lw71 silicibacte	218	38	48.1	156	2	Q63M41_BURPS	Q63mk1 burkholderi
146	38	48.1	282	2	Q9R6G8_9RHI2	Q9r6g8 agrobacteri	219	37.5	47.5	156	2	Q4V2R5_BURMA	Q4v2r5 burkholderi
147	38	48.1	284	2	Q9PHE6_XYLFA	Q9phe6 xyliella fas	220	37.5	47.5	727	2	Q4V9H9_BRARE	Q4v9h9 brachydano
148	38	48.1	297	2	Q8UD90_AGRTS	Q8ud90 agrobacteri	221	37.5	47.5	1385	2	Q53P77_ORYSA	Q53p77 oryza sativ
149	38	48.1	297	2	Q5X294_LEGPA	Q5x294 legionella	222	37.5	47.5	1385	2	Q8X302_SCO57	Q8x3q2 escherichia
150	38	48.1	301	2	Q8NL92_CORGL	Q8nl92 corynebacte	223	37	46.8	161	2	Q8TTE1_METAC	Q8tte1 methanosarc
151	38	48.1	305	1	Y2345_DETRA	Q9rry7 deinococcus	224	37	46.8	168	2	Q5E0P0_VIBP1	Q5e0p0 vibrio fisc
152	38	48.1	306	2	Q5N329_SYNP6	Q5n329 synecchococ	225	37	46.8	138	2	Q5YNM9_NOCFA	Q5ymn9 nocardia fa
153	38	48.1	319	2	Q7CXJ8_AGRTS	Q7cxj8 agrobacteri	226	37	46.8	156	2	Q93DB5_STRMU	Q93db5 streptococc
154	38	48.1	328	2	Q41401_SESRO	Q41401 sesbania ro	227	37	46.8	161	2	Q88XK8_LACPL	Q88xk8 lactobacill
155	38	48.1	330	2	Q69NE3_ORYSA	Q69ne3 oryza sativ	228	37	46.8	171	2	Q8D8P1_VIBVU	Q8d8p1 vibrio vuln
156	38	48.1	339	2	Q6ZV89_HUMAN	Q6zv89 homo sapien	229	37	46.8	179	2	Q8D483_VIBVU	Q8d483 vibrio vuln
157	38	48.1	341	2	Q5R732_PONPY	Q5r732 pongo pygma	230	37	46.8	187	2	Q7MLT8_VIBVY	Q7mlt8 vibrio vuln
158	38	48.1	345	2	Q7WUHO_ESCHIC	Q7wuh0 escherichia	231	37	46.8	192	2	Q7MFO9_VIBVY	Q7mf09 vibrio vuln
159	38	48.1	350	2	Q7UAM4_SHIFL	Q7uam4 shigella fl	232	37	46.8	201	2	Q8AR41_9HIVI	Q8ar41 human immun
160	38	48.1	350	2	Q83P45_SHIFL	Q83p45 shigella fl	233	37	46.8	201	2	Q8AR44_9HIVI	Q8ar44 human immun
161	38	48.1	354	2	Q4PH75_USTMA	Q4ph75 ustilago ma	234	37	46.8	202	2	Q8AS06_9HIVI	Q8as06 human immun
162	38	48.1	364	2	Q4P019_USTMA	Q4p019 ustilago ma	235	37	46.8	202	2	Q7MJN6_VIBVY	Q7mjn6 vibrio vuln
163	38	48.1	369	2	Q51VY2_MAGGR	Q51vy2 magnaporthe	236	37	46.8	202	2	Q8AR55_9HIVI	Q8ar55 human immun
164	38	48.1	377	2	Q64HC5_CONST	Q64hc5 corynebacte	237	37	46.8	202	2	Q8AR64_9HIVI	Q8ar64 human immun
165	38	48.1	388	1	ALGJ_AZOVI	Q52197 azotobacter	238	37	46.8	202	2	Q8AR64_9HIVI	Q8ar64 human immun
166	38	48.1	388	2	Q41X38_AZOVI	Q41x38 azotobacter	239	37	46.8	202	2	Q8AR80_9HIVI	Q8ar80 human immun
167	38	48.1	393	2	Q9EWU0_STRCO	Q9ewu0 streptomyce	240	37	46.8	204	2	Q8AR87_9HIVI	Q8ar87 human immun
168	38	48.1	394	2	Q4HPA6_CAMUP	Q4hpa6 campylobact	241	37	46.8	204	2	Q8AR87_9HIVI	Q8ar87 human immun
169	38	48.1	405	2	Q89JB7_BRADRH	Q89jb7 bradyrhizob	242	37	46.8	204	2	Q8AR87_9HIVI	Q8ar87 human immun
170	38	48.1	415	2	Q92Q05_RHIME	Q92q05 rhizobium m	243	37	46.8	204	2	Q8AR87_9HIVI	Q8ar87 human immun
171	38	48.1	420	2	Q4J410_AZOVI	Q4j410 azotobacter	244	37	46.8	205	2	Q8AR87_9HIVI	Q8ar87 human immun
172	38	48.1	435	2	Q4KEZ7_PSEFS	Q4kez7 pseudomonas	245	37	46.8	205	2	Q8AR87_9HIVI	Q8ar87 human immun
173	38	48.1	437	2	Q5SSJ2_HUMAN	Q5ssj2 homo sapien	246	37	46.8	205	2	Q8AR87_9HIVI	Q8ar87 human immun
174	38	48.1	438	1	SGCE_HUMAN	Q43556 homo sapien	247	37	46.8	205	2	Q8AR87_9HIVI	Q8ar87 human immun
175	38	48.1	443	2	Q5PIH7_SALCH	Q5pih7 salmonella	248	37	46.8	205	2	Q8AR87_9HIVI	Q8ar87 human immun
176	38	48.1	443	2	Q8Z4M1_SALTI	Q8z4m1 salmonella	249	37	46.8	211	1	TRMB_STNY3	P75161 synecchocyst
177	38	48.1	443	2	Q8Z4M1_SALTI	Q8z4m1 salmonella	250	37	46.8				

251	37	46.8	217	2	Q75AX4_ASHGO	Q75AX4_ashbya goss	324	37	46.8	499	2	Q8FC60_ECOL6	Q8fc60 escherichia
252	37	46.8	218	2	Q4NUG9_9DELTA	Q4nug9 anaeromyxob	325	37	46.8	517	2	Q8G678_LEIDO	Q8g678 leishmania
253	37	46.8	219	2	Q95V33_SPOPR	Q95v33 spodoptera	326	37	46.8	517	2	Q4FW28_LEIMA	Q4fw28 leishmania
254	37	46.8	220	2	Q6G7L6_STAAR	Q6g7l6 staphylococ	327	37	46.8	522	2	Q599J4_9ROSI	Q599j4 populus alb
255	37	46.8	221	2	Q6GEY1_STAAR	Q6gey1 staphylococ	328	37	46.8	522	2	Q7PBJ6_FUSNV	Q7pbj6 fusobacteri
256	37	46.8	222	2	Q5HEA5_STAAR	Q5hea5 staphylococ	329	37	46.8	524	2	Q7U475_SYNPX	Q7u475 synechococc
257	37	46.8	223	2	Q7A0C8_STAAR	Q7a0c8 staphylococ	330	37	46.8	526	2	Q9K574_9LACT	Q9k574 lactococcus
258	37	46.8	224	2	Q7A4F3_STAAR	Q7a4f3 staphylococ	331	37	46.8	527	2	Q9KVB5_VIBCH	Q9kvb5 vibrio chol
259	37	46.8	225	2	Q99SG3_STAAR	Q99sg3 staphylococ	332	37	46.8	530	2	Q41FF3_GIBZE	Q41ff3 gibberella
260	37	46.8	226	2	Q6MJG2_BDEBA	Q6mjg2 bdellovibri	333	37	46.8	534	2	Q55QL9_CRYNE	Q55ql9 cryptococcu
261	37	46.8	227	1	RL3_BRJVA	Q89j84 bradyrhizob	334	37	46.8	534	2	Q5KEJ6_CRYNE	Q5kej6 cryptococcu
262	37	46.8	228	1	RL3_RHOFA	R60456 rhodopseudo	335	37	46.8	540	2	Q8XPJ8_RALSO	Q8xpj8 ralstonia s
263	37	46.8	229	1	Q7MAW1_PORGI	Q7maw1 porphyromon	336	37	46.8	545	2	Q6B358_9PROT	Q6b358 uncultured
264	37	46.8	230	2	Q5F7A3_NEIG1	Q5f7a3 neisseria g	337	37	46.8	545	2	Q8RHQ6_FUSNN	Q8rhq6 fusobacteri
265	37	46.8	231	2	Q9JTB7_NEIMA	Q9jtb7 neisseria m	338	37	46.8	567	2	Q6N3E4_RHOPA	Q6n3e4 rhodopseudo
266	37	46.8	232	2	Q9JVE0_NEIMB	Q9jve0 neisseria m	339	37	46.8	573	2	Q9PA14_XYLFA	Q9pa14 xylella fas
267	37	46.8	233	2	Q32816_LACLC	Q32816 lactococcus	340	37	46.8	582	2	Q5F714_NEIG1	Q5f714 neisseria g
268	37	46.8	234	1	RL3_CAUCR	Q9a8v3 caulobacter	341	37	46.8	582	2	Q9JY58_NEIMB	Q9jy58 neisseria m
269	37	46.8	235	1	Q8YA41_LISMO	Q8ya41 listeria mo	342	37	46.8	585	2	Q9JY41_NEIMA	Q9jy41 neisseria m
270	37	46.8	236	2	Q723Y4_LISMF	Q723y4 listeria mo	343	37	46.8	600	2	Q5FNP6_GLOUX	Q5fnp6 gluconobact
271	37	46.8	237	2	Q92EW0_LISIN	Q92ew0 listeria in	344	37	46.8	640	1	AEC33_ARATH	Q9s7z8 arabidopsis
272	37	46.8	238	1	COMT_RAT	P22734 rattus norv	345	37	46.8	642	1	SYT_PHOLL	Q7n3p6 photorhabdu
273	37	46.8	239	2	Q5QBX2_9CAUD	Q5qbx2 enterobacte	346	37	46.8	668	1	UF01_YEAST	Q04511 saccharomyc
274	37	46.8	240	1	G3P_ESCBL	P24749 escherichia	347	37	46.8	676	2	Q5AYG3_EMENI	Q5ayg3 aspergillus
275	37	46.8	241	2	Q94A57_ARATH	Q94a57 arabidopsis	348	37	46.8	735	2	Q5NLH1_ZYMMO	Q5nlh1 zymomonas m
276	37	46.8	242	2	Q5GXR9_XANOR	Q5gx9 arabidomonas	349	37	46.8	739	2	Q82K30_STRAW	Q82k30 streptomyce
277	37	46.8	243	2	Q5LRN5_ARATH	Q5lrn5 arabidopsis	350	37	46.8	743	2	Q4UIF0_THEAN	Q4uif0 theileria a
278	37	46.8	244	2	Q8GHV5_PSERE	Q8ghv5 pseudomonas	351	37	46.8	751	2	Q5W116_BACSK	Q5w116 bacillus cl
279	37	46.8	245	2	Q7KQV8_DROME	Q7kqv8 drosophila	352	37	46.8	768	2	Q6DJF4_ERWCT	Q6djf4 erwina car
280	37	46.8	246	2	Q4UWC7_XANCP	Q4uwc7 xanthomonas	353	37	46.8	779	2	Q4N763_THEPA	Q4n763 theileria p
281	37	46.8	247	2	Q8P7S3_XANCP	Q8p7s3 xanthomonas	354	37	46.8	784	2	Q4RLU8_TSTNG	Q4rlu8 tetraodon n
282	37	46.8	248	2	Q8PJ32_XANAC	Q8pj32 xanthomonas	355	37	46.8	785	2	Q7NH88_GLOVI	Q7nh88 gloeobacter
283	37	46.8	249	2	Q46061_CORGL	Q46061 corynebacte	356	37	46.8	793	1	PHK_RHOBA	Q7uh14 rhodopirell
284	37	46.8	250	2	Q8NN95_CORGL	Q8nn95 corynebacte	357	37	46.8	850	2	Q6C8F7_YARLI	Q6c8f7 yarrowia li
285	37	46.8	251	2	Q4UIP9_XANCP	Q4uip9 xanthomonas	358	37	46.8	865	2	Q5FTV3_GLUOX	Q5ftv3 gluconobact
286	37	46.8	252	2	Q8P5C3_XANCP	Q8p5c3 xanthomonas	359	37	46.8	879	1	SYL_XYLFA	Q7q6t9 anopheles g
287	37	46.8	253	1	YD59_SCHPO	Q10312 schizosacch	360	37	46.8	890	2	Q7Q6T9_ANOGA	Q7q6t9 anopheles g
288	37	46.8	254	2	Q8RL66_PSEFL	Q8rl66 pseudomonas	361	37	46.8	912	2	Q4UQX9_XANCP	Q4uqx9 xanthomonas
289	37	46.8	255	2	Q8YLE1_ANASP	Q8yle1 anaebana sp	362	37	46.8	912	2	Q8PCJ2_XANCP	Q8pcj2 xanthomonas
290	37	46.8	256	2	Q9TPA7_XENLA	Q9tpa7 xenopus lae	363	37	46.8	912	2	Q8PPA0_XANAC	Q8ppa0 xanthomonas
291	37	46.8	257	2	Q7MAJ8_WOLSU	Q7maj8 wolfinella s	364	37	46.8	955	2	Q8G5M4_BIFLO	Q8g5m4 bifidobacte
292	37	46.8	258	1	WNT11_BRARE	Q73864 brachydanio	365	37	46.8	964	2	Q4HW63_GIBZE	Q4hw63 gibberella
293	37	46.8	259	2	Q6IN11_XENLA	Q6ini1 xenopus lae	366	37	46.8	1049	2	Q5VR20_ORVSA	Q5vr20 oryza sativ
294	37	46.8	260	2	Q4V826_XENLA	Q4v826 xenopus lae	367	37	46.8	1093	2	Q55KP7_CRYNE	Q55kp7 cryptococcu
295	37	46.8	261	1	GURAB_SULSO	Q97t28 sulfolobus	368	37	46.8	1093	2	Q5KAS9_CRYNE	Q5kas9 cryptococcu
296	37	46.8	262	2	Q7WTD8_CORGL	Q7wyd8 corynebacte	369	37	46.8	1150	2	Q5OND1_ENTHI	Q5ond1 entamoeba h
297	37	46.8	263	2	Q93QC6_CORGL	Q93qc6 corynebacte	370	37	46.8	1152	2	Q4SEW8_TETNG	Q4sew8 tetraodon n
298	37	46.8	264	2	Q8FND3_COREF	Q8fnd3 corynebacte	371	37	46.8	1173	2	Q4IMT5_GIBZE	Q4imt5 gibberella
299	37	46.8	265	2	Q5L6N8_CHLAB	Q5l6n8 chlamydophi	372	37	46.8	1210	2	Q82Z55_ENTFA	Q82z55 enterococcu
300	37	46.8	266	2	Q7U0S8_MYCBO	Q7u0s8 mycobacteri	373	37	46.8	2477	2	Q9WJD1_9VIRU	Q9wj11 venezuelan
301	37	46.8	267	2	Q824C3_CHLCV	Q824c3 chlamydophi	374	37	46.8	2607	2	Q7QP43_GIALA	Q7qp43 giardia lam
302	37	46.8	268	2	P96353_MYCTU	P96353 mycobacteri	375	36.5	46.2	165	2	Q9AVE8_BRACM	Q9ave8 brassica ca
303	37	46.8	269	2	Q988C3_RHILO	Q988c3 rhizobium l	376	36.5	46.2	250	2	Q5NMF8_ZYMMO	Q5nmf8 zymomonas m
304	37	46.8	270	2	Q8SV17_ENCCU	Q8sv17 encephalito	377	36.5	46.2	255	2	Q4Q9W2_LEIMA	Q4q9w2 leishmania
305	37	46.8	271	2	Q4FXV8_LEIMA	Q4fxv8 leishmania	378	36.5	46.2	255	2	Q7W6Y6_BORPA	Q7w6y6 bordetella
306	37	46.8	272	1	ADIC_ECOL5	P60064 shigella fl	379	36.5	46.2	380	2	Q7WIX3_BORBR	Q7wix3 bordetella
307	37	46.8	273	1	ADIC_ECOL6	P60062 escherichia	380	36.5	46.2	421	2	Q4LRN9_9BURK	Q4lrn9 burkholderi
308	37	46.8	274	1	ADIC_ECOL1	P60061 escherichia	381	36.5	46.2	444	2	Q5UWP8_HALMA	Q5uwp8 haloarcula
309	37	46.8	275	1	ADIC_SALT1	P60065 salmonella	382	36.5	46.2	592	2	Q7SY37_ERARE	Q7sy37 brachydanio
310	37	46.8	276	1	ADIC_SALT1	P60066 salmonella	383	36.5	46.2	598	2	Q8PRD7_XANAC	Q8prd7 xanthomonas
311	37	46.8	277	1	ADIC_SHIFL	P60064 shigella fl	384	36.5	46.2	667	2	Q5B3H6_EMENI	Q5b3h6 aspergillus
312	37	46.8	278	2	Q57GT3_SALCH	Q57gt3 salmonella	385	36.5	46.2	882	1	DM11_MEDTR	Q6hrh6 medicago tr
313	37	46.8	279	2	Q9PJ24_SALPA	Q9pj24 salmonella	386	36.5	46.2	893	2	Q6MEAO_PARUM	Q6meao parachlamyd
314	37	46.8	280	2	Q9KGV3_LACLA	Q9kgv3 lactococcus	387	36.5	46.2	1000	2	Q728I7_DESVH	Q728i7 desulfovibr
315	37	46.8	281	2	Q52DM6_MAGGR	Q52dm6 magnaporthe	388	36.5	46.2	59	2	Q5BSH4_SCHJA	Q5bsh4 schistosoma
316	37	46.8	282	2	Q60414_METCA	Q60414 metcyclothe	389	36	45.6	75	2	Q7PTN0_ANOGA	Q7ptn0 anopheles g
317	37	46.8	283	2	Q82D65_STRAW	Q82d65 streptomyce	390	36	45.6	75	2	Q5OWP1_ENTHI	Q5owp1 entamoeba h
318	37	46.8	284	2	Q562K7_LACRE	Q562k7 lactobacill	391	36	45.6	75	2	Q6ARU4_DESPS	Q6aru4 desulfofale
319	37	46.8	285	2	Q6FIP9_MESFL	Q6fip9 mesoplasma	392	36	45.6	87	2	Q7O867_9SYLV	Q7o867 acrocephalu
320	37	46.8	286	1	GUNA_CLOCE	P17901 clostridium	393	36	45.6	90	2	Q86OD1_9SYLV	Q86od1 acrocephalu
321	37	46.8	287	2	G6CAQ2_YARLI	Q6caq2 yarrowia li	394	36	45.6	90	2	Q86OD4_9SYLV	Q86od4 acrocephalu
322	37	46.8	288	2	Q9CE15_LACLA	Q9ce15 lactococcus	395	36	45.6	91	2	Q86OD0_9SYLV	Q86od0 acrocephalu
323	37	46.8	289	2	Q9CE19_LACLA	Q9ce19 lactococcus	396	36	45.6				

397	36	45.6	102	2	Q50BZ7_9CAUD	Q5qbz7 enterobacte	470	36	45.6	368	2	Q9ALR3_PSEFL	Q9alr3 pseudomonas
398	36	45.6	102	2	P96Z76_MYCTU	P96z76 mycobacteri	471	36	45.6	370	1	GUAB SULTO	Q96y23 sulfolobus
399	36	45.6	102	2	Q7U205_MYCBO	Q7u205 mycobacteri	472	36	45.6	373	2	Q4JBK0_SULAC	Q4jbk0 sulfolobus
400	36	45.6	102	2	Q9CB14_MYCBL	Q9cb14 mycobacteri	473	36	45.6	380	2	Q5QV96_IDILO	Q5qv96 idiomarina
401	36	45.6	109	2	Q9VJ25_DROME	Q9vj25 drosophila	474	36	45.6	383	2	Q6NF15_CORDI	Q6nfi5 corynebacte
402	36	45.6	111	2	Q4UV15_XANCP	Q4uv15 xanthomonas	475	36	45.6	387	2	Q5ZIX6_CHICK	Q5zix6 gallus gall
403	36	45.6	120	2	Q8F323_LEFIN	Q8f323 leptospira	476	36	45.6	389	2	Q6J3J0_BURPS	Q63j0 burkholderi
404	36	45.6	120	2	Q7ZS1F_LEPIC	Q7zs1f leptospira	477	36	45.6	393	2	Q8BQ14_MOUSE	Q8bq14 mus muscu
405	36	45.6	131	1	INEN_SHIDI	P03832 shigella dy	478	36	45.6	395	2	Q8SVAI_ARATH	Q8svai arabidopsis
406	36	45.6	131	2	Q9LA25_SHIDY	Q9la25 shigella dy	479	36	45.6	404	2	Q6NSW5_RHOPA	Q6nsw5 rhodopseu
407	36	45.6	131	2	Q9LA39_SHIDY	Q9la39 shigella dy	480	36	45.6	404	2	Q5PL64_SALPA	Q5pl64 salmoneila
408	36	45.6	135	2	Q7BQ94_SHIDY	Q7bq94 shigella dy	481	36	45.6	411	2	Q8B8U1_SHEON	Q8b8u1 shewabacte
409	36	45.6	135	2	Q6GAU9_BARHE	Q6gau9 bartonella	482	36	45.6	413	2	Q57GP9_SALCH	Q57gp9 bradyrhizob
410	36	45.6	136	2	Q9C2Q5_NEUCR	Q9c2q5 neuropepsa	483	36	45.6	413	2	Q89LS8_BRAJA	Q89ls8 bradyrhizob
411	36	45.6	146	2	Q48381_KLEAE	Q48381 klebsiella	484	36	45.6	413	2	Q8Z1A4_SALTY	Q8z1a4 salmoneila
412	36	45.6	147	2	Q92KG3_RHIME	Q92kg3 rhizobium m	485	36	45.6	413	2	Q8ZKAO_SALTY	Q8zka0 salmoneila
413	36	45.6	148	1	HPCK_ECOLI	P62573 escherichia	486	36	45.6	419	2	Q8GH19_9BURK	Q8gh19 pseudomon
414	36	45.6	170	2	Q7D9U1_MYCTU	P62574 shigella fl	487	36	45.6	424	2	Q5B236_EMENI	Q5b236 pigmentipha
415	36	45.6	170	2	Q8BHF9_SHEON	Q8bhf9 mycobacteri	488	36	45.6	424	2	Q84UD0_BRAOL	Q84ud0 brassica ol
416	36	45.6	170	2	Q6DQC4_ERWCT	Q6dqc4 shewanella	489	36	45.6	424	2	Q4V0B0_XANCP	Q4v0b0 xanthomonas
417	36	45.6	174	2	Q8EW79_MYCPE	Q8ew79 mycoplasma	490	36	45.6	427	2	Q8PE16_XANCP	Q8pe16 xanthomonas
418	36	45.6	174	2	RES18_FAT	P47940 rattus norv	491	36	45.6	427	2	Q8PQ4_XANAC	Q8pq4 xanthomonas
419	36	45.6	177	2	Q6NAS8_RHOPA	Q6nas8 rhodopseu	492	36	45.6	429	1	EXG_KLULA	Q12628 kluyveromyc
420	36	45.6	179	2	Q62P74_BACLD	Q62p74 bacillus li	493	36	45.6	430	1	PYRC_LACPL	P77884 lactobacill
421	36	45.6	180	2	Q6SDQ2_BACLD	Q6sdq2 bacillus li	494	36	45.6	432	2	Q4IB05_GIBZE	Q4ib05 gibberella
422	36	45.6	185	2	Q4WAG6_PLACH	Q4wad6 plasmodium	495	36	45.6	441	2	Q7WKY5_BORBR	Q7wky5 bordetella
423	36	45.6	185	2	Q4ETW8_COREQ	Q4etw8 corynebacte	496	36	45.6	441	1	ADIC_YERPE	Q2zg99 yersinia pe
424	36	45.6	187	2	Q8US28_MIDDV	Q8us28 middelburg	497	36	45.6	444	2	Q6GD09_YERPS	Q6gd09 yersinia ps
425	36	45.6	190	2	Q8SET6_VIRU	Q8set6 cyanophage	498	36	45.6	444	2	Q83CC1_COXBU	Q83cc1 coxiella bu
426	36	45.6	192	1	TRME_PROMP	Q88tc6 enterobacte	499	36	45.6	448	2	Q5SHMT_THET8	Q5shmt thermus the
427	36	45.6	209	1	RL3_WIGBR	Q88tc6 enterobacte	500	36	45.6	451	2	Q72H23_THET2	Q72h23 thermus the
428	36	45.6	215	1	Q9T7X2_9SAUR	Q9t7x2 wiggleswort	501	36	45.6	451	2	Q85Y06_DROME	Q85y06 drosophila
429	36	45.6	221	2	Q4ICC4_GIBZE	Q9t7x2 wiggleswort	502	36	45.6	459	2	Q8VSR0_DROME	Q8vsr0 drosophila
430	36	45.6	225	2	Q4L7X6_STAHL	Q9t7x2 wiggleswort	503	36	45.6	459	2	Q5NGP5_FRATT	Q5ngp5 franciella
431	36	45.6	229	2	Q62P74_BACLD	Q9t7x2 wiggleswort	504	36	45.6	464	2	Q4STW2_TETNG	Q4stw2 tetraodon n
432	36	45.6	230	1	Q6SDQ2_BACLD	Q9t7x2 wiggleswort	505	36	45.6	464	2	Q5NGP5_FRATT	Q5ngp5 franciella
433	36	45.6	237	2	Q4XIF7_PLACH	Q4ixf7 plasmodium	506	36	45.6	466	1	Q6TK71_STRRT	Q6tk71 streptococc
434	36	45.6	237	2	Q99617_SARGL	Q99617 sarcophyton	507	36	45.6	469	2	Q5CP91_PASMU	Q5cp91 pasceucella
435	36	45.6	238	2	Q8UKG9_AGRT5	Q8ukg9 agrobacteri	508	36	45.6	470	2	Q5GU60_XANOR	Q5gu60 xanthomonas
436	36	45.6	247	2	Q565X5_9BACT	Q565x5 uncultured	509	36	45.6	473	2	ARCD_LACSK	Q53092 lactobacill
437	36	45.6	250	2	Q6MNP3_BDEBA	Q6mp3 bdellovibri	510	36	45.6	475	1	Q8CJZM_MOUSE	Q8cjzm mus musculu
438	36	45.6	252	2	Q7N285_PHOLL	Q7n285 photorhabd	511	36	45.6	486	2	Q57C73_BRUAB	Q57c73 brucella me
439	36	45.6	253	2	Q5PAG3_ANAMM	Q5pag3 anaplasma m	512	36	45.6	488	1	MURE_BRUSU	Q9y171 brucella su
440	36	45.6	260	2	Q6FZB6_BARQU	Q6fzb6 bartonella	513	36	45.6	488	2	Q92V88_RHIME	Q92v88 rhizobium m
441	36	45.6	260	2	Q8A411_BACTN	Q8a411 bartonella	514	36	45.6	493	2	SRMS_MOUSE	Q82v88 rhizobium m
442	36	45.6	267	2	Q8A411_BACTN	Q8a411 bartonella	515	36	45.6	496	1	Q8S5N3_ORYSA	Q8s5n3 oryza sativ
443	36	45.6	272	2	Q6ZV82_HUMAN	Q6zv82 homo sapien	516	36	45.6	496	2	Q583L3_9TRYP	Q583l3 trypanosoma
444	36	45.6	288	2	Q64629_ARNTH	Q64629 arabidopsis	517	36	45.6	509	2	Q6LHL4_PHOPR	Q6lhl4 photobacter
445	36	45.6	289	2	Q88CP2_PSEPK	Q88cp2 pseudomonas	518	36	45.6	510	2	Q583L3_9TRYP	Q583l3 trypanosoma
446	36	45.6	291	2	Q92ER8_RHIME	Q92er8 rhizobium m	519	36	45.6	511	1	HUTH_RHIME	Q31197 rhizobium m
447	36	45.6	294	2	Q4SOG7_TETNG	Q4sog7 tetraodon n	520	36	45.6	519	2	Q8ISU4_DROMI	Q8isu4 drosophila
448	36	45.6	322	2	Q66KR3_XENLA	Q66kr3 xenopus lae	521	36	45.6	524	2	Q6NGS9_CORDI	Q6ngs9 corynebacte
449	36	45.6	322	2	Q5E599_VTBFI	Q5e599 vibrio fiesc	522	36	45.6	524	2	PUR9_NEIMA	Q91u58 n bifunctio
450	36	45.6	323	2	Q5KYF5_GEOKA	Q5kyf5 geobacillus	523	36	45.6	530	2	Q9A251_CAUCR	Q9a251 caulobacter
451	36	45.6	324	2	ODPB_RICCP	Q92is2 rickettsia	524	36	45.6	533	2	Q4FEG5_USTMA	Q4feg5 ustilago ma
452	36	45.6	326	1	ODPB_RICCP	Q92is2 rickettsia	525	36	45.6	534	2	Q6JZK6_ORYGA	Q6jzk6 oryza sativ
453	36	45.6	326	1	ODPB_RICCP	Q92is2 rickettsia	526	36	45.6	569	2	Q6UAV9_METCA	Q6uav9 methylococc
454	36	45.6	326	2	Q7PB81_RICSI	Q7pb81 rickettsia	527	36	45.6	583	2	Q5GV13_XANOR	Q5gv13 xanthomonas
455	36	45.6	326	2	Q4UKQ7_RICFE	Q4ukq7 rickettsia	528	36	45.6	602	2	Q6GPP0_XENLA	Q6gpp0 xenopus lae
456	36	45.6	326	2	Q68XA8_RICTY	Q68xa8 wolbachia s	529	36	45.6	610	2	Q5L5B5_GIBZE	Q5l5b5 gibberella
457	36	45.6	332	2	Q5GRX0_WOLTR	Q5grx0 wolbachia s	530	36	45.6	612	2	Q415B5_GIBZE	Q415b5 gibberella
458	36	45.6	332	2	Q73HS0_WOLPM	Q73hs0 wolbachia p	531	36	45.6	633	2	Q5L8Y4_BACFN	Q5l8y4 bacteroides
459	36	45.6	333	2	PUR5_METMA	Q8px06 methanosarc	532	36	45.6	639	2	Q4P47_BACFR	Q4p47 bacteroides
460	36	45.6	333	2	Q41337_GIRZE	Q41337 gibberella	533	36	45.6	643	2	Q4T5N4_TETNG	Q4t5n4 tetraodon n
461	36	45.6	338	1	ST2B1_MOUSE	Q35400 mus musculu	534	36	45.6	652	2	Q9NW82_HUMAN	Q9nw82 homo sapien
462	36	45.6	344	2	Q42944_TOBAC	Q42944 nicotiana t	535	36	45.6	654	2	Q5EB92_RAT	Q5eb92 rattus norv
463	36	45.6	351	2	Q9TPA1_9PIPI	Q9tpa1 xenopus lae	536	36	45.6	655	2	GALT6_DROME	Q6wv16 drosophila
464	36	45.6	352	2	Q670P5_XENLA	Q670p5 xenopus lae	537	36	45.6	666	1	Q4VTM1_XENLA	Q4vtml xenopus lae
465	36	45.6	358	2	Q6ER70_OCEHI	Q6er70 ocellulari	538	36	45.6	669	2	Q6CN70_KLULA	Q6cn70 kluyveromyc
466	36	45.6	358	2	Q6ZAF8_BURMA	Q6zap8 burkholderi	539	36	45.6	672	2	Q6MR04_BDEBA	Q6mr04 bdellovibri
467	36	45.6	359	2	Q98189_9STLV	Q98189 acrocephalu	540	36	45.6	674	2	Q9H053_HUMAN	Q9h053 homo sapien
468	36	45.6	364	2	Q8H291_ANACO	Q8h291 ananas como	541	36	45.6	674	2		
469	36	45.6	364	2	Q4RQ22_TETNG	Q4rq22 tetraodon n	542	36	45.6	674	2		

543	36	45.6	680	2	Q9CNU8_PASMU	Q9cnu8 pasteurella	616	35	44.3	88	2	Q860C6_9SYLV	Q860c6 acrocephalu
544	36	45.6	682	2	Q6FIM0_MESFL	Q6fim0 mesoplasma	617	35	44.3	90	2	Q860C9_9SYLV	Q860c9 acrocephalu
545	36	45.6	686	2	Q4IPAS_GIBZE	Q4ifas gibberella	618	35	44.3	92	2	Q7T209_ORENI	Q7t209 oreochromis
546	36	45.6	696	2	Q741T4_MYCPA	Q741t4 mycobacteri	619	35	44.3	102	2	Q05665_YEAST	Q05665 saccharomyc
547	36	45.6	700	1	EFG2_RALSO	Q8xm7 ralstonia s	620	35	44.3	102	2	Q73102_MYCPA	Q73102 mycobacteri
548	36	45.6	722	2	Q5ZBR5_ORYSA	Q5zbr5 oryza sativ	621	35	44.3	107	2	Q8E222_STRAS	Q8e222 streptococc
549	36	45.6	743	2	Q90194_9VIRU	Q90194 agaricus bi	622	35	44.3	107	2	Q8E7H9_STRAF5	Q8e7h9 pseudomonas
550	36	45.6	743	2	Q712R4_LISMF	Q712r4 listeria mo	623	35	44.3	112	2	Q4K7G9_PSEF5	Q4k7g9 pseudomonas
551	36	45.6	743	2	Q8Y786_LISMO	Q8y786 listeria mo	624	35	44.3	112	2	Q87PX8_VIBPA	Q87px8 vibrio para
552	36	45.6	743	2	Q92BV0_LISIN	Q92bv0 listeria in	625	35	44.3	125	2	Q8BTS2_MOUSE	Q8bts2 mus musculu
553	36	45.6	753	2	Q96917_HUMAN	Q96917 homo sapien	626	35	44.3	126	2	Q4WW83_ASFPU	Q4ww83 aspergillus
554	36	45.6	773	2	Q5WEB7_BACSK	Q5web7 bacillus cl	627	35	44.3	131	2	Q53904_STRCO	Q53904 streptomyc
555	36	45.6	783	2	Q524F9_MAGGR	Q524f9 magnaporthe	628	35	44.3	131	2	Q931Z3_STRCO	Q931z3 streptomyc
556	36	45.6	832	2	Q5LIH3_BACFN	Q5lih3 bacteroides	629	35	44.3	133	2	Q5XXA3_GEOSL	Q5xxa3 geobacillus
557	36	45.6	832	2	Q64ZJ7_BACFR	Q64zj7 bacteroides	630	35	44.3	135	2	Q74A43_GEOSL	Q74a43 geobacteri
558	36	45.6	837	2	Q6P4A6_HUMAN	Q6p4a6 homo sapien	631	35	44.3	137	2	Q70K61_9ACTO	Q70k61 gordonia we
559	36	45.6	861	1	SYL_SYMTH	Q67eb4 symbiobacte	632	35	44.3	139	2	Q6N4L8_RHOPA	Q6n4l8 rhodopseudo
560	36	45.6	864	2	Q4LRK6_9BURK	Q4lrk6 burkholderi	633	35	44.3	144	2	Q7MYB5_PHOLL	Q7myb5 photorhabdu
561	36	45.6	870	2	Q7SD25_NEUCR	Q7sd25 neurospora	634	35	44.3	145	1	Y008_MYCHO	Y008 mycobacteri
562	36	45.6	877	1	SYL_RALSO	Q8xvt3 ralstonia s	635	35	44.3	145	1	Y008_MYCTU	Y008 mycobacteri
563	36	45.6	901	1	SEC4_HAEIN	Q43803 haemophilus	636	35	44.3	149	2	Q8RXE4_ARATH	Q8rxex4 arabidopsis
564	36	45.6	901	2	Q4QM00_HAEI8	Q4qm00 haemophilus	637	35	44.3	150	2	Q8YXZ6_ANASP	Q8yxzx6 anabaena sp
565	36	45.6	902	2	Q8UA54_AGRF5	Q8ua54 agrobacteri	638	35	44.3	155	2	Q8L2C6_PROVU	Q8l2c6 proteus vul
566	36	45.6	905	2	Q7VKT3_HAEDU	Q7vkt3 haemophilus	639	35	44.3	158	2	Q4V067_XANCP	Q4v067 xanthomonas
567	36	45.6	907	2	Q7NFT3_GLOVI	Q7nft3 gloebacter	640	35	44.3	158	2	Q8PDX5_XANCP	Q8pdx5 xanthomonas
568	36	45.6	919	2	Q7CSN9_AGRF5	Q7csn9 agrobacteri	641	35	44.3	160	2	Q4FRC5_9GAMM	Q4frc5 psychrobact
569	36	45.6	926	2	Q4JUH6_CORJK	Q4juh6 corynebacte	642	35	44.3	168	2	Q7SBV1_NEUCR	Q7sbv1 neurospora
570	36	45.6	956	2	Q7SN96_DAUCA	Q7sn96 daucus caro	643	35	44.3	170	2	Q60F51_ORYSA	Q60f51 oryza sativ
571	36	45.6	956	2	Q7SN99_DAUCA	Q7sn99 daucus caro	644	35	44.3	170	2	Q9LIV6_ORYSA	Q9liv6 oryza sativ
572	36	45.6	958	2	Q5GW49_XANOR	Q5gw49 xanthomonas	645	35	44.3	173	2	Q8BT93_MOUSE	Q8bt93 mus musculu
573	36	45.6	964	1	AMPN_RAT	P15684 rattus norv	646	35	44.3	175	1	RES18_MOUSE	RES18 mus musculu
574	36	45.6	965	1	AMPN_MOUSE	P97449 mus musculu	647	35	44.3	175	1	Q5WYU0_NOCPA	Q5wyu0 nocardia fa
575	36	45.6	974	1	Q4PC88_USTMA	Q4pc88 ustilago ma	648	35	44.3	175	1	Q89NE8_BRAJA	Q89ne8 bradyrhizob
576	36	45.6	974	1	POLN_MITDV	P03318 middelburg	649	35	44.3	176	1	DSBB_VERPE	DSBB yersinia pe
577	36	45.6	994	2	Q9Q377_9POKV	Q9q377 rabbit fibr	650	35	44.3	176	2	Q6GAR0_VERPCT	Q6gar0 yersinia ps
578	36	45.6	1006	2	Q9Q8R2_9POKV	Q9q8r2 myxoma viru	651	35	44.3	176	2	Q6D4M8_ERECT	Q6d4m8 erwinia car
579	36	45.6	1096	2	Q61JW2_CAEBR	Q61jw2 caenorhabdi	652	35	44.3	178	2	Q698S0_9HIV1	Q698s0 human immun
580	36	45.6	1481	2	Q54D26_DICDI	Q54d26 dictyosteli	653	35	44.3	180	2	Q89US1_BRAJA	Q89us1 salmonella
581	36	45.6	1853	2	Q59H37_HUMAN	Q59h37 homo sapien	654	35	44.3	181	1	COBU_SALTU	COBU yersinia pe
582	36	45.6	1866	2	Q86W13_HUMAN	Q86w13 homo sapien	655	35	44.3	181	2	Q57MX9_SALCH	Q57mx9 salmonella
583	36	45.6	2481	2	Q9WJD3_9VIRU	Q9wj33 venezuelan	656	35	44.3	181	2	Q5PDU2_SALCPA	Q5pdu2 salmonella
584	36	45.6	3106	1	LAMA2_MOUSE	Q60675 mus musculu	657	35	44.3	181	2	Q8Z5N7_SALTI	Q8z5n7 salmonella
585	36	45.6	3110	1	LAMA2_HUMAN	P24043 homo sapien	658	35	44.3	181	2	Q5LKN3_SILPO	Q5lkn3 silicibacte
586	36	45.6	3122	2	Q5VUM2_HUMAN	Q5vum2 homo sapien	659	35	44.3	187	2	Q846V3_PHOPO	Q846v3 photobacte
587	36	45.6	3758	2	Q4QEN3_LEIMA	Q4qen3 leishmania	660	35	44.3	189	2	Q6MDP1_PARUM	Q6mdp1 parachlamyd
588	36	45.6	4801	2	Q9A1T3_XANAL	Q9ait3 xanthomonas	661	35	44.3	191	2	Q7BUF7_ARYMD	Q7buf7 amycolatamp
589	36	45.6	6879	2	Q70C47_XANAL	Q70c47 xanthomonas	662	35	44.3	194	2	Q8GS14_HORVD	Q8gs14 hordeum vul
590	35.5	44.9	205	2	Q8LNO4_ORYSA	Q8lnq4 oryza sativ	663	35	44.3	194	2	Q8H6C4_PSAJU	Q8h6c4 psathyrosta
591	35.5	44.9	269	2	Q9CT18_MOUSE	Q9ct18 mus musculu	664	35	44.3	195	2	Q20226_CABEL	Q20226 caenorhabdi
592	35.5	44.9	295	2	Q63KN1_BURPS	Q63kn1 burkholderi	665	35	44.3	197	2	Q8H6C5_9POAL	Q8h6c5 leymus trit
593	35.5	44.9	460	2	Q96HD7_HUMAN	Q96hd7 homo sapien	666	35	44.3	197	2	Q8H6C7_9POAL	Q8h6c7 haynaldia v
594	35.5	44.9	464	2	Q4P6N6_USTMA	Q4p6n6 ustilago ma	667	35	44.3	198	1	Y1593_YERPR	Y1593 yersinia pe
595	35.5	44.9	464	2	Q5EGN5_CYTJO	Q5egn5 cytophaga j	668	35	44.3	199	2	Q4YGD4_PLAPR	Q4ygd4 plasmodium
596	35.5	44.9	486	2	Q4S224_TETNG	Q4s224 tetraodon n	669	35	44.3	201	2	Q5YU19_NOCPA	Q5yu19 nocardia fa
597	35.5	44.9	569	2	Q4P2E0_USTMA	Q4p2e0 ustilago ma	670	35	44.3	202	2	Q669K7_YERPS	Q669k7 yersinia ps
598	35.5	44.9	585	1	PTN11_MOUSE	P35235 mus musculu	671	35	44.3	204	2	Q9A168_STRPY	Q9a168 streptococc
599	35.5	44.9	593	1	PTN11_CHICK	P35235 mus musculu	672	35	44.3	205	2	Q98MN2_RHILO	Q98mn2 rhizobium l
600	35.5	44.9	593	1	PTN11_HUMAN	Q90687 gallus gall	673	35	44.3	205	2	Q5QZC3_IDILO	Q5qzc3 idiomarina
601	35.5	44.9	593	1	PTN11_RAT	Q96124 homo sapien	674	35	44.3	206	1	RL3_THET8	RL3 thermus the
602	35.5	44.9	593	1	PTN11_MOUSE	P41499 rattus norv	675	35	44.3	206	1	RL3_THETH	RL3 thermus the
603	35.5	44.9	594	2	Q6PCL5_MOUSE	Q6pcl5 mus musculu	676	35	44.3	206	2	Q72104_THET2	Q72104 thermus the
604	35.5	44.9	594	2	Q7ZW17_BRARE	Q7zw17 brachydanio	677	35	44.3	207	2	Q4H9E8_9DEIO	Q4h9e8 deinococcus
605	35.5	44.9	595	2	Q92124_XENLA	Q92124 xenopus lae	678	35	44.3	209	2	Q72C10_DESVH	Q72c10 desulfovibr
606	35.5	44.9	595	2	Q6GN33_XENLA	Q6gn33 xenopus lae	679	35	44.3	210	2	Q9HVR4_PSEAE	Q9hvr4 pseudomonas
607	35.5	44.9	1059	2	Q64509_MOUSE	Q64509 mus musculu	680	35	44.3	210	2	Q9A170_STRPY	Q9a170 streptococc
608	35.5	44.9	3165	2	Q4P754_USTMA	Q4p754 ustilago ma	681	35	44.3	211	1	RL3_DEIRA	RL3 streptococc
609	35	44.3	20	2	Q8RD09_FUSNN	Q8rd09 fusobacteri	682	35	44.3	211	1	TRMB_SYN7N	TRMB thermoanaer
610	35	44.3	33	2	Q5XDJ9_STRP6	Q5xdj9 yersinia pe	683	35	44.3	213	1	Q5N2X5_SYN6	Q5n2x5 synecococc
611	35	44.3	59	2	Q8FCH6_ECOL6	Q8fch6 escherichia	684	35	44.3	213	2	Q8C7A3_MOUSE	Q8c7a3 mus musculu
612	35	44.3	74	1	CKS1_DROME	Q24152 drosophila	685	35	44.3	214	2	Q7TW40_MYCBO	Q7tw40 mycobacteri
613	35	44.3	74	2	Q8H6C2_9FOAL	Q8h6c2 leymus trit	686	35	44.3	214	2	Q69673_MYCTU	Q69673 mycobacteri
614	35	44.3	74	2	Q8H6C3_9FOAL	Q8h6c3 leymus cine	687	35	44.3	214	2	Q9CHU3_LACLA	Q9chu3 lactococcus
615	35	44.3	82	1	Y4KO_RHISN	P55533 rhizobium s	688	35	44.3	221	2		

689	35	44.3	224	2	Q8B340_COTCH	Q8b340 calturnix ch	762	35	44.3	404	2	Q8CVG5_ECOLI6	Q8cvg5 escherichia
690	35	44.3	225	2	Q8XQV1_RALSO	Q8xqv1 ratstonia ch	763	35	44.3	404	2	Q83IN1_SHIFL	Q83in1 shigella fl
691	35	44.3	226	2	Q5LHN1_MAGR	Q5lhn1 magnaporthe	764	35	44.3	404	2	Q8X554_ECO57	Q8x554 escherichia
692	35	44.3	228	2	Q6ZLG5_ORISA	Q6zlg5 oryza sativ	765	35	44.3	405	2	Q6PP97_3REOV	Q6pp97 muscovy duc
693	35	44.3	228	2	Q5WNR1_NOCFA	Q5wnr1 nocardia fa	766	35	44.3	410	2	Q96463_SKEOV	Q96463 skeletonema
694	35	44.3	232	1	RTF3_HUMAN	Q9bqg7 homo sapien	767	35	44.3	413	2	Q4U402_3REOV	Q4u402 muscovy duc
695	35	44.3	232	2	Q60B81_METCA	Q60b81 methylococc	768	35	44.3	413	2	Q4U403_3REOV	Q4u403 muscovy duc
696	35	44.3	232	2	Q8SUL5_DEIRE	Q8suj15 deirochelys	769	35	44.3	414	2	Q4WT04_ASPFU	Q4wt04 aspergillus
697	35	44.3	236	2	Q6BL00_DEBHA	Q6bli00 debaryomyce	770	35	44.3	416	2	Q4NEC6_9MICC	Q4nec6 arthrobacte
698	35	44.3	237	2	Q8H6C6_9FOAL	Q8h6c6 leymus cine	771	35	44.3	416	2	Q4JWJ6_COROX	Q4jw6 corynebacte
699	35	44.3	237	2	Q87AM1_XYLFT	Q87ami xylella fas	772	35	44.3	416	2	Q6JWJ5_3REOV	Q6jw5 muscovy duc
700	35	44.3	240	2	Q857U2_9CAUD	Q857u2 mycobacteri	773	35	44.3	417	2	Q8W572_BORBR	Q8w572 bordetella
701	35	44.3	243	2	Q57997_PYRHO	Q57997 pyrococcus	774	35	44.3	417	2	Q8DSX7_VIBVU	Q8dsx7 vibrio vuln
702	35	44.3	245	2	Q5V7L6_HALMA	Q5v7l6 haloarcula	775	35	44.3	417	2	Q7WC24_VIBVY	Q7wc24 vibrio vuln
703	35	44.3	247	2	Q6AU61_ORYSA	Q6au61 oryza sativ	776	35	44.3	420	2	Q85993_SPHAR	Q85993 sphingomon
704	35	44.3	248	2	Q4H589_9DEIO	Q4h589 deinococcus	777	35	44.3	420	2	Q87GS9_VIBPA	Q87gs9 vibrio para
705	35	44.3	248	2	Q6A9K1_PROAC	Q6a9k1 propionibac	778	35	44.3	422	2	Q8SUR6_ARATH	Q8sur6 arabidopsis
706	35	44.3	249	2	Q9CBU9_MYCLE	Q9cbu9 mycobacteri	779	35	44.3	422	2	Q4URJ4_XANCP	Q4urj4 xanthomonas
707	35	44.3	255	2	Q8R372_MOUSE	Q8r372 mus musculu	780	35	44.3	422	2	Q8PC05_XANCP	Q8pc05 xanthomonas
708	35	44.3	256	2	Q7X2Y6_9BACT	Q7x2y6 uncultured	781	35	44.3	426	2	Q8JOP5_YEAST	Q8jop5 saccharomyc
709	35	44.3	257	2	Q9PF00_XYLFA	Q9pf00 xylella fas	782	35	44.3	426	2	Q73ZK2_MYCPA	Q73zk2 mycobacteri
710	35	44.3	258	2	Q9PNN5_CAMJR	Q9pnn5 campylobact	783	35	44.3	426	2	Q7P801_RICSI	Q7p801 rickettsia
711	35	44.3	260	2	Q5HU46_CAMJR	Q5hu46 campylobact	784	35	44.3	427	2	Q92HP5_RICCN	Q92hp5 rickettsia
712	35	44.3	271	2	Q5BK78_RAT	Q5bk78 rattus norv	785	35	44.3	427	2	Q6LS34_PHOPR	Q6ls34 photobacter
713	35	44.3	280	2	Q9L390_CABEL	Q9l390 caenorhabd	786	35	44.3	428	2	Q9ZD63_RICPR	Q9zd63 rickettsia
714	35	44.3	280	2	Q6GLK1_XENLA	Q6glk1 xenopus lae	787	35	44.3	429	2	Q68WP9_RICTV	Q68wp9 rickettsia
715	35	44.3	282	2	Q7N5V9_PHOLL	Q7n5v9 photorhabd	788	35	44.3	429	2	Q79LX6_CITFR	Q79lx6 citrobacter
716	35	44.3	282	2	Q5FVY4_XENTR	Q5fvy4 xenopus tro	789	35	44.3	432	2	Q8XYG9_RALSO	Q8xyg9 rickettsia
717	35	44.3	287	1	Y1304_SYNY3	Y73599 synecocyst	790	35	44.3	434	1	EXG_SACKL	EXG01 aspergillus
718	35	44.3	289	2	Q9KHT0_P8EPU	Q9kht0 pseudomonas	791	35	44.3	434	1	EXG_SACKL	EXG01 aspergillus
719	35	44.3	291	2	Q7WM84_BORPA	Q7wm84 bordetella	792	35	44.3	439	2	Q9KLO9_VIBCH	Q9klo9 vibrio chol
720	35	44.3	291	2	Q7WM88_BORBR	Q7wm88 bordetella	793	35	44.3	440	2	Q6FR70_CANGA	Q6fr70 candida gla
721	35	44.3	292	2	Q8LAJ7_ARATH	Q8laj7 arabidopsis	794	35	44.3	443	2	Q8LEN9_ARATH	Q8len9 arabidopsis
722	35	44.3	293	2	Q9ZJ08_RHOFA	Q9zj08 rhodococcus	795	35	44.3	445	2	Q5E419_VIBFI	Q5e419 vibrio fisc
723	35	44.3	296	1	Y1023_VIBCH	Q9kt82 vibrio chol	796	35	44.3	446	2	Q5E419_VIBFI	Q5e419 vibrio fisc
724	35	44.3	301	1	KHSE_HALSA	Q9hp55 halobacteri	797	35	44.3	451	2	Q912S6_PSEAF	Q912s6 pseudomonas
725	35	44.3	301	1	SUMF2_BOVIN	Q58cp2 bos taurus	798	35	44.3	451	2	Q912S6_PSEAF	Q912s6 pseudomonas
726	35	44.3	301	1	SUMF2_HUMAN	Q8nbj7 homo sapien	799	35	44.3	452	2	Q922U0_RHIME	Q922u0 rhizobium m
727	35	44.3	301	1	SUMF2_PONPY	Q5crs5 pongo pygma	800	35	44.3	452	2	Q4U8L0_THEAN	Q4u8l0 theleria a
728	35	44.3	302	2	Q9SVP8_ARATH	Q9svp8 arabidopsis	801	35	44.3	456	2	Q6FNA5_CANGA	Q6fnas candida gla
729	35	44.3	304	2	Q52CM3_MAGGR	Q52cm3 magnaporthe	802	35	44.3	457	1	NUAM_CHICK	NUA939 gallus gall
730	35	44.3	305	2	Q4VYU0_9RHIZ	Q4vyu0 agrobacteri	803	35	44.3	459	2	Q89EX8_BRAJA	Q89ex8 bradyrhizob
731	35	44.3	306	2	Q88SS2_LACPL	Q88ss2 lactobacill	804	35	44.3	459	2	Q6ZLS4_CHICK	Q6zls4 gallus gall
732	35	44.3	308	2	SUMF2_MOUSE	Q8bp66 mus musculu	805	35	44.3	459	2	Q85UJ5_COTCH	Q85uj5 coturnix ch
733	35	44.3	310	2	Q75LP3_HUMAN	Q75lp3 homo sapien	806	35	44.3	459	2	Q8SEW5_COTVA	Q8sew5 coturnix ch
734	35	44.3	313	2	Q4Y3M8_PLACH	Q4y3m8 plasmodium	807	35	44.3	459	2	Q7GTU7_CHICK	Q7gtu7 gallus gall
735	35	44.3	313	2	Q4ZW69_PSESY	Q4zw69 pseudomonas	808	35	44.3	459	2	Q4CMQ3_CHICK	Q4cmq3 gallus gall
736	35	44.3	313	2	Q72Z24_BACCL	Q72z24 bacillus ce	809	35	44.3	459	2	Q4GWP0_CHICK	Q4gwp0 gallus gall
737	35	44.3	314	2	Q7WSC1_9SPHN	Q7wsc1 sphingomon	810	35	44.3	459	2	Q4GWP0_CHICK	Q4gwp0 gallus gall
738	35	44.3	317	2	Q8GV51_9CARY	Q8gv51 mirabilis e	811	35	44.3	459	2	Q4GWP0_CHICK	Q4gwp0 gallus gall
739	35	44.3	319	2	Q4WUB3_ASPFU	Q4wub3 aspergillus	812	35	44.3	459	2	Q4GWL4_GALVA	Q4gw14 gallus vari
740	35	44.3	340	2	Q93308_YEREN	Q933q8 yersinia en	813	35	44.3	459	2	Q4GWL4_GALVA	Q4gw14 gallus vari
741	35	44.3	345	1	T2C1_HERAU	P25258 herpetosiph	814	35	44.3	459	2	Q4GWL4_GALVA	Q4gw14 gallus vari
742	35	44.3	346	2	Q9TF99_RANPI	Q9tp99 rana pipien	815	35	44.3	459	2	Q4GWL4_GALVA	Q4gw14 gallus vari
743	35	44.3	349	2	Q7RV93_NEUCR	Q7rv93 neurospora	816	35	44.3	461	1	FUCO_DICDI	FUCO01 dictyosteli
744	35	44.3	349	2	Q4LX22_9BURK	Q4lx22 burkholderi	817	35	44.3	461	2	Q554R0_DICDI	Q554r0 dictyosteli
745	35	44.3	351	1	AOX_ASPNG	Q74180 aspergillus	818	35	44.3	462	2	Q65F15_BACLD	Q65f15 bacillus li
746	35	44.3	351	2	Q54AC8_ASPNG	Q54ac8 aspergillus	819	35	44.3	462	2	Q65F15_BACLD	Q65f15 bacillus li
747	35	44.3	352	2	Q9TPA0_XENLA	Q9tpa0 xenopus lae	820	35	44.3	469	2	Q9V2Q9_PYRAB	Q9v2q9 pyrococcus
748	35	44.3	352	2	Q4WHK6_ASPFU	Q4whk6 aspergillus	821	35	44.3	469	2	Q36517_PLASU	Q36517 platyomonas
749	35	44.3	352	2	Q6IP23_XENLA	Q6ip23 xenopus lae	822	35	44.3	469	2	Q32204_BACSU	Q32204 bacillus su
750	35	44.3	362	2	Q7SVY4_XENLA	Q7svt4 xenopus lae	823	35	44.3	472	2	Q8TZL5_PYRFU	Q8tzl5 pyrococcus
751	35	44.3	362	2	Q9BD51_MICMU	Q9bd51 micrococcus	824	35	44.3	472	2	Q831F1_ENTFA	Q831f1 enterococcu
752	35	44.3	365	2	Q6CT94_XLULA	Q6ct94 kluyveromyc	825	35	44.3	472	2	Q9AAL5_CAUCR	Q9aal5 caulobacter
753	35	44.3	368	1	YUHT_ECOLI	P39371 escherichia	826	35	44.3	473	2	Q6HJ66_BACCH	Q6hj66 bacillus ce
754	35	44.3	368	1	Q8X671_EC057	Q8x671 escherichia	827	35	44.3	473	2	Q6HJ66_BACCH	Q6hj66 bacillus ce
755	35	44.3	369	2	Q4W191_ASPFU	Q4w191 aspergillus	828	35	44.3	473	2	Q738R0_BACCI	Q738r0 bacillus th
756	35	44.3	370	2	Q7ADL5_EC057	Q7adl5 escherichia	829	35	44.3	473	2	Q81DV0_BACCR	Q81dv0 bacillus ce
757	35	44.3	370	2	Q4S920_TETNG	Q4s920 tetraodon n	830	35	44.3	473	2	Q63BP7_BACCZ	Q63bp7 bacillus an
758	35	44.3	372	2	Q9AK94_STRCO	Q9ak94 streptomyce	831	35	44.3	475	2	Q81QW5_BACAN	Q81qw5 bacillus an
759	35	44.3	383	2	Q5YNE3_NOCFA	Q5yne3 nocardia fa	832	35	44.3	475	2	Q57764_PYRHO	Q57764 pyrococcus
760	35	44.3	400	2	Q5LMT1_SILPO	Q5lmt1 silicibacte	833	35	44.3	476	2	Q8D8U8_VIBVU	Q8d8u8 vibrio vuln
761	35	44.3	401	2	Q73VA1_MYCPA	Q73va1 mycobacteri	834	35	44.3	476	2	Q518C5_ENTHI	Q518c5 entamoeba h

835	35	44.3	477	2	Q7MLM6_VIBVY	Q7mlm6 vibrio vuln	908	35	44.3	667	2	O22979_ARATH	O22979 arabidopsis
836	35	44.3	479	2	Q4UF25_THEAN	Q4uf25 theileria a	909	35	44.3	667	2	Q5KZW6_GEOKA	Q5kzw6 geobacillus
837	35	44.3	484	2	Q7XJW3_ORYSA	Q7xjw3 oryza sativ	910	35	44.3	669	2	O53ET6_HUMAN	O53et6 homo sapien
838	35	44.3	489	2	Q8FC58_ECOLI6	Q8fc58 escherichia	911	35	44.3	669	2	O96005_HUMAN	O96005 homo sapien
839	35	44.3	492	2	Q9HN43_HALSA	Q9hn43 halobacteri	912	35	44.3	671	2	O9VUX3_DROME	O9vux3 drosophila
840	35	44.3	502	2	Q9SLX3_TOBAC	Q9slx3 nicotiana t	913	35	44.3	673	2	Q6R3L0_ARATH	Q6r3l0 arabidopsis
841	35	44.3	504	2	Q9VPD9_DROME	Q9vpd9 drosophila	914	35	44.3	686	2	O9BS85_HUMAN	O9bs85 homo sapien
842	35	44.3	504	2	Q7NM77_PHOUL	Q7nm77 photorhabdu	915	35	44.3	688	2	Q95YGI_PENJP	Q95yg1 penaeus jap
843	35	44.3	510	2	Q5AY59_EMENI	Q5ay59 aspergillus	916	35	44.3	693	2	O8IQN5_DROME	O8iqn5 drosophila
844	35	44.3	511	2	Q5P855_AZOSE	Q5p855 azarcus sp	917	35	44.3	693	2	Q86MV4_APIME	Q86mv4 apis mellif
845	35	44.3	512	2	Q8LG73_ARATH	Q8lg73 arabidopsis	918	35	44.3	696	2	Q8DER6_VIBVU	Q8der6 vibrio vuln
846	35	44.3	513	2	Q9CAT3_ARATH	Q9cat3 arabidopsis	919	35	44.3	709	2	Q8S9F8_UCSTA	Q8s9f8 pseudomonas
847	35	44.3	515	2	Q08708_MOUSE	Q08708 mus musculu	920	35	44.3	713	2	Q4PYX3_ARATH	Q4pyx3 ustiliago ma
848	35	44.3	517	1	ACHG_HUMAN	P07510 homo sapien	921	35	44.3	714	2	Q6CC87_YARLI	Q6cc87 yarrowia li
849	35	44.3	517	2	Q8MN70_CABEL	Q8mn70 caenorhabdi	922	35	44.3	727	2	Q52GB6_MAGGR	Q52gb6 magnaporthe
850	35	44.3	519	2	Q8IST7_DROEQ	Q8ist7 drosophila	923	35	44.3	730	2	Q9RU93_DETRA	Q9ru93 deinococcus
851	35	44.3	519	2	Q8ISU2_DROWI	Q8isu2 drosophila	924	35	44.3	741	2	Q9FCU3_ARATH	Q9fcu3 arabidopsis
852	35	44.3	519	2	Q8ISU3_DROWI	Q8isu3 drosophila	925	35	44.3	745	2	Q95XLI1_CABEL	Q95xli1 caenorhabdi
853	35	44.3	520	2	Q53RG2_HUMAN	O53rg2 homo sapien	926	35	44.3	748	2	Q7MNN9_VIBVY	Q7mnn9 vibrio vuln
854	35	44.3	520	2	Q6MK53_BDEBA	O6mk53 bdellovibri	927	35	44.3	751	2	Q4SEK4_TETNG	Q4sek4 tetradodon n
855	35	44.3	521	2	Q8ISU1_DROWI	Q8isu1 drosophila	928	35	44.3	755	2	Q8S896_ARATH	Q8s896 arabidopsis
856	35	44.3	527	2	Q787L3_NEUCR	Q787l3 neurospora	929	35	44.3	758	2	O82440_ARATH	O82440 arabidopsis
857	35	44.3	528	2	Q4ZTF7_PSESY	Q4ztf7 pseudomonas	930	35	44.3	764	2	Q91311_PSEAE	Q91311 pseudomonas
858	35	44.3	533	2	Q6ZU04_HUMAN	Q6zu04 homo sapien	931	35	44.3	768	2	Q81PH0_DROME	Q81ph0 drosophila
859	35	44.3	536	1	DIT1_YEAST	P21623 saccharomyc	932	35	44.3	772	2	Q9ZSP5_ARATH	Q9zsp5 arabidopsis
860	35	44.3	542	2	Q9VPE0_DROME	Q9vpe0 drosophila	933	35	44.3	776	2	Q9VLJ2_DROME	Q9vlj2 drosophila
861	35	44.3	542	2	Q9HUM7_PSEAE	Q9hum7 pseudomonas	934	35	44.3	778	2	Q9AX30_ORYSA	Q9ax30 oryza sativ
862	35	44.3	547	2	Q4HXJ0_GIBZE	Q4hxj0 gibberella	935	35	44.3	788	2	Q4MMF9_BACCE	Q4mmf9 bacillus ce
863	35	44.3	548	2	Q93XZ2_ARATH	Q93xz2 arabidopsis	936	35	44.3	788	2	Q63FC2_BACCC	Q63fc2 bacillus ce
864	35	44.3	548	2	Q9SVE2_ARATH	Q9sve2 arabidopsis	937	35	44.3	788	2	Q81UI7_BACAN	Q81ui7 bacillus an
865	35	44.3	551	2	Q9ST03_HORVU	Q9st03 hordeum vul	938	35	44.3	791	2	Q9FK76_ARATH	Q9fk76 arabidopsis
866	35	44.3	551	2	Q9ST44_HORVU	Q9st44 hordeum vul	939	35	44.3	798	2	Q4PCF1_USTMA	Q4pcf1 ustiliago ma
867	35	44.3	555	2	Q5R084_IDILO	O5r084 idiomarina	940	35	44.3	803	2	O5C8V6_LEIMA	O5c8v6 leishmania
868	35	44.3	555	2	Q73YE4_MYCPA	Q73ye4 mycobacteri	941	35	44.3	815	2	Q8DSY8_VIBVU	Q8dsy8 vibrio vuln
869	35	44.3	557	1	GLT11_DROME	Q8ia41 drosophila	942	35	44.3	816	1	SYL_CLOPE	Q8xm18 clostridium
870	35	44.3	561	2	Q6QT93_TRYCR	Q6qt93 trypanosoma	943	35	44.3	817	2	Q9AN48_BRAJA	Q9an48 bradyrhizob
871	35	44.3	564	2	Q6CWZ2_KULUA	O6cwz2 kluyveromyc	944	35	44.3	839	2	Q93LD9_BACFR	Q93ld9 bacteroides
872	35	44.3	567	2	Q7UCE6_SHIFL	Q7uce6 shigella fl	945	35	44.3	839	2	O5LBV9_BACFN	O5lbv9 bacteroides
873	35	44.3	567	2	Q4KRW9_PSEF5	Q4kwr9 pseudomonas	946	35	44.3	839	2	O64ST6_BACFR	O64st6 bacteroides
874	35	44.3	567	2	Q83RC5_SHIFL	Q83rc5 shigella fl	947	35	44.3	840	2	P72843_SYNV3	P72843 synechocyst
875	35	44.3	571	2	O8XHF8_CLOPE	Q8xf8 clostridium	948	35	44.3	850	2	Q8GI52_ALTSO	Q8gi52 alteromonas
876	35	44.3	572	2	O5AUG2_EMENI	O5aug2 aspergillus	949	35	44.3	850	2	Q89MT7_BRAJA	Q89mt7 bradyrhizob
877	35	44.3	574	2	Q4P3P4_USTMA	Q4p3p4 ustiliago ma	950	35	44.3	852	2	Q4INB5_GIBZE	Q4inb5 gibberella
878	35	44.3	578	2	Q7RYD9_NEUCR	Q7ryd9 neurospora	951	35	44.3	873	2	Q947C4_GINBI	Q947c4 ginkgo bilo
879	35	44.3	581	2	Q5VTJ2_HUMAN	Q5vtj2 homo sapien	952	35	44.3	881	2	Q7MD07_VIBVY	Q7md07 vibrio vuln
880	35	44.3	587	2	Q8BY59_MOUSE	Q8by59 mus musculu	953	35	44.3	883	2	Q6DCJ5_XENLA	Q6dcj5 xenopus lae
881	35	44.3	598	2	Q8R0Z2_MOUSE	Q8r0z2 mus musculu	954	35	44.3	893	1	RUSCL_MOUSE	Q8bg46 mus musculu
882	35	44.3	599	2	Q8VNV4_CLOPE	Q8vnx4 clostridium	955	35	44.3	902	2	Q6D2V4_ERWCT	Q6d2v4 erwinia car
883	35	44.3	599	2	O8XPI9_CLOPE	Q8xpi9 clostridium	956	35	44.3	910	2	Q98G67_RHILO	Q98g67 rhizobium l
884	35	44.3	599	2	Q64033_SMURI	Q64033 mus sp. ant	957	35	44.3	927	2	O55SR0_DROME	O55sr0 drosophila
885	35	44.3	603	1	EGLR_ECOLI	P05804 escherichia	958	35	44.3	940	2	Q55FR0_DICDI	Q55fi0 dictyosteli
886	35	44.3	603	2	Q93V74_ARATH	Q93v74 arabidopsis	959	35	44.3	943	2	O51RQ7_MAGGR	O51rg7 magnaporthe
887	35	44.3	603	2	Q9AHJ4_ECOLI	Q9ahj4 escherichia	960	35	44.3	943	2	O6MXJ7_BDEBA	O6mcj7 bdellovibri
888	35	44.3	603	2	O8FHA3_ECOLI6	Q8fha3 escherichia	961	35	44.3	946	2	O6NCG2_RHOPA	O6ncg2 rhodopseu
889	35	44.3	604	2	Q9F5N0_RHIME	O9f5n0 rhizobium m	962	35	44.3	968	2	Q7XJU9_ORYSA	Q7xju9 oryza sativ
890	35	44.3	610	1	COVAL_HUMAN	Q16206 homo sapien	963	35	44.3	1033	2	Q6ATV4_ORYSA	Q6atv4 echinosacch
891	35	44.3	610	2	Q5VTU1_HUMAN	Q5vtu1 homo sapien	964	35	44.3	1076	1	YKT5_SCHPO	Q6lm04 schizosacch
892	35	44.3	610	2	Q5SGD1_VITVI	Q5sgd1 vitis vinif	965	35	44.3	1090	2	Q61MT8_CAEBR	Q61mt8 caenorhabdi
893	35	44.3	624	2	O5FYF9_TRICA	O5fyf9 tribolium c	966	35	44.3	1134	2	Q4RY67_TETNG	Q4ry67 tetradodon n
894	35	44.3	624	2	O95ZW0_CAEEL	Q95zw0 caenorhabdi	967	35	44.3	1151	2	O5DTY6_MOUSE	O5dt6 mus musculu
895	35	44.3	626	2	Q95ZV9_CAEEL	Q95zv9 caenorhabdi	968	35	44.3	1205	2	O59946_EMENI	O59946 emerice
896	35	44.3	627	2	Q6LUV9_PHOPR	Q6luv9 photobacter	969	35	44.3	1210	2	O5B8V4_EMENI	O5b8v4 aspergillus
897	35	44.3	637	2	Q4UTU1_XANCP	Q4utu1 xanthomonas	970	35	44.3	1223	2	Q02979_YEAST	Q02979 saccharomyc
898	35	44.3	637	2	Q8P9U4_XANCP	Q8p9u4 xanthomonas	971	35	44.3	1244	2	Q4PLS6_USTMA	Q4pls6 ustiliago ma
899	35	44.3	638	2	Q4UXN7_XANCP	Q4uxn7 xanthomonas	972	35	44.3	1264	2	Q6BGQ6_DEBHA	Q6bgq6 debaryomyc
900	35	44.3	638	2	O8P6C8_XANCP	Q8p6c8 xanthomonas	973	35	44.3	1264	2	O8WV55_SCHMA	O8wpv5 schistosoma
901	35	44.3	639	2	O8PHT4_XANAC	Q8pht4 xanthomonas	974	35	44.3	1374	2	O6CLT0_KLILO	O6clt0 kluyveromyc
902	35	44.3	639	2	Q6LUA7_PHOPR	Q6lua7 photobacter	975	35	44.3	1386	2	O984C1_RHILO	O984c1 rhizobium l
903	35	44.3	654	2	O5H350_XANOR	Q5h350 xanthomonas	976	35	44.3	1439	2	Q4P0P3_USTMA	Q4p0p3 ustiliago ma
904	35	44.3	664	2	O8VBZ3_MOUSE	Q8vzb3 mus musculu	977	35	44.3	1485	2	Q6CFY4_YARLI	Q6cfy4 yarrowia li
905	35	44.3	665	2	O94EY9_ARATH	Q94ey9 arabidopsis	978	35	44.3	1551	2	Q8YMU3_ANASP	Q8ymu3 anabaena sp
906	35	44.3	665	2	Q389Z5_ARATH	Q389z5 arabidopsis	979	35	44.3	1572	2	Q8G7T8_BIFLO	Q8g7t8 bifidobacte
907	35	44.3	665	2	Q9FP29_ARATH	Q9fp29 arabidopsis	980	35	44.3	1678	2	Q924C5_MOUSE	Q924c5 mus musculu

981 35 44.3 1693 1 Y163_SVNY3
 982 35 44.3 1699 2 Q6CD47_YARLI
 983 35 44.3 1757 2 Q4Z41_TETNG
 984 35 44.3 1879 2 P72938_SVNY3
 985 35 44.3 1923 2 Q6TUI4_BOVIN
 986 35 44.3 1962 2 Q7S784_NEUCR
 987 35 44.3 1976 2 Q412S5_GIBZE
 988 35 44.3 2089 2 Q414K8_GIBZE
 989 35 44.3 2266 1 POLI_TBRVM
 990 35 44.3 2635 2 Q7MRJ0_9NOST
 991 35 44.3 2970 2 Q4SFW8_TETNG
 992 35 44.3 3165 2 Q5AR63_EMENI
 993 35 44.3 3591 2 Q9KIE1_STRHY
 994 35 44.3 3615 2 Q6D876_ERWCT
 995 35 44.3 3841 2 Q7Q319_ANOGA
 996 35 44.3 4644 2 Q4Q2F4_LEIMA
 997 34.5 43.7 182 2 Q8H7G0_ARATH
 998 34.5 43.7 298 2 Q5B3D9_EMENI
 999 34.5 43.7 331 2 Q89L06_BRAJA
 1000 34.5 43.7 338 2 Q89K43_BRAJA

ALIGNMENTS

RESULT 1
 Q540D8_MYCTU PRELIMINARY; PRT; 95 AA.

AC Q540D8; 95 AA; 3904 MW; 79BD529ED8F519 CRC64;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DE Secreted low molecular-mass T-cell antigen ESAT6.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium;
 OC Mycobacterium tuberculosis complex.
 OX NCBI_TaxID=1773;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Lee C.F.;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY207398; AAO62007.1; -; Genomic DNA.
 SQ SEQUENCE 95 AA; 3904 MW; 79BD529ED8F519 CRC64;

Query Match 100.0%; Score 79; DB 2; Length 95;
 Best Local Similarity 100.0%; Pred. No. 1.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQWNFAGIEAAA 15
 |||||
 DB 1 MTEQWNFAGIEAAA 15

RESULT 2
 ESXA_MYCBO STANDARD; PRT; 94 AA.

AC POA565; O84901; Q57165;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE 6 kDa early secretory antigenic target (ESAT-6).
 GN Name=esxA; Synonyms=esat6; OrderedLocusNames=Mb3905;
 OS Mycobacterium bovis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium;
 OC Mycobacterium tuberculosis complex.
 OX NCBI_TaxID=1765;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=96200095; PubMed=8631702;
 RA Mahairas G.G., Sabo P.J., Hickey M.J., Singh D.C., Stover C.K.;
 RT "Molecular analysis of genetic differences between Mycobacterium bovis

RT BCG and virulent M. bovis.";
 RL J. Bacteriol. 178:1274-1282(1996).
 RP [2]
 RC NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX STRAIN=AF2122/97; PubMed=12788972; DOI=10.1073/pnas.1130426100;
 RA MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;
 RA Garnier T., Biglener K., Camus J.-C., Medina N., Mansoor H.,
 RA Pryor M., Duthey S., Grondin S., Lacroix C., Mounsepe C., Simon S.,
 RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
 RA Parkhill J., Barrall B.G., Cole S.I., Gordon S.V., Hewison R.G.;
 RL "The complete genome sequence of Mycobacterium bovis.";
 CC Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
 CC -!- FUNCTION: Not known. Elicits high level of IFN-gamma from memory
 CC effector cells during the first phase of a protective immune
 CC response.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the ESAT-6 (esx) family.
 CC
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

DR EMBL: U34848; AAC44033.1; -; Genomic DNA.
 DR EMBL: BX248347; CAD96091.1; -; Genomic DNA.
 KW Antigen; Complete proteome.
 FT INIT_MET 0 BY similarity.
 SQ SEQUENCE 94 AA; 9773 MW; 19245B0EC4785C84 CRC64;

Query Match 93.7%; Score 74; DB 1; Length 94;
 Best Local Similarity 100.0%; Pred. No. 8.5e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TEOQWNFAGIEAAA 15
 |||||
 DB 1 TEOQWNFAGIEAAA 14

RESULT 3
 ESXA_MYCTU STANDARD; PRT; 94 AA.
 ID POA564; O84901; Q57165;
 AC 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE 6 kDa early secretory antigenic target (ESAT-6).
 GN Name=esxA; Synonyms=esat6; OrderedLocusNames=Mb3905; MT3989;
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium;
 OC Mycobacterium tuberculosis complex.
 OX NCBI_TaxID=1773;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RX STRAIN=H37RV;
 RX MEDLINE=95204931; PubMed=7897219;
 RA Andersen P., Andersen A.B., Sorensen A.L., Nagai S.;
 RT "Recall of long-lived immunity to Mycobacterium tuberculosis infection
 RT in mice.";
 RL J. Immunol. 154:3359-3372(1995).
 RP [2]
 RC NUCLEOTIDE SEQUENCE, PROTEIN SEQUENCE OF 1-10, AND CHARACTERIZATION.
 RX STRAIN=Erkman;
 RX MEDLINE=95247251; PubMed=7729876;
 RA Soerensen A.L., Nagai S., Houen G., Anderson P., Anderson A.B.;
 RT "Purification and characterization of a low-molecular-mass T-cell
 RT antigen secreted by Mycobacterium tuberculosis.";
 RL Infect. Immun. 63:1710-1717(1995).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Singh B., Siddiqui Z., Singh S., Sharma P.;

"ESAT-6 gene of a clinical isolate of Mycobacterium tuberculosis from India.";
Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
[4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230; DOI=10.1038/31159;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,
RA Harris D.E., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III,
RA Tekala F., Badcock K., Basham D., Brown D., Chillingworth T.,
RA Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels J., Krogan A., McLellan J., Moule S.,
RA Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,
RA Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544 (1998).
[5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CDC 1551 / OshKosh;
RX MEDLINE=22206494; PubMed=12218036;
RX DOI=10.1128/JB.184.19.5479-5490.2002;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,
RA Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D.,
RA Salzberg S.L., Delcher A., Uterback T.R., Weidman J.F., Khouri H.M.,
RA Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,
RA Fraser C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL J. Bacteriol. 184:5479-5490 (2002).
[6]
RP NUCLEOTIDE SEQUENCE OF 1-70.
RC STRAIN=H37RV;
RX MEDLINE=99061212; PubMed=9846755;
RA Berthet F.-X., Rasmussen P.B., Rosenkrands I., Andersen P.,
RA Gicquel B.;
RT "A Mycobacterium tuberculosis operon encoding ESAT-6 and a novel low-
RT molecular-mass culture filtrate protein (CFP-10).";
RL Microbiology 144:3195-3203 (1998).
CC -!- FUNCTION: Not known. Elicits high level of IFN-gamma from memory
CC effector cells during the first phase of a protective immune
CC response.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the ESAT-6 (esx) family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; X79562; CAAS6099.1; -; Genomic DNA.
CC EMBL; AF420491; AAL16896.1; -; Genomic DNA.
CC EMBL; BX842584; CAP55648.1; -; Genomic DNA.
CC EMBL; AE000316; AAK48357.1; -; Genomic DNA.
CC EMBL; AF004671; AAC83446.1; -; Genomic DNA.
CC FIR; A70803; A70803.
CC TIGR; MT3989; -.
CC Tuberculist; RV3875; -.
KW Antigen; Complete proteome; Direct protein sequencing.
FT INIT_MET 0
FT SEQUENCE 94 AA; 9773 MW; 19245B0EC478BC84 CRC64;
Query Match 93.7%; Score 74; DB 1; Length 94;
Best Local Similarity 100.0%; Pred. No. 8.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TEQOWNFAGIEAAA 15
DB 1 TEQOWNFAGIEAAA 14

RESULT 4

Q5G541 MYCUL
ID Q5G541_MYCUL PRELIMINARY; PRT; 56 AA.
AC Q5G541;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
ESAT-6 (Fragment).
DE Mycobacterium ulcerans.
OS Mycobacteriaceae; Actinobacteridae; Actinomycetales;
OC Bacteria; Actinobacteria; Mycobacteriaceae; Mycobacterium.
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1809;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=98-912, and 7922;
RA Mve-Obiang A., Lee R.E., Umstot E.S., Trott K.A., Grammer T.C.,
RA Parker J.M., Ranger B.S., Small P.C.;
RT "A newly discovered mycobacterial pathogen isolated from lethal
RT infections in laboratory colonies of Xenopus species produces a novel
RT form of the M. ulcerans macrolide toxin, mycolactone.";
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY854677; AAW68024.1; -; Genomic DNA.
DR EMBL; AY854675; AAW68022.1; -; Genomic DNA.
DR NON_TER 1
FT NON_TER 1
SQ SEQUENCE 56 AA; 5787 MW; 4FB7FEBB455D1CEE CRC64;
Query Match 89.9%; Score 71; DB 2; Length 56;
Best Local Similarity 92.9%; Pred. No. 0.00017;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TEQOWNFAGIEAAA 15

DB 1 TEQOWNFAGIEAAA 14

RESULT 5

Q5G545 MYCUL
ID Q5G545_MYCUL PRELIMINARY; PRT; 56 AA.
AC Q5G545;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
ESAT-6 (Fragment).
DE Mycobacterium ulcerans.
OS Mycobacteriaceae; Actinobacteridae; Actinomycetales;
OC Bacteria; Actinobacteria; Mycobacteriaceae; Mycobacterium.
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1809;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=5143;
RA Mve-Obiang A., Lee R.E., Umstot E.S., Trott K.A., Grammer T.C.,
RA Parker J.M., Ranger B.S., Small P.C.;
RT "A newly discovered mycobacterial pathogen isolated from lethal
RT infections in laboratory colonies of Xenopus species produces a novel
RT form of the M. ulcerans macrolide toxin, mycolactone.";
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY854673; AAW68020.1; -; Genomic DNA.
DR NON_TER 1
FT NON_TER 1
SQ SEQUENCE 56 AA; 5788 MW; 4FB7FEBB145FD1CEE CRC64;
Query Match 89.9%; Score 71; DB 2; Length 56;
Best Local Similarity 92.9%; Pred. No. 0.00017;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TEQOWNFAGIEAAA 15

DB 1 TEQOWNFAGIEAAA 14

RESULT 6

```

Q4VQH8_9MYCO
ID Q4VQH8_9MYCO PRELIMINARY; PRT; 72 AA.
AC Q4VQH8;
DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE Small secreted antigenic protein Esat6 (Fragment).
OS Mycobacterium lifilandiil.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=261524;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=XT-128;
RX PubMed=15908356; DOI=10.1128/IAI.73.6.3307-3312.2005;
RA Mve-Obiang A., Lee R.E., Umstot E.S., Trott K.A., Grammer T.C.,
RA Parker J.M., Ranger B.S., Grainger R., Mahrous E.A., Small P.L.;
RT "A Newly Discovered Mycobacterial Pathogen Isolated from Laboratory
RT Colonies of Xenopus Species with Lethal Infections Produces a Novel
RT Form of Mycolactone, the Mycobacterium ulcerans Macrolide Toxin.";
RL Infect. Immun. 73:3307-3312(2005).
DR EMBL: AY736851; AAX20068.1; -; Genomic_DNA.
FT NON_TER 1
FT TER 72
SQ SEQUENCE 72 AA; 7527 MW; BBE8911F7654352D CRC64;

Query Match 83.5%; Score 66; DB 2; Length 72;
Best Local Similarity 92.3%; Pred. No. 0.0016;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 EOMNPFAGIEAAA 15
DB 1 EOMNPFAGIEAAS 13

RESULT 7
Q87WZ3_PSESM
ID Q87WZ3_PSESM PRELIMINARY; PRT; 913 AA.
AC Q87WZ3;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Preprotein translocase, SecA subunit.
GN Name=secA; OrderedLocName=PSPT04400;
OS Pseudomonas syringae (pv. tomato).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=323;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=DC3000;
RX MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
RA Buell C.R., Joardar V., Lindeberg M., Seiwung J., Paulsen I.I.,
RA Gwin M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,
RA Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H.,
RA Nelson W.C., Davidse T.M., Zafar N., Zhou L., Liu J., Yuan Q.,
RA Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,
RA Utterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M.,
RA Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K.,
RA Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X.,
RA Bender C.L., White O., Fraser C.M., Collmer A.;
RT "The complete genome sequence of the Arabidopsis and tomato pathogen
RT Pseudomonas syringae pv. tomato DC3000.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
DR EMBL: AE016853; BAO57849.1; -; Genomic_DNA.
DR HSPB; O05885; INKT.
DR TIGR; PSPT04400;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005324; F:ATP binding; IEA.
DR GO; GO:0004386; F:nicotinic activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0017038; P:protein import; IEA.

GO; GO:0006605; P:protein targeting; IEA.
DR InterPro; IPR001650; Helicase C.
DR InterPro; IPR004027; SEC_C_motif.
DR InterPro; IPR000185; SecA.
DR InterPro; IPR011115; SecA DEAD.
DR InterPro; IPR011130; SecA PP bind.
DR InterPro; IPR011116; SecA SW.
DR Pfam; PF00271; Helicase C; 1.
DR Pfam; PF02810; SEC-C_1_C; 1.
DR Pfam; PF0517; SecA DEAD; 1.
DR Pfam; PF01043; SecA_PP_bind; 1.
DR Pfam; PF07516; SecA SW; 1.
DR PRINTS; PR00906; SEC_A.
DR TIGRFAMs; TIGR00963; secA; 1.
KW Complete proteome.
SQ SEQUENCE 913 AA; 103430 MW; DCE7A1A79A312222 CRC64;

Query Match 60.8%; Score 48; DB 2; Length 913;
Best Local Similarity 72.7%; Pred. No. 27;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 QOMNPFAGIEAA 14
DB 699 EQMNVAGIEAA 709

RESULT 8
Q4J587_AZOV1
ID Q4J587_AZOV1 PRELIMINARY; PRT; 284 AA.
AC Q4J587;
DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DE Senescence marker protein-30 (SMP-30).
GN ORFName=AvinDRAFT_8270;
OS Azotobacter vinelandii AVOP.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=322710;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AVOP;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Azotobacter vinelandii
RT AVOP.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AVOP;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Laxner F., Land M.;
RT "Annotation of the draft genome assembly of Azotobacter vinelandii
RT AVOP.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AVOP;
RG US DOE Joint Genome Institute;
RA Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AVOP;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; ARAU0300001; EAM07254.1; -; Genomic DNA.
DR SEQUENCE 284 AA; 31315 MW; 1B3171C77C6A9A46 CRC64;

```

Query Match 58.2%; Score 46; DB 2; Length 284;
 Best Local Similarity 57.1%; Pred. No. 18;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 2 TEQWQNFAGIEAAA 15
 | | | | | | | | | |
 Db 43 TRQWQNFDFGVSA 56

RESULT 9

Q5CX78 CRYPV Q5CX78 CRYPV PRELIMINARY; PRT; 2151 AA.
 AC Q5CX78;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Large uncharacterized low complexity protein.
 GN ORFNames=cgd7_4980;
 OS Cryptosporidium parvum.
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
 OC Cryptosporidiidae; Cryptosporidium.
 OC NCBI_TaxID=5807;
 [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Iowa type II;
 RC PubMed=15044751; DOI=10.1126/science.1094786;
 RA Abrahamson M.S., Templeton T.J., Enomoto S., Abrahamte J.E., Zhu G.,
 RA Lantto C.A., Deng M., Liu C., Widmer G., Tzipori S., Buck G.A., Xu P.,
 RA Bankier A.T., Dear P.H., Konfortov B.A., Spriggs H.F., Iyer L.,
 RA Anantharaman V., Aravind L., Kapur V.;
 RT "Complete genome sequence of the apicomplexan, Cryptosporidium
 parvum.";
 RT Science 304:441-445 (2004).
 RL EMBL; AAEE01000001; EAK90461.1; -; Genomic_DNA.
 DR InterPro; IPR000873; AMP_bind.
 DR InterPro; IPR011989; ARM-like.
 DR InterPro; IPR011058; Cytochrome_N.
 DR InterPro; IPR012282; Cytochrome_C_R.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR007117; Expan_Lol_pl_C.
 DR InterPro; IPR012287; Homeodomain-rel.
 DR InterPro; IPR001093; IMPdh/GMPRTase.
 DR InterPro; IPR000471; Interferon_abd.
 DR InterPro; IPR011986; Liga.
 DR InterPro; IPR003086; MPTase_inhib_138.
 DR InterPro; IPR000535; MSP.
 DR InterPro; IPR012128; Phycocyanin.
 DR InterPro; IPR000403; PI3/4_kinase_cat.
 DR InterPro; IPR008916; Retrov_capsid_C.
 DR InterPro; IPR009095; TRADD_N.
 DR InterPro; IPR009032; Vpu_cyt.
 DR InterPro; IPR011991; Wing_hlx_DNA_bd.
 DR PROSITE; PS00455; AMP_BINDING; UNKNOWN 1.
 SQ SEQUENCE 2151 AA; 246626 MW; 055F1D6E01CFB0C9 CRC64;

Query Match 58.2%; Score 46; DB 2; Length 2151;
 Best Local Similarity 66.7%; Pred. No. 1.4e+02;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 MTEQWQNFAGIE 12
 | | | | | | | | | |
 Db 156 MDERQWKFAGYE 167

RESULT 10

Q5Y972 PLEOS Q5Y972 PLEOS PRELIMINARY; PRT; 290 AA.
 AC Q5Y972;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Metalloprotease.

OS Pleurotus ostreatus (Oyster mushroom) (White-rot fungus).
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Agaricales; Pleurotaceae; Pleurotus.
 OX NCBI_TaxID=5322;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC PubMed=15451101; DOI=10.1016/j.femsle.2004.08.020;
 RA Joh J.H., Kim B.G., Kong W.S., Yoo Y.B., Kim N.K., Park H.R.,
 RA Cho B.G., Lee C.S.;
 RT "Cloning and developmental expression of a metzincin family
 metalloprotease cDNA from oyster mushroom Pleurotus ostreatus.";
 RL FEMS Microbiol. Lett. 239:57-62 (2004).
 DR EMBL; AY640032; AAU94648.1; -; mRNA.
 DR GO; GO:0008237; F:metalloproteinase activity; IEA.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.
 KW Metalloprotease; Protease.
 SQ SEQUENCE 290 AA; 31897 MW; CES8A4BC76283533 CRC64;

Query Match 57.0%; Score 45; DB 2; Length 290;
 Best Local Similarity 53.8%; Pred. No. 28;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 MTEQWQNFAGIEA 13
 | | | | | | | | | |
 Db 272 MREQSWYRGVEA 284

RESULT 11

NOEA RHIME NOEA RHIME STANDARD; PRT; 476 AA.
 ID NOEA RHIME
 AC Q52892;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Modulation protein noeA.
 GN Name=noeA; OrderedLocNames=RA0416; ORFNames=Sma0773;
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OG Plasmid pSymba (megaplasmid 1).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Sinorhizobium.
 OC NCBI_TaxID=382;
 [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=RCR2011 / SU47;
 RC MEDLINE=96111489; PubMed=8801423;
 RA Ardourel M., Lortet G., Maillet F., Roche P., Truchet G., Promé J.-C.,
 RA Rosenberg C.;
 RT "In Rhizobium meliloti, the operon associated with the nod box n5
 comprises nodL, noeA and noeB, three host-range genes specifically
 required for the modulation of particular Medicago species.";
 RT Mol. Microbiol. 17:687-699 (1995).
 RL [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=1021;
 RC MEDLINE=21396509; PubMed=11481432; DOI=10.1073/pnas.161294798;
 RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
 RA Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
 RA Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
 RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
 RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
 RT "Nucleotide sequence and predicted functions of the entire
 Sinorhizobium meliloti pSymba megaplasmid.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888 (2001).
 CC -!- FUNCTION: Not known; does not seem to participate in nod factor
 synthesis but required for nodulation on some specific Medicago
 species such as M.littoralis.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

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CC -----
DR EMBL: U26430; AAC44091.1; -; Genomic DNA.
DR EMBL: AF007232; AAK5074.1; -; Genomic DNA.
DR PIR: H95313; H95313.
DR PIR: S71360; S71360.
DR InterPro: IPR000051; SAM bd.
KW Complete proteome; Modulation; Plasmid.
SQ SEQUENCE 476 AA; 53674 MW; EF0A4009B5F4965E CRC64;

Query Match 57.0%; Score 45; DB 1; Length 476;
Best Local Similarity 63.6%; Pred. No. 46;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 5 QWNPAGIEAAA 15
Db 100 ENSFAGLKAAA 110

RESULT 12
Q6PW80 RHIME PRELIMINARY; PRT; 476 AA.
AC Q6PW80;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE NoaA.
GN NoaA;
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=042BW;
RA Du B.H., Jiang J.Q., Li X.H., Wang L., Yang S.S.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY573929; AAS79316.1; -; Genomic DNA.
DR GO: GO:0008757; F:S-adenosylmethionine-dependent methyltransf. .; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR InterPro: IPR000051; SAM bd.
SQ SEQUENCE 476 AA; 53719 MW; 71B86963E865ECD CRC64;

Query Match 57.0%; Score 45; DB 2; Length 476;
Best Local Similarity 63.6%; Pred. No. 46;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 5 QWNPAGIEAAA 15
Db 100 ENSFAGLKAAA 110

RESULT 13
Q4ZN28 PSESY PRELIMINARY; PRT; 913 AA.
AC Q4ZN28;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE SecA protein.
GN ORFNames=Psyr_4094;
OS Pseudomonas syringae pv. syringae B728a.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=205918;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B728a;
RG DOE Joint Genome Institute;
RA Chain P., Larimer F., DiBartolo G., Copeland A., Lykidis A., Trong S.,
RA Nolan M., Goitsman E., Thiel J., Melfatti S., Lapidus A., Detter J.C.,
RA Land M., Richardson P.M., Kyrpides N.C., Ivanova N.;
RT "Comparison of two complete genome sequences of Pseudomonas syringae
pv. syringae B728a and pv. tomato DC3000.";

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Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B728a;
RA Loper J.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B728a;
RA Fell H., Fell W.S., Lindow S.E.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: CF000075; AAX39124.1; -; Genomic DNA.
DR InterPro: IPR001410; DEAD.
DR InterPro: IPR001650; Helicase_C.
DR InterPro: IPR011539; RHD.
DR InterPro: IPR004027; SEC_C motif.
DR InterPro: IPR000185; SecA.
DR InterPro: IPR011115; SecA DEAD.
DR InterPro: IPR011130; SecA PP bind.
DR InterPro: IPR011116; SecA SW.
DR Pfam: PF00271; Helicase_C; 1.
DR Pfam: PF02810; SEC-C; 1.
DR Pfam: PF07517; SecA DEAD; 1.
DR Pfam: PF01043; SecA_PP bind; 1.
DR Pfam: PF07516; SecA_SW; 1.
DR PRINTS: PR00906; SECA.
DR TIGRFAMs: TIGR00963; secA. 1.
SQ SEQUENCE 913 AA; 103258 MW; B30D5B96F620668A CRC64;

Query Match 57.0%; Score 45; DB 2; Length 913;
Best Local Similarity 63.6%; Pred. No. 89;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 QWNPAGIEAAA 14
Db 699 EQMNVAGLESA 709

RESULT 14
Q4IYL2 AZOVI PRELIMINARY; PRT; 4331 AA.
AC Q4IYL2;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Non-ribosomal peptide synthase: Amino acid adenylation.
GN ORFNames=AvinDRAFT_3823;
OS Azotobacter vinelandii AvOP.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=322710;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AVOP;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Azotobacter vinelandii
AvOP.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AVOP;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Azotobacter vinelandii
AvOP.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AVOP;
RG DOE Joint Genome Institute;
RT "Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.

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RN RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AVOP;
RG US DOE Joint Genome Institute (JGI-PGP);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Picluc S., Richardson P.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAU03000004; EMB05898.1; -; Genomic DNA.
SQ SEQUENCE 4331 AA; 478712 MW; 5D701A8C0E294F4E CRC64;

Query Match 57.0%; Score 45; DB 2; Length 4331;
Best Local Similarity 53.8%; Pred. No. 4.4e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 EQOWNFAGIEAAA 15
Db 3729 DAQWYAGLNARA 3741
: |||: |||

RESULT 15
Q9KMY8 VIBCH
ID Q9KMY8 VIBCH PRELIMINARY; PRT; 217 AA.
AC Q9KMY8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE FNE protein.
GN OrderedLocusNames=VCA0178;
OS Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OX NCBI_TaxID=666;
RN [1]
NUCLEOTIDE SEQUENCE.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301; DOI=10.1038/35020000;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.L.,
RA Ermolaeva M.D., Vamathevan J.J., Bass S., Qin H., Dragoi I.,
RA Sellers P., McDonald L.A., Uterback T.R., Fleischmann R.D.,
RA Niernan W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R.,
RA Mekalanos J.J., Venter J.C., Fraser C.W.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae."
RL Nature 406:477-483(2000).
CC -!- SUBCELLULAR LOCATION: Periplasmic (By similarity).
DR EMBL; AE004358; AAF96091.1; -; Genomic DNA.
DR PIR; A82491; A82491.
DR TIGR; VCA0178; -.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact...; IEA.
DR GO; GO:0015035; F:protein disulfide oxidoreductase activity; IEA.
DR InterPro; IPR001853; DSB.
DR InterPro; IPR012336; Thioresdoxin-like.
DR InterPro; IPR012335; Thioresdoxin_fold.
DR Pfam; PF01323; DSB.1.
KW Complete proteome; Periplasmic.
SQ SEQUENCE 217 AA; 24897 MW; 79B473E32313B5E8 CRC64;

Query Match 54.4%; Score 43; DB 2; Length 217;
Best Local Similarity 75.0%; Pred. No. 46;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TEQOWNFAGIEA 13
Db 170 TEQOWLQAGIHA 181
||||| |||||

RESULT 16
Q8X3F8_EC057

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ID Q8X3F8_EC057 PRELIMINARY; PRT; 247 AA.
AC Q8X3F8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein EC01576.
GN OrderedLocusNames=EC01576;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
NUCLEOTIDE SEQUENCE.
RC STRAIN=O157:H7 / Sakai / RIMD 0509952 / EHCC;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayaishi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Oheubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasaki C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12."
RL DNA Res. 8:11-22(2001).
DR EMBL; BA000007; BAB34999.1; -; Genomic DNA.
DR PIR; H90825; H90825.
DR InterPro; IPR000223; Peptidase_S26A.
DR PROSITE; PS00761; SPASE_I_3; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 247 AA; 27429 MW; 676680113259AB70 CRC64;

Query Match 54.4%; Score 43; DB 2; Length 247;
Best Local Similarity 53.9%; Pred. No. 52;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 EQOWNFAGIEAAA 15
Db 22 QQWGFSGIKKAA 34
: |||: |||: |||

RESULT 17
Q5NGF1_FRATT
ID Q5NGF1_FRATT PRELIMINARY; PRT; 770 AA.
AC Q5NGF1;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Fusion protein PurC/PurD (EC 6.3.2.6) (EC 6.3.4.13).
GN Names=purC; OrderedLocusNames=FT0894;
OS Francisella tularensis (subsp. tularensis).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Thiotrichales;
OC Francisellaceae; Francisella.
OX NCBI_TaxID=119856;
RN [1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SCHU S4 / Schu 4;
RX PubMed=15640799; DOI=10.1038/ng1499;
RA Larsson P., Oyston P.C.F., Chain P., Chu M.C., Duffield M.,
RA Fuxelius H.-H., Garcia E., Haelltorp G., Johansson D., Isherwood K.E.,
RA Karp P.D., Larsson E., Liu Y., Michell S., Prior J., Prior R.,
RA Malfatti S., Sjoestedt A., Svensson K., Thompson N., Vergez L.,
RA Wagg J.K., Wren B.W., Lindler L.E., Andersson S.G.E., Forsman M.,
RA Titball R.W.;
RT "The complete genome sequence of Francisella tularensis, the causative
RT agent of tularemia."
RL Nat. Genet. 37:153-159(2005).
CC -!- CATALYTIC ACTIVITY: ATP + 5-phospho-D-riboseylamine + glycine = ADP
CC + phosphate + N(1)-(5-phospho-D-riboseyl)glycinamide.
CC -!- PATHWAY: De novo purine biosynthesis; second step.
DR EMBL; AJ749949; CAG45527.1; -; Genomic DNA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0004637; F:phosphoribosylamine-glycine ligase activity; IEA.
DR GO; GO:0004639; F:phosphoribosylaminimidazolesuccinocarboxam...; IEA.
DR GO; GO:0009113; P:purine base biosynthesis; IEA.
DR GO; GO:0006164; P:purine nucleotide biosynthesis; IEA.

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DR InterPro; IPR011761; ATP_GRASP.
DR InterPro; IPR000115; Gars.
DR InterPro; IPR001636; SAICAR_synt.
DR Pfam; PF02842; GARS_A; 1.
DR Pfam; PF02842; GARS_B; 1.
DR Pfam; PF02843; GARS_C; 1.
DR Pfam; PF02844; GARS_D; 1.
DR Pfam; PF02844; GARS_E; 1.
DR Pfam; PF01259; SAICAR_synt; 1.
DR Pfam; PF01259; SAICAR_synt; 1.
DR Pfam; PF01259; SAICAR_synt; 1.
DR TIGRFAMS; TIGR00877; purD; 1.
DR PROSITE; PSS0975; ATP_GRASP; 1.
DR PROSITE; PSS0184; GARS; 1.
DR PROSITE; PSS0157; SAICAR_SYNTHETASE_1; 1.
DR PROSITE; PSS0157; SAICAR_SYNTHETASE_2; UNKNOWN 1.
DR PROSITE; PSS0158; SAICAR_SYNTHETASE; Purine biosynthesis.
KW Complete proteome; ligase; Purine biosynthesis.
SQ SEQUENCE 770 AA; 86352 MW; C5D66AA2CAFD03CA3 CRC64;

Query Match 54.4%; Score 43; DB 2; Length 770;
Best Local Similarity 53.8%; Pred. No. 1.7e+02;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTEQQWNFAGIEA 13
Db 174 LTQQQWDFASQKA 186

RESULT 18
OBIDJ8 SYNEL
ID Q8DJEB_SYNEL PRELIMINARY; PRT; 785 AA.
AC Q8DJEB;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE T11277 protein.
GN OrderedLocusNames=t11277;
OS Synechococcus elongatus (Thermosynechococcus elongatus).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=32046;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BP-1;
RX MEDLINE=22225144; PubMed=12240834;
RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
RA Watanabe A., Iriquchi M., Kawashima K., Kimura T., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,
RA Shimo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
RA "Complete genome structure of the thermophilic cyanobacterium
RT Thermosynechococcus elongatus BP-1.";
RL DNA Res. 9:123-130(2002).
DR EMBL; BA000039; BAC06829.1; -; Genomic DNA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR004300; Glyco_hydro_57.
DR Pfam; PF03065; Glyco_hydro_57; 1.
DR Complete proteome.
KW Complete proteome.
SQ SEQUENCE 785 AA; 90977 MW; 4960ADA9529C9A01 CRC64;

Query Match 54.4%; Score 43; DB 2; Length 785;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 EQQWNFAG 10
Db 614 EQQWNFAG 621

RESULT 19
QWFTL_BORBR
ID Q7WFTL_BORBR PRELIMINARY; PRT; 911 AA.
AC Q7WFTL;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Preprotein translocase secA subunit.
GN Name=secA; Synonyms=azi, pea, prID; OrderedLocusNames=BPP3743;
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OX Alcaligenaceae; Bordetella.
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=12822 / ATCC BAA-587;

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DE Preprotein translocase secA subunit.
GN Name=secA; Synonyms=azi, pea, prID; OrderedLocusNames=B84189;
OC Bordetella bronchiseptica (Alcaligenes bronchiseptica).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OX Alcaligenaceae; Bordetella.
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RB50 / ATCC BAA-588;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640449; CAE34553.1; -; Genomic_DNA.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004366; F:ATPase activity; IEA.
DR GO; GO:0003678; F:nucleic acid binding; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0017038; P:protein import; IEA.
DR GO; GO:0008605; P:protein targeting; IEA.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR004027; SEC_C_motif.
DR InterPro; IPR000185; SecA.
DR InterPro; IPR011115; SecA_DEAD.
DR InterPro; IPR011130; SecA_PP_bind.
DR InterPro; IPR011116; SecA_SW.
DR Pfam; PF00271; Helicase_C; 1.
DR Pfam; PF02810; SEC-C; 1.
DR Pfam; PF07517; SecA_DEAD; 1.
DR Pfam; PF01043; SecA_PP_bind; 1.
DR Pfam; PF07516; SecA_SW; 1.
DR PRINTS; PR00906; SFCA.
DR TIGRFAMS; TIGR00963; secA; 1.
DR PROSITE; PS01312; SECA; 1.
DR Complete proteome.
SQ SEQUENCE 911 AA; 103302 MW; 3E25B9B0D59A2597 CRC64;

Query Match 54.4%; Score 43; DB 2; Length 911;
Best Local Similarity 58.3%; Pred. No. 2e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 EQQWNFAGIEAA 14
Db 705 EQQWDFAGLEKA 716

RESULT 20
Q7W4C3_BORPA
ID Q7W4C3_BORPA PRELIMINARY; PRT; 911 AA.
AC Q7W4C3;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Preprotein translocase secA subunit.
GN Name=secA; Synonyms=azi, pea, prID; OrderedLocusNames=BPP3743;
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OX Alcaligenaceae; Bordetella.
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=12822 / ATCC BAA-587;

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[illegible]

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CC removed.
CC EMBL; AE005696; AAK22209.1; -; Genomic_DNA.
DR PIR; E87276; E87276.
DR HSSP; PG6744; LIAT.
DR TIGR; CC0222; -.
DR HAMAP; MF 00473; -; 1.
DR InterPro; IPR001672; G6P Isomerase.
DR PANTHER; PTHR11469; G6P_Isomerase; 1.
DR Pfam; PF00342; PGI; 1.
DR PRINTS; PR0662; G6PISOMERASE.
DR PROSITE; PS00765; P-GLUCOSE-ISOMERASE_1; 1.
DR PROSITE; PS00174; P-GLUCOSE-ISOMERASE_2; 1.
KW Complete proteome; Gluconeogenesis; Glycolysis; Isomerase.
FT ACT_SITE 380 380 By similarity.
FT ACT_SITE 508 508 By similarity.
SQ SEQUENCE 539 AA; 57526 MW; B233DFBAF7FD1595 CRC64;

Query Match 53.2%; Score 42; DB 1; Length 539;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 1 MTEQWNFAGIEAAA 14
DB 48 LSKQWDEAGLEAA 61

RESULT 26
Q9A279 CAUCR PRELIMINARY; PRT; 723 AA.
AC Q9A279;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Prolyl oligopeptidase family protein.
GN OrderedLocusNames=CC3687;
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;

[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;
RA Nieman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,
RA Berry K.J., Utterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,
RA Ermlaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
RA Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RT Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL; AE006026; AAK25649.1; -; Genomic_DNA.
DR PIR; E87706; E87706.
DR TIGR; CC3687; -.
DR GO; GO:0003824; F: catalytic activity; IEA.
DR GO; GO:0004287; F: prolyl oligopeptidase activity; IEA.
DR GO; GO:0006508; P: proteolysis and peptidolysis; IEA.
DR InterPro; IPR001375; Peptidase_S9.
DR InterPro; IPR002470; Peptidase_S9A.
DR InterPro; IPR004106; Peptidase_S9A_N.
DR InterPro; IPR000379; Ser_estr.
DR Pfam; PF00326; Peptidase_S9; 1.
DR Pfam; PF02897; Peptidase_S9_N; 1.
DR PRINTS; PR00862; PROLIGOPTASE.
KW Complete proteome.
SQ SEQUENCE 723 AA; 78547 MW; 05FB0515D74819A8 CRC64;

Query Match 53.2%; Score 42; DB 2; Length 723;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

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OY 2 TEQQWNFAGIEAAA 15
DB 316 TEPTWTFAGVAIPA 329

RESULT 27
Q8PQM3 XANAC PRELIMINARY; PRT; 418 AA.
AC Q8PQM3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Serine-pyruvate aminotransferase.
GN OrderedLocusNames=XAC0300;
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;

[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A.,
RA Almeida N.F. Jr., Alves L.M.C., do Amaral A.M., Bertolini M.C.,
RA Camargo L.E.A., Camarotte G., Cannavan F., Cardozo J., Chambergo F.,
RA Ciapina L.P., Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R.,
RA El-Dorri H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Gruber A.,
RA Ferro M.I.T., Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C. de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.B., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities.";
RN Nature 417:459-463(2002).
DR EMBL; AE011655; AAM35192.1; -; Genomic_DNA.
DR HSSP; P21549; 1H0C.
DR GO; GO:0008483; F: transaminase activity; IEA.
DR GO; GO:0008152; P: metabolism; IEA.
DR InterPro; IPR000192; Aminotrans_V.
DR Pfam; PF00266; Aminotran_5; 1.
KW Aminotransferase; Complete proteome; Pyruvate; Transferase.
SQ SEQUENCE 418 AA; 44746 MW; 7F9B577CD39DE843 CRC64;

Query Match 52.5%; Score 41.5; DB 2; Length 418;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 7; Gaps 1;

OY 2 TEQQWNFAGIEAAA 14
DB 66 TENRTWFLVDGTARAGIEA 85

RESULT 28
Q5QWV0 IDILO PRELIMINARY; PRT; 98 AA.
AC Q5QWV0;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Uncharacterized conserved secreted protein.
GN OrderedLocusNames=II0566;
OS Idiomarina loihiensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Idiomarinaceae; Idiomarina.
OX NCBI_TaxID=135577;

[1]

```

```
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=L2-TR / DSM 15497 / ATCC BAA-735;
RX PubMed=1559722; DOI=10.1073/pnas.0407638102;
RA Hou S., Saw J.H., Lee K.S., Freitas T.A., Belisle C., Kawarabayashi Y.,
RA Donachie S.P., Pikina A., Galperin M.Y., Koonin E.V., Makarova K.S.,
RA Omelchenko M.V., Sorokin A., Wolf Y.I., Li Q.X., Keum Y.S.,
RA Campbell S., Deney J., Aizawa S.-I., Shibata S., Malahoff A.,
RA Alam M.;
RT "Genome sequence of the deep-sea gamma-proteobacterium Idiomarina
RT loihiensis reveals amino acid fermentation as a source of carbon and
RT energy.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:18036-18041 (2004).
DR EMBL; AEO17340; AAV81407.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 98 AA; 9411 MW; 4098B547D53D40C4 CRC64;

Query Match 51.9%; Score 41; DB 2; Length 98;
Best Local Similarity 46.7%; Pred. No. 45;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 MTEQOWNFAGIEAA 15
   : : | | | | |
Db 38 LSTEAVVFGVAA 52

RESULT 29
DSBB_ECOLI
ID DSBB_ECOLI STANDARD; PRT; 176 AA.
AC P0A6M5; P30018; Q47408;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DE Disulfide bond formation protein B (Disulfide oxidoreductase).
GN Name=dsbB; Synonyms=roxB; OrderedLocusNames=z1948, EC81680;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA Perna N.T., Plunkett G., III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.P., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533 (2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / Sakai / RIMD 050952 / EHEC;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22 (2001).
CC -!- FUNCTION: Required for disulfide bond formation in some
CC periplasmic proteins such as phoA or ompA. Acts by oxidizing the
CC deaB protein (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (By similarity).
CC -!- SIMILARITY: Belongs to the dsbB family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
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CC EMBL; AEO051174; AAG56036.1; -; Genomic_DNA.
DR EMBL; BAO00007; BAB35103.1; -; Genomic_DNA.
DR PIR; H90838; H90838.
DR HAMAP; MF_00286; -; 1.
DR InterPro; IPR003752; DsbB.
DR InterPro; IPR012139; DsbB_proteobact.
DR Pfam; PF02600; DsbB; 1.
DR PIRSF; PIRSF000258; DsbB; 1.
KW Chaperone, Complete proteome, Electron transport, Inner membrane,
KW Membrane, Oxidoreductase, Redox-active center, Transmembrane;
KW Transport.
FT TOPO_DOM 1 14 Cytoplasmic (By similarity).
FT TRANSMEM 15 31 By similarity.
FT TOPO_DOM 32 49 Periplasmic (By similarity).
FT TRANSMEM 50 65 By similarity.
FT TOPO_DOM 66 71 Cytoplasmic (By similarity).
FT TRANSMEM 72 89 By similarity.
FT TOPO_DOM 90 144 Periplasmic (By similarity).
FT TRANSMEM 145 163 By similarity.
FT TOPO_DOM 164 176 Cytoplasmic (By similarity).
FT DISULFID 41 44 Redox-active (By similarity).
FT DISULFID 104 130 Redox-active (By similarity).
SQ SEQUENCE 176 AA; 20142 MW; 9C8D673D51E9F09B CRC64;

Query Match 51.9%; Score 41; DB 1; Length 176;
Best Local Similarity 60.0%; Pred. No. 82;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 EQQWNFAGIE 12
   | : | | | | |
Db 132 EQQWDFLGLE 141

RESULT 30
DSBB_ECOLI
ID DSBB_ECOLI STANDARD; PRT; 176 AA.
AC P0A6M2; P30018; Q47408;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DE Disulfide bond formation protein B (Disulfide oxidoreductase).
GN Name=dsbB; Synonyms=roxB; OrderedLocusNames=b1185;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND CHARACTERIZATION.
RX MEDLINE=93157338; PubMed=8430071;
RA Bardwell J.C.A., Lee J.-O., Jander G., Martin N., Belin D.,
RA Beckwith J.;
RT "A pathway for disulfide bond formation in vivo.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:1038-1042 (1993).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93348217; PubMed=7688471;
RA Missiakas D., Georgopoulos C., Raina S.;
RT "Identification and characterization of the Escherichia coli gene
RT dsbB, whose product is involved in the formation of disulfide bonds in
RT vivo.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:7084-7088 (1993).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kikagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
```

corresponding to the 12.7-28.0 min region on the linkage map.";
 RL DNA Res. 3:137-155(1996).
 [4]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Ferna N.T., Burland V.,
 Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 Mau B., Shao Y.;
 RA "The complete genome sequence of *Escherichia coli* K-12.";
 RT Science 277:1453-1474(1997).
 RL [5]
 RN PRELIMINARY NUCLEOTIDE SEQUENCE OF 1-169.
 RC STRAIN=K12;
 RX MEDLINE=92283803; PubMed=1317851;
 RA Pinner E., Padan E., Schuldiner S.;
 RT "Cloning, sequencing, and expression of the rhaB gene, encoding a
 RT Na⁺/H⁺ antiporter in *Escherichia coli*.";
 RL J. Biol. Chem. 267:11064-11068(1992).
 RN [6]
 RN TOPOLOGY, AND MUTAGENESIS OF CYSTEINE RESIDUES.
 RP MEDLINE=95045404; PubMed=7957076;
 RX Jander G., Martin N.L., Beckwith J.;
 RA "Two cysteines in each periplasmic domain of the membrane protein DsbB
 RT are required for its function in protein disulfide bond formation.";
 RL EMBO J. 13:5121-5127(1994).
 RN [7]
 RP ACTIVE SITES.
 RX MEDLINE=99164086; PubMed=10064586; DOI=10.1093/emboj/18.5.1192;
 RA Kobayashi T., Ito K.;
 RT "Respiratory chain strongly oxidizes the CXXC motif of DsbB in the
 RT *Escherichia coli* disulfide bond formation pathway.";
 RL EMBO J. 18:1192-1198(1999).
 RN [8]
 RN TOPOLOGY.
 RC STRAIN=K12 / MG1655;
 RX PubMed=15919996; DOI=10.1126/science.1109730;
 RA Daley D.O., Rapp M., Granseth E., Melen K., Drew D., von Heijne G.;
 RT "Global topology analysis of the *Escherichia coli* inner membrane
 RT proteome.";
 RL Science 308:1321-1323(2005).
 CC -1- FUNCTION: Required for disulfide bond formation in some
 CC periplasmic proteins such as phoA or ompA. Acts by oxidizing the
 CC dsbA protein. Integral membrane protein. Inner membrane.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
 CC -1- SIMILARITY: Belongs to the dsbB family.
 CC -1- CAUTION: Ref.7 sequence differs from that shown due to a
 CC frameshift in position 130.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC removed.
 CC -----
 DR EMBL; L03721; AAA23711.1; ALT INIT; Genomic_DNA.
 DR EMBL; U00096; AAC74269.1; -; Genomic_DNA.
 DR EMBL; D90753; BAA36040.1; ALT INIT; Genomic_DNA.
 DR EMBL; D90752; BAA36032.1; ALT INIT; Genomic_DNA.
 DR EMBL; M83655; AAA24220.1; ALT_FRAME; Genomic_DNA.
 DR FIR; F64864; F64864.
 DR ECHOBASE; EBI366; -.
 DR EcoGene; EG11393; dsbB.
 DR HAMAP; MF 00286; -; 1.
 DR InterPro; IPR003752; DsbB.
 DR InterPro; IPR012139; DsbB_proteobact.
 DR Pfam; PF02600; DsbB; 1.
 DR PIRSF; PIRSF00258; DsbB; 1.
 KW Chaperone; Complete proteome; Electron transport; Inner membrane;
 KW Membrane; Oxidoreductase; Redox-active center; Transmembrane;
 KW Transport.
 TOPO_DOM 1 14 Cytoplasmic (Probable).
 FT

FT TRANSMEM 15 31 Probable.
 FT TOPO_DOM 32 49 Periplasmic (Probable).
 FT TRANSMEM 50 65 Probable.
 FT TOPO_DOM 66 71 Cytoplasmic (Probable).
 FT TRANSMEM 72 89 Probable.
 FT TOPO_DOM 90 144 Periplasmic (Probable).
 FT TRANSMEM 145 163 Probable.
 FT TOPO_DOM 164 176 Cytoplasmic (Probable).
 FT DISULFID 41 44 Redox-active.
 FT DISULFID 104 130 Redox-active.
 FT CONFLICT 74 74 M -> MM (in Ref. 5).
 SQ SEQUENCE 176 AA; 20142 MW; 9CBD673D51E9F09B CRC64;
 Query Match 51.9%; Score 41; DB 1; Length 176;
 Best Local Similarity 60.0%; Pred. No. 82;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 3 EQOWNPAGIE 12
 DB 132 ERQWDFLGIE 141
 RESULT 31
 ID P95622 RHILE PRELIMINARY; PRT; 182 AA.
 AC P95622;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Cytochrome c1 (fragment).
 OS Rhizobium leguminosarum.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
 OX NCBI_TaxID=384;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=97158229; PubMed=9004501;
 RA Wu G., Delgado M.J., Vargas C., Davies A.E., Poole R.K., Downie J.A.;
 RT "The cytochrome bcl complex but not CymC is necessary for symbiotic
 RT nitrogen fixation by *Rhizobium leguminosarum*.";
 RL Microbiology 142:3381-3388(1996).
 DR EMBL; X98018; CAA6651.1; -; Genomic DNA.
 DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0020037; F:heme binding; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR012282; Cytochrome_c_r.
 DR InterPro; IPR002326; Cyt_c1.
 DR Pfam; PF02167; Cytochrom C1; 1.
 DR PRINTS; PR00603; CYTOCHROMECL.
 FT NON_TER 182 182
 SQ SEQUENCE 182 AA; 19787 MW; BC1C7255859D4488 CRC64;
 Query Match 51.9%; Score 41; DB 2; Length 182;
 Best Local Similarity 66.7%; Pred. No. 85;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 2 TEQOWNPAG 10
 DB 51 TEEWTFAG 59
 RESULT 32
 TRMB_PROMA
 ID TRMB_PROMA STANDARD; PRT; 213 AA.
 AC Q7VDU8;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE tRNA (Guanine-N(7)-)-methyltransferase (EC 2.1.1.33) (tRNA (m7G46) -
 DE methyltransferase).
 GN Name=trmb; OrderedLocusNames=Pro0270;
 OS Prochlorococcus marinus.

OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
 OC Prochlorococcus.
 OX NCBI_TaxID=1219;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=SRG / CCMF 1375 / SS120;
 RX MEDLINE=22810154; PubMed=12917486; DOI=10.1073/pnas.1733211100;
 RA Darlene A., Salanoubat M., Partensky F., Artiguenave F., Axmann I.M.,
 RA Burre V., Duprat S., Galperin M.Y., Koonin E.V., Le Gall F.,
 RA Makarova K.S., Ostrowski M., Ozdas S., Robert C., Rogozin I.B.,
 RA Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Winkler P.,
 RA Wolf Y.I., Hess W.R.;
 RT "Genome sequence of the cyanobacterium Prochlorococcus marinus SS120,
 RT a nearly minimal oxyphototrophic genome.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025(2003).
 CC -!- FUNCTION: Catalyzes the formation of N(7)-methylguanine at
 CC position 46 (m7G46) in tRNA (By similarity).
 CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-
 CC homocysteine + tRNA containing N(7)-methylguanine.
 CC -!- SIMILARITY: belongs to the RNA m7G methyltransferase family.
 CC
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; AE017161; AAP99316.1; -; Genomic_DNA.
 DR HAMAP; MF 01057; -; 1.
 DR InterPro; IPR004395; CHP91.
 DR InterPro; IPR003358; Methyltransf_4.
 DR PANTHER; PTHR12793; Methyltransf_4; 1.
 DR Pfam; PF02390; Methyltransf_4; 1.
 DR TIGRFAMs; TIGR00091; Cons_hypoth91; 1.
 DR Complete proteome; Methyltransferase; Transferase; tRNA processing.
 SK SEQUENCE 213 AA; 25154 MW; 6413A68BC374A5DC CRC64;
 QY
 Query Match 51.9%; Score 41; DB 1; Length 213;
 Best Local Similarity 75.0%; Pred. No. 1e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 5 QWNFAGIE 12
 ||||| |||
 DB 53 QWNFLGVE 60
 ||||| |||
 RESULT 33
 Q8KU04_RHLV PRELIMINARY; PRT; 217 AA.
 ID Q8KU04_RHLV PRELIMINARY;
 AC Q8KU04;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE FbcC' (Fragment).
 GN Name=fbcC;
 OS Rhizobium leguminosarum (biovar viciae).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
 OX NCBI_TaxID=387;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=UPM791;
 RA Sidler S., Ruiz-Arques T., Imperial J.;
 RL Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
 RE EMBL; AF466752; RAN03341.1; -; Genomic DNA.
 DR GO; GO:0005746; C-mitochondrial electron transport chain; IEA.
 DR GO; GO:0005489; F-electron transporter activity; IEA.
 DR GO; GO:0020037; F-iron binding; IEA.
 DR GO; GO:0006118; F-electron transport; IEA.
 DR InterPro; IPR012282; Cytochrome_c_R.
 DR InterPro; IPR002326; Cyt_C1.
 DR InterPro; IPR009056; Cyt_c_monohaem.
 DR Pfam; PF02167; Cytochrom_C1; 1.

DR PRINTS; PR00603; CYTOCHROME C1.
 DR PROSITE; PS51007; CYTC; 1.
 FT NON TER 217
 SQ SEQUENCE 217 AA; 23460 MW; A020BBB947007876 CRC64;
 Query Match 51.9%; Score 41; DB 2; Length 217;
 Best Local Similarity 66.7%; Pred. No. 1e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 OY 2 TEQOWNFAG 10
 ||:| |||
 DB 51 TEEEWTFAG 59
 ||:| |||
 RESULT 34
 Q83LH0_SHIFL PRELIMINARY; PRT; 248 AA.
 ID Q83LH0_SHIFL PRELIMINARY;
 AC Q83LH0;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=SF1133;
 OS Shigella flexneri.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Shigella.
 OX NCBI_TaxID=623;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=301 / Serotype 2a;
 RX MEDLINE=22272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
 RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
 RA Sun J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
 RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
 RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
 RA Yu J.;
 RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
 RT through comparison with genomes of Escherichia coli K12 and O157.";
 RL Nucleic Acids Res. 30:4432-4441 (2002).
 DR EMBL; AR005674; AAN42751.1; -; Genomic DNA.
 SK Complete proteome; Hypothetical protein.
 QY SEQUENCE 248 AA; 27647 MW; 34896D1FE05CF9B2 CRC64;
 Query Match 51.9%; Score 41; DB 2; Length 248;
 Best Local Similarity 58.3%; Pred. No. 1.2e+02;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 OY 4 QQWNFAGIEAAA 15
 ||||| |||
 DB 23 QWGFSGIKKAA 34
 ||||| |||
 RESULT 35
 Q6ABJ4_PROAC PRELIMINARY; PRT; 319 AA.
 ID Q6ABJ4_PROAC PRELIMINARY;
 AC Q6ABJ4;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=PPA0113;
 OS Propionibacterium acnes.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Propionibacteriaceae; Propionibacteriaceae; Propionibacterium.
 OX NCBI_TaxID=1747;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=KPA171202 / DSM 16379;
 RX PubMed=15286373; DOI=10.1126/science.1100330;
 RA Brueggemann H., Henne A., Hoster F., Liesegang H., Wierer A.,
 RA Stittgatter A., Hujer S., Puere P., Gottschalk G.;
 RT "The complete genome sequence of Propionibacterium acnes, a commensal
 RT of human skin."


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GN OrderedLocusNames=VF2058;
OS Vibrio fischeri (strain ATCC 700601 / ES114).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OX Vibrionaceae; Vibrio.
NCBI_TaxID=312309;
[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15703294; DOI=10.1073/pnas.040900102;
RA Ruby E.G., Urbanowicz M., Campbell J., Dunn A., Faini M., Gunsalus R.,
RA Lestroth P., Lupp C., McCann J., Millikan D., Schaefer A., Stabb E.,
RA Stevens A., Visick K., Whistler C., Greenberg E.P.;
RT "Complete genome sequence of Vibrio fischeri: a symbiotic bacterium
RT with pathogenic congeners.";
RL Proc. Natl. Acad. Sci. U.S.A. 102:3004-3009 (2005).
DR EMBL; CP000020; AAW86553.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; P:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/rel_permeasel.
DR InterPro; IPR004841; Permease_region.
DR Pfam; PF00324; AA_permease; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 444 AA; 46393 MW; 3A3073C0E26ED4BA CRC64;

Query Match 51.9%; Score 41; DB 2; Length 444;
Best Local Similarity 60.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 WNFAGIEAAA 15
|:|:|:|
DB 199 WSFVGVSAA 208

RESULT 40
QBDA6 VIBVU PRELIMINARY; PRT; 445 AA.
AC QBDA67
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cadaverine/lysine antiporter.
GN OrderedLocusNames=V12059;
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OX Vibrionaceae; Vibrio.
NCBI_TaxID=672;
[1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=CMCP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA Choy H.E.;
RT "Complete genome sequence of Vibrio vulnificus CMCP6.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE016803; AAO10448.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; P:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/rel_permeasel.
DR InterPro; IPR004841; Permease_region.
DR Pfam; PF00324; AA_permease; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 445 AA; 46856 MW; 558CA9B01FC7CFA9 CRC64;

Query Match 51.9%; Score 41; DB 2; Length 445;
Best Local Similarity 60.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 WNFAGIEAAA 15
|:|:|:|

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DB 199 WSFVGVSAA 208

RESULT 41
QSKV76 VIBCH PRELIMINARY; PRT; 445 AA.
AC QSKV76;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cadaverine/lysine antiporter Cadd, putative.
GN OrderedLocusNames=VC0280;
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OX Vibrionaceae; Vibrio.
NCBI_TaxID=666;
[1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301; DOI=10.1038/35020000;
RA Heidelberg J.P., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.L.,
RA Ermolaeva M.D., Vamathevan J.J., Bass S., Qin H., Dragoi I.,
RA Sellers P., McDonald L.A., Utterback T.R., Fleischmann R.D.,
RA Niernan W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R.,
RA Mekalanos J.J., Venter J.C., Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483 (2000).
DR EMBL; AE004116; AAF93455.1; -; Genomic DNA.
DR FTR; D82342; D82342.
DR TIGR; VC0280; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; P:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/rel_permeasel.
DR InterPro; IPR004841; Permease_region.
DR Pfam; PF00324; AA_permease; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 445 AA; 46908 MW; 3A64F21B9680684C CRC64;

Query Match 51.9%; Score 41; DB 2; Length 445;
Best Local Similarity 60.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 WNFAGIEAAA 15
|:|:|:|
DB 199 WSFVGVSAA 208

RESULT 42
Q7SVK9 VIBPA PRELIMINARY; PRT; 447 AA.
AC Q7SVK9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Lysine:cadaverine antiporter.
GN Name=cadb;
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OX Vibrionaceae; Vibrio.
NCBI_TaxID=670;
[1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=VO2-64;
RA Tanaka Y., Kimura B., Watanabe T., Iwase K., Fujii T.;
RA Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB124819; BAB12082.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.

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DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/rel_permease1.
DR InterPro; IPR004841; Permease_region.
DR Pfam; PF00324; AA_permease; 1.
KW Transmembrane; Transport.
SQ SEQUENCE 447 AA; 47082 MW; 1A4E14027C225903 CRC64;

Query Match 51.9%; Score 41; DB 2; Length 447;
Best Local Similarity 60.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 WNPAGIEAAA 15
Db 199 WSPFVGESAA 208
|:|:|:|:|

RESULT 43
Q87KT5_VIBPA PRELIMINARY; PRT; 447 AA.
AC Q87KT5_2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Putative cadaverine/lysine antiporter CadB (lysine/cadaverine
DE antiporter).
GN Name=cadB; OrderedLocNames=VP2891;
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=RIMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Tijina Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae."
RN Lancet 361:743-749 (2003).
[2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=Vp +11;
RA Kimura B., Tanaka Y., Iwase K., Fujii T.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BA000031; BAC61154.1; -; Genomic DNA.
DR EMBL; AB089504; BAC77061.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/rel_permease1.
DR InterPro; IPR004841; Permease_region.
DR Pfam; PF00324; AA_permease; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 447 AA; 47070 MW; 359CE2DB780866F0 CRC64;

Query Match 51.9%; Score 41; DB 2; Length 447;
Best Local Similarity 60.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 WNPAGIEAAA 15
Db 199 WSPFVGESAA 208
|:|:|:|:|

RESULT 44
Q7MIY1_VIBVY PRELIMINARY; PRT; 452 AA.
ID Q7MIY1_VIBVY
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AC Q7MIY1;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cadaverine/lysine antiporter.
DE OrderedLocNames=VW2382; YJ016).
OS Vibrio vulnificus (Strain YJ016).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=196600;
[1]
RN NUCLEOTIDE SEQUENCE.
RP PubMed=14656965; DOI=10.1101/gr.1295503;
RX Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
RA Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,
RA Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;
RT "Comparative genome analysis of Vibrio vulnificus, a marine
RT pathogen."
RL Genome Res. 13:2577-2587 (2003).
DR EMBL; BA000037; BAC95146.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/rel_permease1.
DR InterPro; IPR004841; Permease_region.
DR Pfam; PF00324; AA_permease; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 452 AA; 47628 MW; 5E552E3796BC2E7A CRC64;

Query Match 51.9%; Score 41; DB 2; Length 452;
Best Local Similarity 60.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 WNPAGIEAAA 15
Db 206 WSPFVGESAA 215
|:|:|:|:|

RESULT 45
O28786_ARCFU PRELIMINARY; PRT; 471 AA.
ID O28786_ARCFU
AC O28786;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein AFI486.
GN OrderedLocNames=AFI486;
OS Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxID=2234;
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475; DOI=10.1038/37052;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M.L., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.R.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.J.,
RA Peterson S.N., Reich C.I., McNeil L.K., Badger J.H., Glodek A.,
RA Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L.A.,
RA Uitterback T.R., Cotton M.D., Spriggs T., Artiach P., Kaine B.P.,
RA Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C.,
RA Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O.,
RA Woese C.R., Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus."
RL Nature 390:364-370 (1997).
DR EMBL; AE001000; AAB89769.1; -; Genomic DNA.
DR PIR; E69435; E69435.
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DR TIGR: AF1486; -.
DR InterPro: IPR007566; DUF557.
DR Pfam: PR04477; DUF557; 1.
DR FRSF: FR5706677; UCR006677; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 471 AA; 54165 MW; 892A03A47FBD4771 CRC64;

Query Match 51.9%; Score 41; DB 2; Length 471;
Best Local Similarity 61.5%; Pred. No. 2.2e+02;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 EQOWNFAGIEAAA 15
DB 45 EQWDFEGKEADA 57

RESULT 46
Q4L323 STAHU PRELIMINARY; PRT; 601 AA.
AC Q4L323.
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Beta-glucuronidase.
GN ORFNames=SH2645;
OS Staphylococcus haemolyticus (strain JCSG1435).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=279808;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JCSG1435;
RA Takeuchi F., Watanabe S., Baba T., Yuzawa H., Ito T., Cui L.,
RA Morimoto Y., Kuroda M., Takahashi M., Ankaï A., Baba S., Fukui S.,
RA Lee J.C., Hiramatsu K.;
RT "Whole genome sequencing of Staphylococcus haemolyticus uncovers
RT extreme plasticity of its genome and dynamism in the evolution of
RT human-colonizing staphylococcal species.";
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP006716; BAE05954.1; -; Genomic DNA.
SQ SEQUENCE 601 AA; 68799 MW; DB43162EF0ADA25 CRC64;

Query Match 51.9%; Score 41; DB 2; Length 601;
Best Local Similarity 58.3%; Pred. No. 2.9e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 EQOWNFAGIEAA 14
DB 549 EQWNFADPETS 560

RESULT 47
Q7UWA6 RHOB PRELIMINARY; PRT; 719 AA.
AC Q7UWA6.
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alpha-amylase (EC 3.2.1.1).
GN OrderedLocusNames=RB2160;
OS Rhodopirella baltica.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [1]_TaxID=117;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA Schlesner H., Anann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
RT strain 1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).
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DR EMBL: BX294136; CAD72460.1; -; Genomic_DNA.
DR HSP: Q32462; 1K1W.
DR GO: GO:0004556; F:alpha-amylase activity; IEA.
DR GO: GO:0015798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO: GO:0005925; F:carbohydrate metabolism; IEA.
DR InterPro: IPR004300; Glyco_hydro_57.
DR Pfam: PF03065; Glyco_hydro_57; 1_57.
KW Complete proteome; Glycosidase; Hydrolase.
SQ SEQUENCE 719 AA; 81466 MW; 39642E0732728CA8 CRC64;

Query Match 51.9%; Score 41; DB 2; Length 719;
Best Local Similarity 54.5%; Pred. No. 3.4e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 OMNFAGIEAAA 15
DB 598 EWNFAGLPSGA 608

RESULT 48
Q7NOS9 CHRVO PRELIMINARY; PRT; 903 AA.
AC Q7NOS9.
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Preprotein translocase secA subunit.
GN Name=secA; OrderedLocusNames=CV4281;
OS Chromobacterium violaceum.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OX Neisseriaceae; Chromobacterium.
OX NCBI_TaxID=536;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 12472 / DSM 30191;
RX MEDLINE=22882880; PubMed=14500782; DOI=10.1073/pnas.1832124100;
RA Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,
RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,
RA Alves-Gomes J.A., Andrade E.M., Araripe J., de Araujo M.F.F.,
RA Ascófi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,
RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
RA Bordignon J., Brígido M.M., Brito C.A., Brocchi M., Burty H.A.,
RA Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carriro D.M.,
RA Creczynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,
RA Fantinatti F., Farias I.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,
RA Ferri M.T., Franco G.R., Freitas N.S.A., Furlan L.R.,
RA Gazzinelli R.T., Gomes E.A., Gonçalves P.R., Grangeiro T.B.,
RA Grattapaglia D., Grisard E.C., Hanna E.S., Jardim S.N., Laurino J.,
RA Leoi L.C.T., Lima I.P.A., Loureiro M.F., Lyra M.C.C.P., Martins W.S.,
RA Madeira H.M.F., Manfio G.P., Maranhão A.Q., Meissner R.V., Moreira M.A.M.,
RA di Mauro S.M.Z., de Medeiros S.R.B., Oliveira J.G., Oliveira S.C., Pereira J.O.,
RA Paixao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Potrich D.P.,
RA Pereira M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Rondinelli E.,
RA Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,
RA Santos E.B.P., Santos F.R., Schneider M.P.C., Seunanez H.N.,
RA Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,
RA Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,
RA Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Urmenyi T.,
RA Vettore A., Wessens R., Zaha A., Simpson A.J.G.;
RT "The complete genome sequence of Chromobacterium violaceum reveals
RT remarkable and exploitable bacterial adaptability.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665 (2003).
DR EMBL: AE016925; AAQ61941.2; -; Genomic_DNA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0005515; F:protein binding; IEA.
DR GO: GO:0017038; P:protein import; IEA.
DR GO: GO:0004605; P:protein targeting; IEA.
DR InterPro: IPR004027; SEC_C_motif.
DR InterPro: IPR000185; SecA_DEAD.
DR InterPro: IPR011115; SecA_DEAD.
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DR InterPro; IPR011130; SecA_PP_bind.
 DR InterPro; IPR011116; SecA_SW.
 DR Pfam; PF02810; SEC-C; 1.
 DR Pfam; PF07517; SecA_DEAD; 1.
 DR Pfam; PF01043; SecA_PP_bind; 1.
 DR Pfam; PF07516; SecA_SW; 1.
 DR PRINTS; PR00906; SECA.
 DR TIGRFAMs; TIGR00963; secA; 1.
 DR PROSITE; PS01312; SECA; 1.
 KW ATP-binding; Complete proteome; Nucleotide-binding; Protein transport;
 KW Translocation; Transport.
 SQ SEQUENCE 903 AA; 101273 MW; 328A076D764845F3 CRC64;

Query Match 51.9%; Score 41; DB 2; Length 903;
 Best Local Similarity 60.0%; Pred. No. 4.3e+02;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 EQWNPAGIE 12
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 Db 700 EQQWDLAGLE 709

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 Q8XVJ6 RALSO
 ID Q8XVJ6 RALSO PRELIMINARY; PRT; 934 AA.
 AC Q8XVJ6;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE PROBABLE PRPTEININ TRANSLOCASE SECA SUBUNIT.
 GN Name=secA; OrderedLocNames=RSC2834; ORFNames=RSC00271;
 OS Ralstonia solanacearum (Pseudomonas solanacearum).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Ralstonia.
 OX NCBI_TaxID=305;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=GMI1000;
 RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
 RA Ariat M., Billaut A., Brotter P., Camus J.C., Cattolico L.,
 RA Chandler M., Choise N., Claudel-Renard C., Cunac S., Demange N.,
 RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
 RA Signier P., Thebaud P., Whalen M., Wincker P., Levy M.,
 RA Weissenbach J., Boucher C.A.;
 RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
 RL Nature 415:497-502(2002).
 DR EMBL; AL646072; CAP16541.1; -; Genomic_DNA.
 DR HSSP; P28366; 1M6N.
 DR GO; GO:0016020; C-membrane; IEA.
 DR GO; GO:0005224; F:ATP binding; IEA.
 DR GO; GO:0005515; F:protein binding; IEA.
 DR GO; GO:0017038; P:protein import; IEA.
 DR GO; GO:0006605; P:protein targeting; IEA.
 DR InterPro; IPR004027; SEC_C motif.
 DR InterPro; IPR000185; SecA_DEAD.
 DR InterPro; IPR011115; SecA_DEAD.
 DR InterPro; IPR011130; SecA_PP_bind.
 DR InterPro; IPR011116; SecA_SW.
 DR Pfam; PF02810; SEC-C; 1.
 DR Pfam; PF07517; SecA_DEAD; 1.
 DR Pfam; PF01043; SecA_PP_bind; 1.
 DR Pfam; PF07516; SecA_SW; 1.
 DR PRINTS; PR00906; SECA.
 DR TIGRFAMs; TIGR00963; secA; 1.
 DR PROSITE; PS01312; SECA; 1.
 KW ATP-binding; Complete proteome; Nucleotide-binding; Protein transport;
 KW Translocation; Transport.
 SQ SEQUENCE 934 AA; 105242 MW; F9C3FA601EA62095 CRC64;

Query Match 51.9%; Score 41; DB 2; Length 934;
 Best Local Similarity 60.0%; Pred. No. 4.5e+02;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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 Db 708 EQQWDLAGLE 717

RESULT 50
 Q4HUJ5 GIBZE
 ID Q4HUJ5 GIBZE PRELIMINARY; PRT; 947 AA.
 AC Q4HUJ5;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=FGI1363.1;
 OS Gibberella zeae PH-1.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
 OX NCBI_TaxID=229533;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PH-1;
 RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
 RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
 RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
 RA Choepel Y., Collamore A., Cook A., Cooke P., Corum B., DeArelano K.,
 RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
 RA Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
 RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
 RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
 RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
 RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
 RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,
 RA Matthews C., Mauceli E., McCarthy M., Meldrum J., Meneus L.,
 RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
 RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
 RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
 RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
 RA Roman J., Schauer S., Schuback R., Seaman S., Severy P., Smirnov S.,
 RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
 RA Talanas J., Tesfaye S., Theodore J., Topham K., Travers M.,
 RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
 RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
 RA Lander E.;
 RT "Fusarium graminearum genome sequence.";
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC preliminary data.
 CC EMBL; AACW01000465; EAA78676.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 947 AA; 104687 MW; CD71625E06FALL149 CRC64;

Query Match 51.9%; Score 41; DB 2; Length 947;
 Best Local Similarity 54.5%; Pred. No. 4.6e+02;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 EQWNPAGIEA 13
 |:|:|:|:|:
 Db 146 DQWNPFGTKA 156

Search completed: May 4, 2006, 15:17:41
 Job time : 193 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 15:13:52 ; Search time 24 Seconds
(without alignments)
60.135 Million cell updates/sec

Title: US-09-830-839-1

Perfect score: 79

Sequence: 1 MTEQQWNFAIEAAA 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

PIR 80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	100.0	95	2 A70803	early secretory an
2	45	57.0	476	2 H95313	NoeA host specific
3	45	57.0	476	2 S71360	noeA protein - Rhi
4	43	54.4	217	2 A82491	frnE protein VCA01
5	43	54.4	247	2 H90825	hypothetical prote
6	42	53.2	369	2 G72069	conserved hypothet
7	42	53.2	369	2 E86554	Fe-S oxidoreductas
8	42	53.2	539	2 E87276	glucose-6-phosphat
9	42	53.2	723	2 E87706	prolyl oligopeptid
10	41	51.9	176	1 F64864	protein-disulfide
11	41	51.9	176	2 H85696	hypothetical prote
12	41	51.9	176	2 H90838	protein-disulfide
13	41	51.9	445	2 D82342	probable cadaverin
14	41	51.9	471	2 E69435	hypothetical prote
15	40	50.6	38	2 H82256	hypothetical prote
16	39	49.4	219	2 AG2036	hypothetical prote
17	39	49.4	328	2 A70145	prolipoprotein dia
18	39	49.4	393	2 AH2150	hypothetical prote
19	39	49.4	482	2 T01762	hypothetical prote
20	39	49.4	714	2 G86844	hypothetical prote
21	39	49.4	916	2 D83093	secretion protein
22	38.5	48.7	392	2 A87572	aminotransferase,
23	38	48.1	252	2 FC1140	cellulase (EC 3.2.
24	38	48.1	284	2 E82868	hypothetical prote
25	38	48.1	297	2 AD2851	cytochrome c1 fbcC
26	38	48.1	305	1 H75285	probable phosphos
27	38	48.1	319	2 B97628	cytochrome c1 (AF1
28	38	48.1	443	2 AE0826	probable cadaverin
29	38	48.1	444	2 H86108	transport of lysin

30	38	48.1	444	2 A41842	lysine/cadaverine
31	38	48.1	444	2 B91268	transport proteoin
32	38	48.1	593	2 I51213	drebrin - chicken
33	38	48.1	607	2 A43776	drebrin E2 - chick
34	37	46.8	61	2 E86084	hypothetical prote
35	37	46.8	192	1 S75273	hypothetical prote
36	37	46.8	229	2 D90002	hypothetical prote
37	37	46.8	251	2 C81816	hypothetical prote
38	37	46.8	256	2 AD1115	hypothetical prote
39	37	46.8	257	2 AE1476	hypothetical prote
40	37	46.8	264	2 S22090	catechol O-methylt
41	37	46.8	267	2 A87404	ribosomal protein
42	37	46.8	294	2 I41220	glyceraldehyde-3-p
43	37	46.8	326	2 A41862	C-S lyase (ORF326)
44	37	46.8	335	2 T39033	hypothetical prote
45	37	46.8	348	2 A12475	hypothetical prote
46	37	46.8	367	2 G90508	GMP synthase, pp-A
47	37	46.8	371	2 C70626	hypothetical prote
48	37	46.8	445	2 AF1022	probable amino aci
49	37	46.8	445	2 B65221	probable amino aci
50	37	46.8	445	2 A91266	probable amino aci
51	37	46.8	445	2 F86106	probable amino aci
52	37	46.8	475	1 CZCLCA	cellulase (EC 3.2.
53	37	46.8	490	2 C86879	arginine/ornitine
54	37	46.8	497	2 G86878	arginine/ornitine
55	37	46.8	527	2 C82349	hypothetical prote
56	37	46.8	573	2 C82525	hypothetical prote
57	37	46.8	582	2 B81048	conserved hypothet
58	37	46.8	585	2 B81827	hypothetical prote
59	37	46.8	640	2 G96733	auxin transport pr
60	37	46.8	668	2 S49639	probable membrane
61	37	46.8	887	2 E82590	leucyl-tRNA synthe
62	36	45.6	102	2 B87150	conserved hypothet
63	36	45.6	102	2 D70631	hypothetical prote
64	36	45.6	131	1 IE8BC1	insB protein homol
65	36	45.6	148	2 S30280	hpcR protein - Esc
66	36	45.6	175	2 A53523	endocrinal secretor
67	36	45.6	230	2 S51274	terminal protein -
68	36	45.6	237	2 T12403	H+-transporting tw
69	36	45.6	238	2 AH3176	conserved hypothet
70	36	45.6	288	2 T00862	probable serine/th
71	36	45.6	326	2 D97743	hypothetical prote
72	36	45.6	326	2 B71681	pyruvate dehydroge
73	36	45.6	338	2 JE0196	hydroxyteroid sul
74	36	45.6	344	2 S46495	glucan endo-1,3-be
75	36	45.6	395	2 T09373	hypothetical prote
76	36	45.6	413	2 AC1045	probable permease
77	36	45.6	466	2 AE0147	probable amino aci
78	36	45.6	475	2 T46745	RV8167 protein hom
79	36	45.6	493	2 F95940	arginine/ornitine
80	36	45.6	496	2 A56040	probable xanthine
81	36	45.6	499	2 AH3323	protein-tyrosine k
82	36	45.6	511	2 G95945	UDP-N-acetylmuramo
83	36	45.6	530	2 H81885	probable histidine
84	36	45.6	533	2 A87710	purH bifunctional
85	36	45.6	724	2 T00495	hypothetical prote
86	36	45.6	743	2 AF1250	I5 protein - white
87	36	45.6	743	2 AB1613	pyruvate formate-1
88	36	45.6	901	2 H64101	pyruvate formate-1
89	36	45.6	902	2 AG2989	preprotein translo
90	36	45.6	919	2 B98294	preprotein translo
91	36	45.6	965	2 A32852	membrane alanyl am
92	36	45.6	994	1 MNWTM	nonstructural prot
93	36	45.6	3106	1 S53868	laminin alpha-2 ch
94	36	45.6	585	2 A46209	protein-tyrosine-p
95	35.5	44.9	593	1 JN0805	protein-tyrosine-p
96	35.5	44.9	593	1 JN0805	protein-tyrosine-p
97	35.5	44.9	593	1 JN0805	protein-tyrosine-p
98	35.5	44.9	593	1 JN0805	protein-tyrosine-p
99	35.5	44.9	593	1 JN0805	protein-tyrosine-p
100	35	44.3	20	2 AE0120	insertion element
101	35	44.3	82	2 T10869	y4KO protein - Rhi
102	35	44.3	102	4 S59295	hypothetical prote

103	35	44.3	131	2	S18540	hypothetical prote	176	34	43.0	154	2	F90632	prolipoprotein sig
104	35	44.3	145	2	F70698	hypothetical prote	177	34	43.0	154	2	E85483	signal peptidase I
105	35	44.3	150	2	A11938	hypothetical prote	178	34	43.0	166	2	AB0508	lipoprotein signal
106	35	44.3	175	2	I51385	glucocorticoid-reg	179	34	43.0	169	2	A10058	signal peptidase I
107	35	44.3	176	2	AD0261	disulfide bond for	180	34	43.0	183	2	H82290	conserved hypoteth
108	35	44.3	181	2	AB0757	cobinamide kinase	181	34	43.0	216	2	AB1052	probable hexulose-
109	35	44.3	195	2	T22032	hypothetical prote	182	34	43.0	216	2	D91275	probable hexulose-
110	35	44.3	198	2	AD0194	conserved hypoteth	183	34	43.0	216	2	D86116	probable membrane
111	35	44.3	210	2	G83082	hypothetical prote	184	34	43.0	230	2	S03348	hypothetical prote
112	35	44.3	211	2	G75533	riboemul protein	185	34	43.0	232	2	S70211	conserved hypoteth
113	35	44.3	221	2	A86703	hypothetical prote	186	34	43.0	245	2	F95430	probable oxidoradu
114	35	44.3	221	2	D71450	hypothetical prote	187	34	43.0	246	2	AH0190	probable tryptopha
115	35	44.3	243	2	G87105	hypothetical prote	188	34	43.0	252	2	G72488	probable permease
116	35	44.3	249	2	D82751	probable amidotran	189	34	43.0	282	2	E83605	hypothetical prote
117	35	44.3	257	2	E81308	conserved hypoteth	190	34	43.0	285	2	H82323	hypothetical prote
118	35	44.3	258	2	E81308	hypothetical prote	191	34	43.0	289	2	B84950	amino acid ABC tra
119	35	44.3	263	2	I54780	APK1 antigen - hum	192	34	43.0	275	2	B83671	hypothetical prote
120	35	44.3	280	2	T25829	hypothetical prote	193	34	43.0	286	2	AH2416	chitinase (EC 3.2.
121	35	44.3	287	2	S77309	hypothetical prote	194	34	43.0	290	2	UX0076	hypothetical prote
122	35	44.3	296	2	E88250	conserved hypoteth	195	34	43.0	303	2	T17774	hypothetical prote
123	35	44.3	301	2	E84331	homoserine kinase	196	34	43.0	314	2	D97538	ribosomal large ch
124	35	44.3	302	2	S02333	hypothetical prote	197	34	43.0	329	2	AG2757	hypothetical prote
125	35	44.3	345	2	T19706	type II site-speci	198	34	43.0	334	2	H87192	probable isomerase
126	35	44.3	368	2	A85768	partial beta-D-glu	199	34	43.0	350	2	F69112	hypothetical prote
127	35	44.3	370	2	D90919	beta-D-glucuronida	200	34	43.0	350	2	T31820	hypothetical prote
128	35	44.3	404	2	S58535	hypothetical 43.7K	201	34	43.0	372	2	S76427	phospho-2-dehydro-
129	35	44.3	404	2	E86128	hypothetical prote	202	34	43.0	376	2	A75449	probable membrane
130	35	44.3	415	2	E91287	hypothetical prote	203	34	43.0	379	2	S46187	septin- yeast cdc1
131	35	44.3	420	2	T42379	PH05-like protein	204	34	43.0	380	2	T39234	actin-related prot
132	35	44.3	422	2	T31285	biphenyl dioxygena	205	34	43.0	398	2	S44028	aminotransferase l
133	35	44.3	422	2	T05592	tyrosine transamin	206	34	43.0	402	2	C87133	probable aminotran
134	35	44.3	427	2	F97790	putrescine-ornithi	207	34	43.0	407	2	B07033	LIS-1 protein - hu
135	35	44.3	429	2	F71651	conserved hypoteth	208	34	43.0	409	2	S46113	platelet-activatin
136	35	44.3	440	2	C82410	probable tyrosine	209	34	43.0	410	2	E84052	glycosyltransferas
137	35	44.3	451	2	E83418	putrescine/ornithi	210	34	43.0	411	2	E82993	hypothetical 42.6K
138	35	44.3	452	2	G95306	probable amino aci	211	34	43.0	423	2	S47761	hypothetical 47.3K
139	35	44.3	459	2	S10196	NADH2 dehydrogenas	212	34	43.0	423	2	G86027	probable transport
140	35	44.3	461	1	A30364	alpha-L-fucosidase	213	34	43.0	423	2	C91181	probable transport
141	35	44.3	461	1	A30364	alpha-L-fucosidase	214	34	43.0	438	2	A47702	glucan 1,3-beta-gl
142	35	44.3	469	2	S62702	H+-transporting tw	215	34	43.0	438	2	T52149	beta-glucanase (im
143	35	44.3	469	2	D70048	ABC transporter (a	216	34	43.0	441	2	S14441	retinol-binding pr
144	35	44.3	469	2	D75186	hypothetical prote	217	34	43.0	441	2	S14441	sucrase-6-phosphat
145	35	44.3	472	2	D87321	succinylglutamic s	218	34	43.0	487	2	B83882	conserved hypoteth
146	35	44.3	475	2	E71219	hypothetical prote	219	34	43.0	488	2	AD0735	probable bacteriop
147	35	44.3	492	2	F84376	hypothetical prote	220	34	43.0	488	2	AG0621	hypothetical prote
148	35	44.3	513	2	G96757	probable protein A	221	34	43.0	513	2	T03916	phosphoribosylamin
149	35	44.3	517	2	A23261	nicotinic acetylch	222	34	43.0	526	2	A81135	ribosomal protein
150	35	44.3	536	2	R36395	spore wall maturat	223	34	43.0	557	1	R3EC1	308 ribosomal prot
151	35	44.3	542	2	D83041	probable two-compo	224	34	43.0	557	2	AC0614	308 ribosomal subu
152	35	44.3	548	2	T05671	hypothetical prote	225	34	43.0	557	2	B90753	308 ribosomal subu
153	35	44.3	599	2	I53395	antigen LEC-A mo	226	34	43.0	557	2	H85616	308 ribosomal subu
154	35	44.3	603	1	GBEGGC	beta-glucuronidase	227	34	43.0	558	2	AB0170	308 ribosomal subu
155	35	44.3	730	2	E75387	NADH dehydrogenase	228	34	43.0	616	2	S38060	hypothetical prote
156	35	44.3	758	2	T51335	subtilisin-like pr	229	34	43.0	632	1	VGNSY	carboxylic acid tr
157	35	44.3	764	2	F83431	periplasmic beta-g	230	34	43.0	639	2	D70720	surface glycoprote
158	35	44.3	840	2	S74707	nitrogen fixation	231	34	43.0	655	2	A12556	hypothetical prote
159	35	44.3	1223	2	S62011	PH085 protein - ye	232	34	43.0	655	2	A12556	heat shock protein
160	35	44.3	1551	2	AB2410	WD-repeat protein	233	34	43.0	656	2	A87112	coagulation factor
161	35	44.3	1693	2	S76086	beta transducin-l1	234	34	43.0	673	2	A49878	probable ribonucle
162	35	44.3	1741	2	T15978	hypothetical prote	235	34	43.0	693	2	G72805	polynucleotide
163	35	44.3	1879	2	S74915	extracellular nucl	236	34	43.0	714	2	AC3497	subtilisin homolog
164	34.5	43.7	382	2	F82428	iron-containing al	237	34	43.0	736	2	T12963	subtilisin homolog
165	34.5	43.7	546	1	SVBYHM	histidine-tRNA lig	238	34	43.0	739	2	T12964	secreted protease
166	34.5	43.7	589	2	T19216	hypothetical prote	239	34	43.0	781	2	G96991	lipoprotein (impor
167	34.5	43.7	611	2	T19217	hypothetical prote	240	34	43.0	789	2	G90587	homolog to drosoph
168	34.5	43.7	942	2	C96574	hypothetical prote	241	34	43.0	790	2	T50337	subtilisin-like pr
169	34	43.0	90	2	H69159	hypothetical prote	242	34	43.0	803	2	T04190	protein F33E2.2 li
170	34	43.0	96	2	AD2869	conserved hypoteth	243	34	43.0	848	2	B87950	hypothetical prote
171	34	43.0	96	2	F97845	hypothetical prote	244	34	43.0	855	2	T20082	preproteinal transi
172	34	43.0	138	2	E87846	hypothetical prote	245	34	43.0	914	2	F82760	hypothetical prote
173	34	43.0	147	2	D86943	conserved hypoteth	246	34	43.0	1084	2	T15616	interphotoreceptor
174	34	43.0	155	2	AG0214	homoproteaschut	247	34	43.0	1285	1	RJBOP	1-pyrroline-5-carb
175	34	43.0	164	1	ZPECL	signal peptidase I	248	34	43.0	1323	2	AH0225	

249	34	43.0	1530	2	AH1396	peptidoglycan anch	322	41.8	418	2	B98269	probable transport
250	34	43.0	2500	2	G88493	protein F57B9.2 [i	323	41.8	419	2	A81651	conserved hypothet
251	34	43.0	26926	1	I38344	titin, cardiac mus	324	41.8	421	2	S76827	hypothetical prote
252	33.5	42.4	610	2	B83745	aspartate transami	325	41.8	426	2	JC5086	polytropic cytoplas
253	33.5	42.4	630	2	JC5374	angiotensin-conver	326	41.8	428	2	D83861	hypothetical prote
254	33	41.8	73	2	AD1043	transcription regu	327	41.8	435	2	E86515	oligopeptide bindi
255	33	41.8	79	2	B36670	cell division cont	328	41.8	435	2	C72107	peptide ABC transp
256	33	41.8	87	2	B96708	hypothetical prote	329	41.8	451	2	F83793	DNA-damage-inducib
257	33	41.8	107	2	B74298	hypothetical prote	330	41.8	453	2	AG0353	probable RNA-bindi
258	33	41.8	122	2	A13427	transposase BME114	331	41.8	455	2	T44519	putrescine/ornithi
259	33	41.8	122	2	AI3478	transposase BME118	332	41.8	464	2	B86079	probable glycoprot
260	33	41.8	122	2	AD3377	transposase BME110	333	41.8	464	2	C91232	probable glycoprot
261	33	41.8	122	2	AE3599	transposase BME110	334	41.8	468	2	G83931	L-lysine 2,3-amino
262	33	41.8	122	2	AG3383	transposase BME110	335	41.8	468	2	H82321	arginine/ornithine
263	33	41.8	122	2	B82854	hypothetical prote	336	41.8	470	2	F83022	probable amino aci
264	33	41.8	131	1	CKKCV	cytochrome c' [val	337	41.8	472	2	E83497	probable amino aci
265	33	41.8	140	2	I46638	rearranged T-cell	338	41.8	475	2	A10010	probable membrane
266	33	41.8	140	2	F83128	probable transcrip	339	41.8	477	2	H83389	hypothetical prote
267	33	41.8	146	2	AG0630	homoprotocatechua	340	41.8	481	2	T10470	transcription init
268	33	41.8	158	2	AE1555	glutathione peroxi	341	41.8	481	2	D86619	arginine/ornithine
269	33	41.8	159	2	AG1197	glutathione peroxi	342	41.8	482	2	JH0110	probable arginine/
270	33	41.8	159	2	T46620	chemotaxis protein	343	41.8	483	2	G71523	probable rhamnose
271	33	41.8	161	2	T32027	hypothetical prote	344	41.8	484	2	T36427	arginine/ornithine
272	33	41.8	163	2	AC3526	homoprotocatechua	345	41.8	485	2	A72006	aspartate oxidase
273	33	41.8	167	2	C95056	RNA methyltransfer	346	41.8	487	2	E90251	hypothetical prote
274	33	41.8	173	2	G90351	disulfide bond for	347	41.8	490	2	T27095	probable amino aci
275	33	41.8	176	2	AH0723	probable kinase fr	348	41.8	500	2	AD1047	probable transport
276	33	41.8	177	2	H97205	rRNA methylase (EC	349	41.8	501	2	A86112	L-lysine transport
277	33	41.8	180	2	H97925	22K extracellular	350	41.8	501	2	S18573	probable membrane
278	33	41.8	183	2	A32851	hypothetical prote	351	41.8	501	2	A11031	photosystem II chl
279	33	41.8	183	2	G75378	ribosomal protein	352	41.8	507	2	S06272	photosystem II chl
280	33	41.8	191	2	G71835	ribosomal protein	353	41.8	509	2	JA0148	photosystem II chl
281	33	41.8	191	2	G64684	dermatopontin prec	354	41.8	509	2	AB1824	photosystem II pro
282	33	41.8	201	2	A47220	hypothetical prote	355	41.8	509	2	T06855	L-aspartate oxidas
283	33	41.8	218	2	D64162	hypothetical prote	356	41.8	514	2	B70368	hypothetical 56.3K
284	33	41.8	224	2	D89836	hypothetical prote	357	41.8	514	2	A91271	probable transport
285	33	41.8	229	2	F83879	thioesterase II BH	358	41.8	517	2	E95920	probable PSR type
286	33	41.8	242	2	F87640	exsB protein (impo	359	41.8	517	2	T45254	probable anthranil
287	33	41.8	243	2	G86701	hypothetical prote	360	41.8	529	2	T45254	hypothetical prote
288	33	41.8	244	2	S40698	riboflavin biosynt	361	41.8	535	2	D84340	hypothetical prote
289	33	41.8	248	2	S77407	hypothetical prote	362	41.8	536	2	E86550	hypothetical prote
290	33	41.8	264	2	AG2095	probable hydrolase	363	41.8	536	2	E72073	hypothetical prote
291	33	41.8	265	2	T35850	cytochrome c1 - Rh	364	41.8	552	2	AI2256	probable cerebrosi
292	33	41.8	282	1	JQ0347	nirV precursor [im	365	41.8	555	2	D95377	methanol dehydrog
293	33	41.8	283	2	AB3633	prolipoprotein dia	366	41.8	591	2	S68591	pyruvate oxidase (
294	33	41.8	289	2	E84098	conserved hypothet	367	41.8	591	2	F95084	hypothetical prote
295	33	41.8	290	2	C87208	hypothetical prote	368	41.8	591	2	G70713	pyruvate oxidase (
296	33	41.8	291	2	AG1065	homoserine kinase	369	41.8	606	2	S60090	radl7 protein - fi
297	33	41.8	306	2	S77133	protein F27J15.20	370	41.8	612	2	B95067	hypothetical prote
298	33	41.8	314	2	F96527	hypothetical prote	371	41.8	612	2	A97935	hypothetical prote
299	33	41.8	320	2	G84676	hypothetical prote	372	41.8	612	2	A97935	hypothetical integ
300	33	41.8	323	2	T21569	chitinase (EC 3.2.	373	41.8	625	2	T40742	hypothetical prote
301	33	41.8	333	2	T05187	hypothetical prote	374	41.8	630	2	T48369	electron transfer
302	33	41.8	339	2	AF2252	cymA protein precu	375	41.8	641	2	T38167	hypothetical prote
303	33	41.8	346	2	S55403	sulfate-binding pr	376	41.8	641	2	AI2524	hypothetical prote
304	33	41.8	352	2	S76739	MHC class I protei	377	41.8	659	2	T40383	hypothetical prote
305	33	41.8	361	2	I48160	conserved hypothet	378	41.8	670	2	T09205	hypothetical prote
306	33	41.8	369	2	F81674	probable Fe-S oxid	379	41.8	670	2	T09274	hypothetical prote
307	33	41.8	369	2	B71516	hypothetical prote	380	41.8	682	2	S40459	ribosomal protein
308	33	41.8	371	2	T05213	probable D-amino a	381	41.8	690	2	T11749	transferrin - Atla
309	33	41.8	371	2	B84615	3-dehydroquinat s	382	41.8	706	2	T01351	subtilisin-like pr
310	33	41.8	378	2	AF3257	probable membrane	383	41.8	711	2	S68443	double-stranded RN
311	33	41.8	383	2	S67813	hypothetical prote	384	41.8	723	2	H81794	receptor tyrosine
312	33	41.8	386	2	F87684	aromatic-amino-aci	385	41.8	766	2	G81216	ATP-dependent DNA
313	33	41.8	397	2	G81821	hypothetical prote	386	41.8	766	2	A37956	sulfate permease I
314	33	41.8	397	2	H70753	probable zinc fing	387	41.8	797	1	PHCGM	phosphorylase (EC
315	33	41.8	399	2	T48267	hypothetical prote	388	41.8	797	2	C91161	maltodextrin phosp
316	33	41.8	401	2	E87531	tniQ protein - Xan	389	41.8	797	2	B86007	maltodextrin phosp
317	33	41.8	405	2	S70150	probable permease	390	41.8	802	2	E91210	hypothetical prote
318	33	41.8	416	2	AB0081	aminopeptidase - D	391	41.8	802	2	H86056	hypothetical prote
319	33	41.8	417	2	F75303	hypothetical 44.8K	392	41.8	805	2	A64453	H+-exporting Anpas
320	33	41.8	418	2	S56369	probable transport	393	41.8	805	2	A64453	outer envelope mem
321	33	41.8	418	2	H86109		394	41.8	809	2	S55344	

395	33	41.8	817	2	T15138	hypothetical prote	468	32	40.5	146	2	F86081	hypothetical prote
396	33	41.8	833	1	S20387	outer membrane pro	469	32	40.5	146	2	S40864	hypothetical 16.5K
397	33	41.8	833	2	T14703	Fl capsule anchori	470	32	40.5	151	2	S37013	transposase (clone
398	33	41.8	856	2	I58411	protein-tyrosine k	471	32	40.5	166	2	B83700	hypothetical prote
399	33	41.8	873	2	E83148	leucyl-tRNA synth	472	32	40.5	176	1	S10202	parathyroid hormon
400	33	41.8	876	2	I45152	protein-tyrosine k	473	32	40.5	180	2	A56836	bone marrowstroma
401	33	41.8	879	2	A10728	conserved hypothet	474	32	40.5	185	2	S77003	hypothetical prote
402	33	41.8	880	1	JC4166	protein-tyrosine k	475	32	40.5	188	2	T41706	probable phosphopr
403	33	41.8	882	2	B53743	protein-tyrosine k	476	32	40.5	192	2	AH3385	hypothetical prote
404	33	41.8	882	2	I38912	receptor tyrosine	477	32	40.5	192	2	C96680	hypothetical 16 (
405	33	41.8	890	1	A53743	protein-tyrosine k	478	32	40.5	195	2	T46002	DNA binding protei
406	33	41.8	905	2	S75035	H+-exporting ATPas	479	32	40.5	204	2	H2256	conserved hypothet
407	33	41.8	911	2	AD2271	cation-transportin	480	32	40.5	211	2	E83116	SOS ribosomal prot
408	33	41.8	916	2	B84473	copia-like retroir	481	32	40.5	213	2	T24389	hypothetical prote
409	33	41.8	931	2	F84637	probable plasma me	482	32	40.5	215	2	A23012	conserved hypothet
410	33	41.8	977	2	I52657	seizure-related pr	483	32	40.5	216	2	S56421	Probable hexokinase-
411	33	41.8	1014	2	T24412	hypothetical prote	484	32	40.5	220	2	S45409	nuclear protein RO
412	33	41.8	1035	2	B90656	ICMF-like protein	485	32	40.5	226	2	C84852	hypothetical prote
413	33	41.8	1043	2	A56037	DNA-binding protei	486	32	40.5	228	1	C46335	vif protein - Maed
414	33	41.8	1067	2	T30061	hypothetical prote	487	32	40.5	229	2	T32772	hypothetical prote
415	33	41.8	1086	2	T33893	hypothetical prote	488	32	40.5	232	2	B83732	hypothetical prote
416	33	41.8	1112	2	T28048	hep70-related prot	489	32	40.5	240	2	I40335	hypothetical prote
417	33	41.8	1144	2	C85507	probable macrophag	490	32	40.5	244	2	T29079	hypothetical prote
418	33	41.8	1230	2	T13899	hypothetical prote	491	32	40.5	247	2	T01907	hypothetical prote
419	33	41.8	1247	2	A33812	interphotoreceptor	492	32	40.5	247	2	T11654	hypothetical prote
420	33	41.8	1289	2	E90098	RNA polymerase III	493	32	40.5	247	2	T43015	conserved hypothet
421	33	41.8	1353	2	TQ0407	xanthine dehydroge	494	32	40.5	251	2	H87692	hypothetical prote
422	33	41.8	1377	2	I54632	tsn protein - Esch	495	32	40.5	252	2	T44299	probable oxidoredu
423	33	41.8	1526	2	T19473	hypothetical prote	496	32	40.5	258	2	A96013	lipase-protein li
424	33	41.8	1547	2	T28657	blackjack protein,	497	32	40.5	264	2	E30500	MG068 homolog D02
425	33	41.8	1584	2	S57161	hypothetical prote	498	32	40.5	265	2	S73587	hypothetical prote
426	33	41.8	1607	2	T03022	MAP kinase kinase	499	32	40.5	266	2	A93369	cytochrome c1 (lamp
427	33	41.8	1616	2	E90704	Rhs core protein w	500	32	40.5	283	2	A33311	hypothetical prote
428	33	41.8	1645	2	H85554	hypothetical prote	501	32	40.5	283	2	S65215	monofunctional bio
429	33	41.8	1711	2	AD1842	WD-40 repeat prote	502	32	40.5	273	2	A80682	probable secreted
430	33	41.8	1779	2	T23130	hypothetical prote	503	32	40.5	273	2	F82646	hypothetical prote
431	33	41.8	2013	2	AD1129	probable peptidogl	504	32	40.5	273	2	B95765	Putative protease
432	33	41.8	2013	2	AI1489	probable peptidogl	505	32	40.5	273	2	H64915	hypothetical prote
433	33	41.8	2078	2	T25400	hypothetical prote	506	32	40.5	275	2	B98880	hypothetical prote
434	33	41.8	2241	2	T02857	conserved hypothet	507	32	40.5	277	2	H22226	hypothetical prote
435	33	41.8	2330	2	T26836	hypothetical prote	508	32	40.5	283	2	T51091	hypothetical prote
436	33	41.8	2338	2	T25810	hypothetical prote	509	32	40.5	285	2	B84316	halocyanin precurs
437	33	41.8	2492	1	A44213	nonstructural poly	510	32	40.5	288	2	T24066	exonuclease III ho
438	33	41.8	2492	1	C44213	nonstructural poly	511	32	40.5	291	2	AF0740	probable cation tr
439	33	41.8	2492	1	NNWVTD	nonstructural poly	512	32	40.5	312	2	H64162	hypothetical prote
440	33	41.8	2519	2	S43048	polyketide synthas	513	32	40.5	314	2	S52223	hypothetical prote
441	33	41.8	2519	2	S43048	polyketide synthas	514	32	40.5	314	2	T03524	cobD protein - Rho
442	32.5	41.1	2538	2	C82139	RTX toxin BtXA Vcl	515	32	40.5	317	2	T04201	hypothetical prote
443	32.5	41.1	2538	2	C82139	conserved hypothet	516	32	40.5	317	2	H95143	conserved hypothet
444	32.5	41.1	2538	2	C82139	conserved hypothet	517	32	40.5	317	2	F98011	conserved hypothet
445	32.5	41.1	2538	2	C82139	conserved hypothet	518	32	40.5	319	2	E75068	dipteric abc tran
446	32.5	41.1	2538	2	C82139	conserved hypothet	519	32	40.5	321	1	LNHUEP	IgE Fc receptor II
447	32.5	41.1	2538	2	C82139	conserved hypothet	520	32	40.5	321	2	F71163	probable oligopept
448	32.5	41.1	2538	2	C82139	conserved hypothet	521	32	40.5	322	2	D75142	oligopeptide trans
449	32.5	41.1	2538	2	C82139	conserved hypothet	522	32	40.5	322	2	T03928	probable peroxidase
450	32	40.5	81	2	AG0590	calcium channel pr	523	32	40.5	326	2	T27003	hypothetical prote
451	32	40.5	94	2	T29829	hypothetical prote	524	32	40.5	328	2	T29625	urate oxidase (EC
452	32	40.5	97	2	T07747	hypothetical prote	525	32	40.5	332	2	JC4535	hypothetical prote
453	32	40.5	107	2	I68725	IgE chain C2 regio	526	32	40.5	334	2	T19860	probable cathepsin
454	32	40.5	109	2	B97192	hypothetical prote	527	32	40.5	335	2	T37280	hypothetical prote
455	32	40.5	110	2	D82628	hypothetical prote	528	32	40.5	340	2	T34423	probable amino aci
456	32	40.5	111	2	T46490	hypothetical prote	529	32	40.5	341	2	H83162	hypothetical prote
457	32	40.5	113	2	E30560	Ig kappa chain V r	530	32	40.5	343	2	S25644	adhesin P1 precurs
458	32	40.5	113	2	A99915	hypothetical prote	531	32	40.5	347	2	S73381	translation initia
459	32	40.5	115	2	S68316	iron regulatory pr	532	32	40.5	351	2	S71960	maternal protein -
460	32	40.5	115	2	AI2743	hypothetical prote	533	32	40.5	353	2	IS1572	Wnt-11 protein pre
461	32	40.5	122	2	C69490	tungsten formylmet	534	32	40.5	354	2	JC4152	fructose-bisphosph
462	32	40.5	132	2	T35141	hypothetical prote	535	32	40.5	360	2	AH2272	hypothetical prote
463	32	40.5	138	2	H97524	hypothetical prote	536	32	40.5	362	2	T20686	hypothetical prote
464	32	40.5	140	2	H70632	hypothetical prote	537	32	40.5	362	2	A45845	MHC class I histoc
465	32	40.5	142	2	AB0940	probable membrane	538	32	40.5	362	2	B43680	K'362 protein - Af
466	32	40.5	144	2	AG0011	conserved membrane	539	32	40.5	364	2	T43361	probable potassium
467	32	40.5	146	2	F91234	hypothetical prote	540	32	40.5	366	2	T32598	hypothetical prote

541	32	40.5	367	2	B75597	first mannoseyl tra	614	32	40.5	645	2	S20138	probable protein k
542	32	40.5	374	2	AD1854	hypothetical prote	615	32	40.5	657	2	A87648	senser histidine k
543	32	40.5	376	2	A96643	hypothetical prote	616	32	40.5	658	1	S73805	DNA ligase (NAD) (
544	32	40.5	377	2	T27010	diphosphomevalonat	617	32	40.5	660	2	C86877	hypothetical prote
545	32	40.5	378	2	B98272	hypothetical prote	618	32	40.5	670	2	T05222	hypothetical prote
546	32	40.5	383	2	S57191	hypothetical prote	619	32	40.5	679	2	S28366	recombination repa
547	32	40.5	383	2	B83922	short-chain-specif	620	32	40.5	691	2	S39867	competence protein
548	32	40.5	384	2	T51423	formate dehydrogen	621	32	40.5	691	2	G81167	competence protein
549	32	40.5	385	2	S64340	hypothetical prote	622	32	40.5	691	2	B81937	protein-glutamine
550	32	40.5	388	1	BHMS	Ig epsilon chain C	623	32	40.5	695	2	S66662	translation elonga
551	32	40.5	388	2	E95007	sugar isomerase do	624	32	40.5	701	2	C81234	translation elonga
552	32	40.5	388	2	H97879	tagatose-6-phospha	625	32	40.5	705	2	E82006	hypothetical prote
553	32	40.5	388	2	D84992	hypothetical prote	626	32	40.5	705	2	T01911	hypothetical prote
554	32	40.5	389	2	D49263	potential oncogene	627	32	40.5	713	1	A34782	sperm-binding glyc
555	32	40.5	389	2	A59392	Wnt10b protein pre	628	32	40.5	721	2	T41942	hypothetical prote
556	32	40.5	392	2	G83575	conserved hypothet	629	32	40.5	722	2	H96986	endo-1,4-beta gluc
557	32	40.5	393	2	AE1896	hypothetical prote	630	32	40.5	732	2	AB0991	heavy metal-transp
558	32	40.5	399	1	AJFFIM	glutamate-ammonia	631	32	40.5	732	2	F86014	zinc-transporting
559	32	40.5	399	2	A69893	hypothetical prote	632	32	40.5	732	2	F91168	zinc-transporting
560	32	40.5	402	2	S58477	rdsl protein - fis	633	32	40.5	732	2	S47688	cd2+-exporting ATP
561	32	40.5	413	2	S73336	adhesin P1 precurs	634	32	40.5	736	2	JC7518	subtilisin-like se
562	32	40.5	423	1	BHMS	Ig epsilon chain C	635	32	40.5	743	2	E84767	hypothetical prote
563	32	40.5	435	2	E64079	putrescine/ornithi	636	32	40.5	752	2	S61505	glycogen(starch) s
564	32	40.5	439	2	A10586	putrescine/ornithi	637	32	40.5	754	2	G90484	beta-xylosidase [i
565	32	40.5	439	2	B40839	putrescine/ornithi	638	32	40.5	764	2	S49849	aconitate hydrat
566	32	40.5	439	2	H90718	putrescine transpo	639	32	40.5	766	1	CDH026	dipeptidyl-peptida
567	32	40.5	439	2	H85568	putrescine transpo	640	32	40.5	770	2	JC7728	xylan 1,4-beta-xy
568	32	40.5	439	2	D82384	putrescine-ornithi	641	32	40.5	795	2	D64343	hypothetical prote
569	32	40.5	445	2	A40639	exo-1,3-beta-gluc	642	32	40.5	795	2	H70934	hypothetical prote
570	32	40.5	446	2	AD0995	low-affinity gluco	643	32	40.5	802	2	S49252	penicillin amidase
571	32	40.5	448	2	T05591	tyrosine transamin	644	32	40.5	822	2	S77112	DNA mismatch repai
572	32	40.5	450	2	B83530	probable RNA meth	645	32	40.5	837	2	AF1388	translocase bindin
573	32	40.5	454	1	MHHY	Ig mu chain C regi	646	32	40.5	837	2	AH1763	translocase bindin
574	32	40.5	455	1	MHMS	Ig mu chain C regi	647	32	40.5	848	2	G86708	aconitate hydrat
575	32	40.5	455	2	A24976	NADH dehydrogenase	648	32	40.5	859	2	F84981	leucine-tRNA ligas
576	32	40.5	458	2	B90621	NADH2 dehydrogen	649	32	40.5	860	2	F86349	hypothetical prote
577	32	40.5	458	2	T11333	NADH2 dehydrogen	650	32	40.5	864	2	S60441	hypothetical prote
578	32	40.5	459	2	T11202	NADH2 dehydrogen	651	32	40.5	870	2	E72541	probable aconitate
579	32	40.5	459	2	T11543	NADH2 dehydrogen	652	32	40.5	874	2	B70945	hypothetical prote
580	32	40.5	462	2	S61332	IgA-specific metal	653	32	40.5	878	2	H83184	phosphoenolpyruv
581	32	40.5	464	2	C75186	L-aspartate oxidas	654	32	40.5	878	2	A97854	aconitate hydrat
582	32	40.5	467	2	B97213	FAD/FMN-containing	655	32	40.5	879	1	B64945	probable membrane
583	32	40.5	476	1	MHMS	Ig mu chain C regi	656	32	40.5	879	2	D85795	hypothetical prote
584	32	40.5	476	2	A90071	arginine/ornithin	657	32	40.5	879	2	H90946	hypothetical prote
585	32	40.5	476	2	H87352	hypothetical prote	658	32	40.5	881	1	A64040	hypothetical prote
586	32	40.5	481	2	D64883	Aminobenzoyl-gluta	659	32	40.5	883	2	C86729	hypothetical prote
587	32	40.5	481	2	A90869	hypothetical prote	660	32	40.5	885	2	T32771	hypothetical prote
588	32	40.5	481	2	H85749	hypothetical prote	661	32	40.5	887	2	D82049	phosphoenolpyruv
589	32	40.5	487	2	T28804	lipoprotein lipase	662	32	40.5	887	2	T27868	hypothetical prote
590	32	40.5	490	1	S04331	BRF-2 protein - hu	663	32	40.5	888	2	S50801	AMP deaminase homo
591	32	40.5	492	2	S49147	hypothetical prote	664	32	40.5	889	1	A44153	aconitate hydrat
592	32	40.5	502	2	T21935	hypothetical prote	665	32	40.5	889	2	A44154	aconitate hydrat
593	32	40.5	504	2	H86272	hypothetical prote	666	32	40.5	889	2	S26403	aconitate hydrat
594	32	40.5	510	2	F96987	2,3-bisphosphoglyc	667	32	40.5	889	2	S18720	aconitate hydrat
595	32	40.5	522	2	F75391	2-isopropylmalate	668	32	40.5	890	2	AB0270	aconitate hydrat
596	32	40.5	525	2	T01108	cellulase [EC 3.2.	669	32	40.5	891	2	AH0654	Clp Arpase [import
597	32	40.5	545	2	F84533	Mutator-like trans	670	32	40.5	891	2	B48642	aconitate hydrat
598	32	40.5	548	2	S38864	Ig epsilon chain C	671	32	40.5	891	2	A90860	aconitate hydrase
599	32	40.5	553	2	S53080	hypothetical prote	672	32	40.5	891	2	E85759	aconitate hydrase
600	32	40.5	557	2	D83478	gamma-glutamyltran	673	32	40.5	891	2	G64875	aconitate hydrat
601	32	40.5	561	2	S63388	probable membrane	674	32	40.5	891	2	G64875	aconitate hydrat
602	32	40.5	566	2	A49880	alpha-N-acetylglala	675	32	40.5	895	2	A13483	aconitate hydrat
603	32	40.5	569	2	JS0101	glucokinase regula	676	32	40.5	897	2	AD2906	cytoplasmic aconit
604	32	40.5	569	2	S32494	hypothetical prote	677	32	40.5	897	2	E97681	aconitate hydrat
605	32	40.5	584	2	C84325	hypothetical prote	678	32	40.5	898	2	B84471	aconitate hydrat
606	32	40.5	585	1	BWSAM1	mesR1 protein - St	679	32	40.5	898	2	T0101	aconitate hydrat
607	32	40.5	585	2	T44117	methicillin resist	680	32	40.5	898	2	A11279	aconitate hydrat
608	32	40.5	585	2	S20575	mesR1 protein - St	681	32	40.5	900	2	A11642	aconitate hydrat
609	32	40.5	604	2	A84753	hypothetical prote	682	32	40.5	901	2	F89910	aconitate hydrat
610	32	40.5	609	2	AH0388	alpha-glucosidase	683	32	40.5	901	2	A11642	aconitate hydrat
611	32	40.5	611	2	D84423	probable WD-40-rep	684	32	40.5	903	2	A87704	aconitate hydrat
612	32	40.5	627	1	S41745	glucokinase regula	685	32	40.5	906	2	G75362	aconitate hydrat
613	32	40.5	644	2	B87089	probable apolipop	686	32	40.5	907	2	T04820	aconitate hydrat

687	32	40.5	907	2	T02417	probable C2H2-type	760	31	39.2	159	2	A72660	hypothetical prote
688	32	40.5	908	2	G82824	acnitate XF0290 [761	31	39.2	162	1	RDEBDT	dihydrofolate redu
689	32	40.5	909	2	G63599	acnitate hydrat	762	31	39.2	167	2	S29579	ig light chain - r
690	32	40.5	910	2	B83451	acnitate hydrat	763	31	39.2	169	2	AC0556	conserved hypotet
691	32	40.5	943	2	F70873	acnitate hydrat	764	31	39.2	169	2	AB2076	hypothetical prote
692	32	40.5	944	2	G82135	acnitate hydrat	765	31	39.2	170	2	C86652	hypothetical prote
693	32	40.5	946	2	T16297	hypothetical prote	766	31	39.2	175	2	D86787	hypothetical prote
694	32	40.5	974	1	FXLMFD	H+-exporting ATPa	767	31	39.2	180	2	A00134	probable prophage
695	32	40.5	978	1	RG8R13	regulatory protein	768	31	39.2	182	2	A72240	conserved hypotet
696	32	40.5	1037	2	T13943	phospholipase D (E	769	31	39.2	184	2	S41960	Ras-related GTP-bi
697	32	40.5	1066	2	T06001	phospholipase D (E	770	31	39.2	184	2	I55401	conserved hypotet
698	32	40.5	1075	2	T46635	hypothetical prote	771	31	39.2	188	2	D82240	internal protein I
699	32	40.5	1078	2	D87647	hypothetical prote	772	31	39.2	183	1	HB8P4	transcription regu
700	32	40.5	1091	2	AF2953	DNA polymerase III	773	31	39.2	193	2	A82806	hypothetical prote
701	32	40.5	1091	2	G98329	probable DNA polym	774	31	39.2	197	2	T15923	weakly phosphoglyc
702	32	40.5	1142	2	T46155	hypothetical prote	775	31	39.2	199	2	AG1583	conserved hypotet
703	32	40.5	1146	2	S59376	hypothetical prote	776	31	39.2	203	2	D87567	probable DNA-bindi
704	32	40.5	1188	2	S48861	gene ei protein -	777	31	39.2	204	2	D97388	transforming prote
705	32	40.5	1228	2	S00873	paraspoxal crystal	778	31	39.2	206	1	TVH0AA	conserved hypotet
706	32	40.5	1271	2	T49009	protein kinase lik	779	31	39.2	215	2	D87199	conserved hypotet
707	32	40.5	1275	2	T18556	O-antigen biosynth	780	31	39.2	219	2	F86153	Germin-like protei
708	32	40.5	1328	2	T43060	agrin - electric r	781	31	39.2	224	2	G82913	conserved hypotet
709	32	40.5	1345	2	S55669	tegument protein 7	782	31	39.2	224	2	T51638	probable transcrip
710	32	40.5	1451	2	I40325	demonocrotic toxi	783	31	39.2	230	2	A42579	C-reactive protein
711	32	40.5	1650	2	S28721	hypothetical prote	784	31	39.2	236	2	T23941	hypothetical prote
712	32	40.5	1661	2	T43260	RNA polymerase (BC	785	31	39.2	237	2	T15924	hypothetical prote
713	32	40.5	1955	1	AGCH	agrin precursor -	786	31	39.2	237	2	B97560	hypothetical prote
714	32	40.5	1959	1	AGRI	agrin rat	787	31	39.2	237	2	T37790	acetacetyl-CoA re
715	32	40.5	2364	2	A56577	microtubule-associ	788	31	39.2	241	1	S06998	probable 30s ribos
716	32	40.5	2471	2	T42977	large tegument pro	789	31	39.2	241	2	AC0857	hypothetical prote
717	32	40.5	4199	2	S76412	hypothetical prote	790	31	39.2	241	2	AC0857	minor tail protein
718	32	40.5	4342	2	H83343	probable non-ribos	791	31	39.2	243	2	T13105	hypothetical prote
719	31.5	39.9	101	2	T09149	late-embryogenesis	792	31	39.2	243	2	T13105	hypothetical prote
720	31.5	39.9	140	2	AB1428	transcription regu	793	31	39.2	249	2	A83161	hypothetical prote
721	31.5	39.9	140	2	AB1428	transcription regu	794	31	39.2	249	2	B45392	hypothetical prote
722	31.5	39.9	159	2	AI1801	hypothetical 17.8K	795	31	39.2	249	2	C36861	orf2 protein - bel
723	31.5	39.9	215	2	T50576	probable heme oxyg	796	31	39.2	251	2	H65007	vacuoliprotein p
724	31.5	39.9	283	2	T20734	hypothetical prote	797	31	39.2	251	2	E91032	lipoprotein precu
725	31.5	39.9	289	2	A97388	nitrilase-related	798	31	39.2	251	2	F85876	lipoprotein precu
726	31.5	39.9	289	2	AB2606	carbon-nitrogen hy	799	31	39.2	251	2	S67191	hypothetical prote
727	31.5	39.9	392	2	B64017	probable RNA meth	800	31	39.2	252	2	B71956	type II DNA modifi
728	31.5	39.9	445	2	S37779	porin precursor, m	801	31	39.2	252	2	G45552	site-specific DNA-
729	31.5	39.9	450	2	G71364	probable aminopep	802	31	39.2	256	2	H86163	hypothetical prote
730	31.5	39.9	465	2	T34984	probable integral	803	31	39.2	256	2	T46597	hypothetical prote
731	31.5	39.9	473	2	B87504	glucose-6-phosphat	804	31	39.2	259	1	B70314	hypothetical prote
732	31.5	39.9	556	2	A84018	hypothetical prote	805	31	39.2	266	2	H90286	hypothetical prote
733	31.5	39.9	793	2	TC5831	kinasein-related pr	806	31	39.2	268	2	C64234	conserved hypotet
734	31.5	39.9	872	1	S53319	acetaldehyde dehyd	807	31	39.2	276	2	G82108	hypothetical prote
735	31.5	39.9	953	1	B30169	leukotoxin A - Pas	808	31	39.2	276	2	T08773	hypothetical prote
736	31.5	39.9	955	1	A35254	leukotoxin A - Pas	809	31	39.2	286	2	T19460	sugar ABC transpor
737	31.5	39.9	1000	2	C82630	serine proteinase	810	31	39.2	286	2	C72378	hypothetical prote
738	31.5	39.9	1231	2	AF2220	hypothetical prote	811	31	39.2	286	2	E95404	hypothetical prote
739	31	39.2	66	2	H97818	hypothetical prote	812	31	39.2	286	2	I40265	outer surface prot
740	31	39.2	75	2	F83630	hypothetical prote	813	31	39.2	286	2	I40265	outer surface prot
741	31	39.2	76	2	S42789	cell division cont	814	31	39.2	286	2	I40265	outer surface prot
742	31	39.2	76	2	B64423	hypothetical prote	815	31	39.2	286	2	I40265	outer surface prot
743	31	39.2	79	2	A36670	cell division cont	816	31	39.2	286	2	I40265	outer surface prot
744	31	39.2	81	2	AH2795	conserved hypotet	817	31	39.2	286	2	I40250	outer surface prot
745	31	39.2	82	2	AD3480	hypothetical prote	818	31	39.2	286	2	I40250	outer surface prot
746	31	39.2	86	2	AD3565	transposase BME110	819	31	39.2	286	2	I40252	outer surface prot
747	31	39.2	96	2	S20781	ig heavy chain V r	820	31	39.2	286	2	I40260	outer surface prot
748	31	39.2	98	2	A75393	conserved hypotet	821	31	39.2	286	2	I40260	outer surface prot
749	31	39.2	99	2	S70645	cell division cont	822	31	39.2	286	2	S03894	ADP,ATP carrier pr
750	31	39.2	120	2	AF3193	hypothetical prote	823	31	39.2	288	1	A64922	probable oxidoredu
751	31	39.2	122	2	AF3193	transposase BME11	824	31	39.2	298	2	AH0289	probable aido/keto
752	31	39.2	122	2	H97574	hypothetical 9.2K	825	31	39.2	298	2	B43646	ADP,ATP carrier pr
753	31	39.2	140	2	S77039	hypothetical prote	826	31	39.2	299	2	T47917	probable transcrip
754	31	39.2	145	2	T41313	hypothetical heme	827	31	39.2	299	2	D71051	hypothetical prote
755	31	39.2	150	1	OKR51	cell division cont	828	31	39.2	300	2	H64121	type II site-speci
756	31	39.2	150	2	G83840	ferric uptake regu	829	31	39.2	301	2	AH1824	hypothetical prote
757	31	39.2	150	2	E90279	Conserved hypotet	830	31	39.2	302	2	C90929	probable ARAC-type
758	31	39.2	155	2	A12780	hypothetical prote	831	31	39.2	303	2	G85777	probable ARAC-type
759	31	39.2	158	2	S68978	Na+/Ca2+,K+-exchan	832	31	39.2	303	2	H64927	hypothetical prote

833	31	39.2	305	2	S58822	probable membrane	906	31	39.2	417	2	B59392	Wnt10a protein pro
834	31	39.2	306	2	S73676	hypothetical prote	907	31	39.2	422	2	AB3473	3-oxoacyl-acyl car
835	31	39.2	308	2	F95405	conserved hypothet	908	31	39.2	424	2	AB2725	threonine dehydrat
836	31	39.2	309	2	S23096	protein kinase (EC	909	31	39.2	425	2	A38153	paired box protein
837	31	39.2	311	2	C84807	probable cell divi	910	31	39.2	425	2	S69796	pectate lyase (EC
838	31	39.2	311	2	T09586	probable cdc2-like	911	31	39.2	426	2	T31278	biphenyl dioxygena
839	31	39.2	317	2	A83783	hypothetical prote	912	31	39.2	428	2	E71415	probable coll wall
840	31	39.2	321	2	E81668	conserved hypothet	913	31	39.2	429	2	B97500	ribonuclease D (PA
841	31	39.2	321	2	A71510	hypothetical prote	914	31	39.2	431	2	E83304	hypothetical prote
842	31	39.2	321	2	E69009	cation antiporter	915	31	39.2	434	2	D83928	melibiase (alpha-g
843	31	39.2	323	2	T20331	hypothetical prote	916	31	39.2	435	2	B86149	TrnG.17 protein -
844	31	39.2	326	2	AF0495	Probable D-isomer	917	31	39.2	437	2	F97506	threonine dehydrat
845	31	39.2	327	1	RDVZAS	Ribonucleoside-dip	918	31	39.2	439	1	A48099	transcription fact
846	31	39.2	327	2	A13308	glutathione transf	919	31	39.2	439	2	S20489	S-locus-specific g
847	31	39.2	327	2	A82335	conserved hypothet	920	31	39.2	440	2	T48064	beta-glucosidase-1
848	31	39.2	328	2	A70871	probable quinone o	921	31	39.2	440	2	I61183	transcription fact
849	31	39.2	328	2	T36963	hypothetical prote	922	31	39.2	440	2	AP2934	probable transport
850	31	39.2	329	2	F86675	mevalonate kinase	923	31	39.2	442	2	F71930	probable transport
851	31	39.2	330	2	H69020	probable Na+/Ca2+	924	31	39.2	447	2	D81093	aldehyde dehydroge
852	31	39.2	332	1	S41003	protein kinase (EC	925	31	39.2	447	2	H81848	probable aldehyde
853	31	39.2	333	2	S46984	indole-3-pyruvate	926	31	39.2	448	2	AF1615	manganese transpor
854	31	39.2	333	2	C37145	probable helvetic	927	31	39.2	448	2	G53610	ntpJ protein - Ent
855	31	39.2	335	2	B86594	Yop translocation	928	31	39.2	448	2	D83518	cis,cis-muconate t
856	31	39.2	335	2	F72030	type III secretion	929	31	39.2	451	2	AG2117	hypothetical prote
857	31	39.2	338	2	T05902	auxin-induced prot	930	31	39.2	453	2	T10995	NADH2 dehydrogenas
858	31	39.2	339	2	B86906	oxidoreductase yrd	931	31	39.2	460	2	T11296	NADH2 dehydrogenas
859	31	39.2	339	2	C86978	hypothetical prote	932	31	39.2	460	2	AI0689	probable amino aci
860	31	39.2	339	2	T00632	hypothetical prote	933	31	39.2	460	2	G64916	probable membrane
861	31	39.2	339	2	AG0165	L-allo-threonine a	934	31	39.2	460	2	G90917	probable arginine/
862	31	39.2	341	2	F72215	oligopeptide ABC c	935	31	39.2	460	2	D85766	probable arginine/
863	31	39.2	341	2	B83298	conserved hypothet	936	31	39.2	460	2	C84591	probable tyrosine
864	31	39.2	341	2	AC2819	cyclopropane-fatty	937	31	39.2	462	2	H97292	UDP-N-acetylmuramo
865	31	39.2	341	2	D97597	cyclopropane fatty	938	31	39.2	462	2	AC0281	probable amino aci
866	31	39.2	343	2	S74438	iron(III) dicitrat	939	31	39.2	463	2	D71219	probable L-asparta
867	31	39.2	344	2	S62020	probable membrane	940	31	39.2	464	2	T40697	hypothetical prote
868	31	39.2	344	2	AG3489	Cytochrome o ubiqu	941	31	39.2	465	2	A70434	hypothetical prote
869	31	39.2	346	2	D72705	hypothetical prote	942	31	39.2	477	2	T02623	hypothetical prote
870	31	39.2	347	2	A41048	extracellular meta	943	31	39.2	479	2	T20715	hypothetical prote
871	31	39.2	350	2	T10498	UDPglucose 4-epime	944	31	39.2	488	2	AD2834	hypothetical prote
872	31	39.2	350	2	T06526	UDPglucose 4-epime	945	31	39.2	489	2	T11894	NADH2 dehydrogenas
873	31	39.2	352	2	I51541	MHC class I antige	946	31	39.2	491	2	AD2834	cytosol aminopepti
874	31	39.2	353	2	D70466	cathepsin B-like c	947	31	39.2	493	2	A87459	protein Fln1.12 l
875	31	39.2	353	2	D96657	hypothetical prote	948	31	39.2	493	2	F96696	anthranilate synth
876	31	39.2	354	2	S34378	wnt-11 protein - m	949	31	39.2	497	2	S11891	probable purine pe
877	31	39.2	362	2	S78515	single-stranded nu	950	31	39.2	502	2	A98348	hypothetical prote
878	31	39.2	362	2	S19511	hypothetical prote	951	31	39.2	508	2	H97611	hypothetical prote
879	31	39.2	364	2	G87597	conserved hypothet	952	31	39.2	526	2	H75595	probable cycloprop
880	31	39.2	365	2	S42471	hnRNP protein E2 -	953	31	39.2	532	2	T18571	hypothetical prote
881	31	39.2	369	2	I56077	MHC class I antige	954	31	39.2	533	2	AG2293	hypothetical prote
882	31	39.2	370	2	A75569	probable phosphori	955	31	39.2	537	2	D86299	hypothetical prote
883	31	39.2	370	2	B95420	probable sideropho	956	31	39.2	543	2	B87474	steroid monooxygen
884	31	39.2	376	2	S27015	GTP-binding regula	957	31	39.2	547	2	T37793	probable zinc fing
885	31	39.2	378	2	D69817	sulfate starvation	958	31	39.2	549	2	JC7158	steroid monooxygen
886	31	39.2	379	2	T46002	hypothetical prote	959	31	39.2	552	2	T10850	y4np protein - Rhi
887	31	39.2	389	2	T04612	tyrosine transamin	960	31	39.2	557	2	S21733	FACC protein - hum
888	31	39.2	390	2	T04096	glucose-6-phosphat	961	31	39.2	557	2	A36347	glypican 1 precurs
889	31	39.2	393	2	I64043	serine-type D-Ala-	962	31	39.2	558	2	T26053	hypothetical prote
890	31	39.2	393	2	S59383	probable membrane	963	31	39.2	564	2	T26053	hypothetical prote
891	31	39.2	393	2	C71254	hypothetical prote	964	31	39.2	566	2	T50536	succinate dehydrog
892	31	39.2	394	2	T35996	conserved hypothet	965	31	39.2	570	2	A36337	oligopeptidase
893	31	39.2	396	2	T04100	glucose-6-phosphat	966	31	39.2	578	1	F64578	oligopeptidase - H
894	31	39.2	400	2	C75336	serine proteinase,	967	31	39.2	578	2	B71934	alpha,alpha-trehal
895	31	39.2	402	2	C83508	two-component sens	968	31	39.2	581	2	T05232	hypothetical prote
896	31	39.2	405	2	G72463	probable acyl-CoA	969	31	39.2	583	2	JC6504	alpha, alpha-trehal
897	31	39.2	405	2	A84007	hypothetical prote	970	31	39.2	585	1	A41292	glutamate decarbox
898	31	39.2	407	2	S74213	formamidase (EC 3.	971	31	39.2	585	1	S38533	glutamate decarbox
899	31	39.2	410	2	T39115	formamidase-like p	972	31	39.2	585	2	JC4064	glutamate decarbox
900	31	39.2	410	2	T03819	phosphate/phosphoe	973	31	39.2	585	2	S46825	hypothetical prote
901	31	39.2	411	2	T03836	phosphate/phosphoe	974	31	39.2	588	2	T26193	hypothetical prote
902	31	39.2	413	2	C89780	hypothetical prote	975	31	39.2	589	2	AB1151	hypothetical prote
903	31	39.2	413	2	G95965	conserved hypothet	976	31	39.2	591	2	S73708	internalin protein
904	31	39.2	416	2	S25764	connexin 46 - rat	977	31	39.2	591	2	MG321	homolog H08
905	31	39.2	417	2	JC7693	soluble-type glyco	978	31	39.2	591	2	S77287	N-acetylmuramoyl-L

```

979 31 39.2 596 2 D84972 ABC transporter AT
980 31 39.2 599 2 G90539 heat shock protein
981 31 39.2 602 2 T35782 probable secreted
982 31 39.2 603 2 T27901 hypothetical prote
983 31 39.2 609 2 S67616 probable membrane
984 31 39.2 611 2 T44880 probable acyl-coA
985 31 39.2 618 2 B87566 voltage gated chlo
986 31 39.2 625 1 S52485 glucokinase regula
987 31 39.2 631 2 AG0082 topoisomerase IV c
988 31 39.2 634 2 F82079 probable 2',3'-cyc
989 31 39.2 637 2 F90257 hypothetical prote
990 31 39.2 638 2 T20944 hypothetical prote
991 31 39.2 639 2 C42049 leishmanolysin (BC
992 31 39.2 640 2 G72339 threonine-LRNA lig
993 31 39.2 644 2 A43370 capsid protein - N
994 31 39.2 646 2 T26427 hypothetical prote
995 31 39.2 648 2 F69848 transcription anti
996 31 39.2 657 2 S77543 short-chain alcoh
997 31 39.2 658 2 G81727 conserved hypothet
998 31 39.2 665 2 B83577 transketolase PA05
999 31 39.2 669 2 T28028 hypothetical prote
1000 31 39.2 678 2 H91228 probable glycosida

```

ALIGNMENTS

```

RESULT 1
A70803
early secretory antigen target esat6 - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: A70803; S49174
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.;
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: A70803
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-95 <COL>
A:Cross-references: UNIPROT:Q57165; UNIPARC:UPI0000036DD3; GB:AL123456; NID
A:Experimental source: strain H37RV
R:Soerensen, A.L.; Nagai, S.; Houen, G.; Andersen, P.; Andersen, A.B.
submitted to the EMBL Data Library, June 1994
A:Reference number: S49174
A:Accession: S49174
A:Molecule type: DNA
A:Residues: 1-13,'R',15-22,'S',24-95 <SOE>
A:Cross-references: UNIPARC:UPI000017AD5F; EMBL:X79562; NID:G531708
C:Genetics:
A:Gene: esat6

```

```

Query Match 100.0%; Score 79; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MTEQQNWFAGIEAAA 15
|||||
Db 1 MTEQQNWFAGIEAAA 15
|||||

```

```

RESULT 2
H95313
NoeA host specific nodulation protein [imported] - Sinorhizobium meliloti (strain 1021)
C:Species: Sinorhizobium meliloti
C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: H95313
R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowe
.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.]

```

```

Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
A:Reference number: A95262; MUID:21396509; PMID:11481432
A:Accession: H95313
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-476 <KUR>
A:Cross-references: UNIPROT:Q52892; UNIPARC:UPI000013032A; GB:AB006469; PIDN:AAK65074.1.A
A:Experimental source: strain 1021, megaplasmid pSymA
R:Galibert, F.; Finan, T.M.; Long, S.R.; Wong, K.; Yeh, K.; Barloy-Hubler, F.;
; peia, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, B.; Komp, C.; Lelaure,
; hebaull, P.; Vandenbol, M.; Vorholter, P.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
C:Contents: annotation
C:Genetics:
A:Gene: noeA
A:Genome: plasmid
C:Superfamily: Rhizobium meliloti noeA protein

```

```

Query Match 57.0%; Score 45; DB 2; Length 476;
Best Local Similarity 63.6%; Pred. No. 5.7;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 5 QWNPAGIEAAA 15
|||||
Db 100 EWSFAGLKAAA 110
|||||

```

```

RESULT 3
S71360
noeA protein - Rhizobium meliloti
C:Species: Rhizobium meliloti
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
R:Ardourel, M.; Lortet, G.; Maillet, F.; Roche, P.; Truchet, G.; Promé, J.C.; Rosenberg,
submitted to the EMBL Data Library, May 1995
A:Reference number: S71360
A:Accession: S71360
A:Molecule type: DNA
A:Residues: 1-476 <ARD>
A:Cross-references: UNIPROT:Q52892; UNIPARC:UPI000013032A; EMBL:U26430; NID:G1326069; P
A:Experimental source: strain RCR2011
R:Ardourel, M.; Lortet, G.; Maillet, P.; Roche, P.; Truchet, G.; Promé, J.C.; Rosenberg,
Mol. Microbiol. 17, 687-699, 1995
A:Title: In Rhizobium meliloti, the operon associated with the nod box n5 comprises nodI

```

```

A:Reference number: S71357; MUID:96111489; PMID:8801423

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A:Accession: S71358
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 304-339 <ARW>
A:Cross-references: UNIPARC:UPI00001792D2; EMBL:U26430
A:Experimental source: strain RCR2011 (=S047)
C:Genetics:
A:Gene: noeA
C:Superfamily: Rhizobium meliloti noeA protein
C:Keywords: nodulation

```

```

Query Match 57.0%; Score 45; DB 2; Length 476;
Best Local Similarity 63.6%; Pred. No. 5.7;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 5 QWNPAGIEAAA 15
|||||
Db 100 EWSFAGLKAAA 110
|||||

```

```

RESULT 4
AB2491

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```

frnE protein VCA0178 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: A82491
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
R;Harrison, D.; Ermolaeva, M.D.; Vamathevan, J.; Bacs, S.; Qin, H.; Dragoi, I.; Sellers, P.
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: A82491
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-217 <HEI>
A;Cross-references: UNIPROT:Q9KMY8; UNIPARC:UPI00000C3460; GB:AE004356; GB:AE003853; NID
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VCA0178
A;Map position: 2

Query Match 54.4%; Score 43; DB 2; Length 217;
Best Local Similarity 75.0%; Pred. No. 5.4;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TEQQWNFAGIEA 13
Db 170 TEQQWLGAGIHA 181

RESULT 5
H90825
hypothetical protein ECs1576 [imported] - Escherichia coli (strain O157:H7, substrain R1)
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: H90825
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasaawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: H90825
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-247 <HAY>
A;Cross-references: UNIPROT:Q8X3F8; UNIPARC:UPI00000D2994; GB:BA000007; PIDN:BA834999.1;
A;Experimental source: strain O157:H7, substrain R1MD 0509952
C;Genetics:
A;Gene: ECs1576

Query Match 54.4%; Score 43; DB 2; Length 247;
Best Local Similarity 53.8%; Pred. No. 6.2;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 EQQWNFAGIEAAA 15
Db 22 QQNWGFSGIKKAA 34

RESULT 6
G72069
conserved hypothetical protein CP0240 [imported] - Chlamydophila pneumoniae (strains CWI
N;Alternate names: fe-s oxidoreductase
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: G72069; F81599
R;Kallman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606; PMID:10192388
A;Accession: G72069
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-369 <ARN>

```

```

A;Cross-references: UNIPROT:Q9Z839; UNIPARC:UPI00000D403D; GB:AE001636; GB:AE001363; NID
A;Experimental source: strain CWL029
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: F81599
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-369 <REA>
A;Cross-references: UNIPARC:UPI00000D403D; GB:AE002184; GB:AE002161; NID:97189156; PIDN
A;Experimental source: strain AR39, HL cells
C;Genetics:
A;Gene: CPn0513; CP0240
C;Superfamily: hypothetical protein AF0390

Query Match 53.2%; Score 42; DB 2; Length 369;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 WNPAGIEAA 14
Db 305 WNYLGIEAA 313

RESULT 7
E86554
Pe-S oxidoreductase [imported] - Chlamydophila pneumoniae (strain J138)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: E86554
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; I
Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: E86554
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-369 <STO>
A;Cross-references: UNIPROT:Q9Z839; UNIPARC:UPI00000D403D; GB:BA000008; NID:G8978883; P
A;Experimental source: strain J138
C;Genetics:
A;Gene: CPJ0513
C;Superfamily: hypothetical protein AF0390

Query Match 53.2%; Score 42; DB 2; Length 369;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 WNPAGIEAA 14
Db 305 WNYLGIEAA 313

RESULT 8
E87276
glucose-6-phosphate isomerase [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: E87276
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolo
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.N
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: E87276
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-539 <STO>
A;Cross-references: UNIPROT:Q9ABK5; UNIPARC:UPI000012AF47; GB:AE005673; NID:gl3421349;
C;Genetics:

```

A:Gene: CC0222
C:Superfamily: glucose-6-phosphate isomerase

Query Match 53.2%; Score 42; DB 2; Length 539;
Best Local Similarity 50.0%; Pred. No. 22;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTEQQWNFAGIEAA 14
: : : : :
DB 48 LSKQWDEAGLEAA 61

RESULT 9
E87706
prolyl oligopeptidase family protein [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: E87706
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: E87706
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-723 <STO>
A:Cross-references: UNIPROT:Q9A279; UNIPARC:UPI000000C7B7A; GB:AE005673; MID:gl3425449; P
C:Genetics:
A:Gene: CC3687

Query Match 53.2%; Score 42; DB 2; Length 723;
Best Local Similarity 50.0%; Pred. No. 30;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 TEQQWNFAGIEAAA 15
: : : : :
DB 316 TERPWFAGVAIPA 329

RESULT 10
F64864
protein-disulfide oxidoreductase (EC 1.8.4.-) dabb [validated] - Escherichia coli (strain
N)Alternate names: disulfide bond formation protein B
C:Species: Escherichia coli
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 31-Dec-2004
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: F64864
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-176 <BLAT>
A:Cross-references: UNIPROT:P30018; UNIPARC:UPI0000031A36; GB:AE0000216; MID:g
A:Experimental source: strain K-12, substrain MG1655
R:Missiakas, D.; Georgopoulos, C.; Raina, S.
Proc. Natl. Acad. Sci. U.S.A. 90, 7084-7088, 1993
A:Title: Identification and characterization of the Escherichia coli gene dabb, whose pr
A:Reference number: A48288; MUID:93348217; PMID:7688471
A:Accession: A48288
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-176 <MIS>
A:Cross-references: UNIPARC:UPI000016EF3C; GB:L03721; MID:g398017; PIDN:AAA23711.1; PID
R:Finer, E.; Padan, E.; Schuldiner, S.
J. Biol. Chem. 267, 11064-11068, 1992
A:Title: Cloning, sequencing, and expression of the nhaB gene, encoding a Na⁺/H⁺ antipor
A:Reference number: JCI108; MUID:92283803; PMID:1317851
A:Accession: JCI109

A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 'MI', 1-129, 'LRRASGVGFRSGNAVAARYFVRLDCRSAGG', 136-137, 'PAV' <PIN>
A:Cross-references: UNIPARC:UPI000017214A; GB:M83655
A:Experimental source: strain K-12, substrain W1333
C:Genetics:
A:Gene: dabb; toxB
A:Map position: 25.5 min
C:Function:
A:Description: reoxidizes dabb protein specifically
A>Note: reaction depends on the presence of oxygen
C:Superfamily: disulfide bond formation protein B (disulfide oxidoreductase B)
C:Keywords: oxidoreductase; redox-active disulfide; transmembrane protein
C:Keywords: oxidoreductase; redox-active disulfide; transmembrane protein
F16-32/Domain: transmembrane #status predicted <TM>
F146-65/Domain: transmembrane #status predicted <TM>
F141-44/Disulfide bonds: redox-active #status predicted
Query Match 51.9%; Score 41; DB 1; Length 176;
Best Local Similarity 60.0%; Pred. No. 9.6;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 EQQWNFAGIE 12
: : : : :
DB 132 ERQWDFLGLE 141

RESULT 11
H85696
hypothetical protein dabb [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Dec-2004
C:Accession: H85696
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dialanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: H85696
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-176 <STO>
A:Cross-references: UNIPARC:UPI0000165784; GB:AE005174; MID:gl2514882; PIDN:AAG5036.1;
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: dabb
C:Superfamily: disulfide bond formation protein B (disulfide oxidoreductase B)
Query Match 51.9%; Score 41; DB 2; Length 176;
Best Local Similarity 60.0%; Pred. No. 9.6;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 EQQWNFAGIE 12
: : : : :
DB 132 ERQWDFLGLE 141

RESULT 12
H90838
protein-disulfide oxidoreductase Ecs1680 [imported] - Escherichia coli (strain O157:H7,
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 31-Dec-2004
C:Accession: H90838
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G
sasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: H90838
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-176 <HAV>
A:Cross-references: UNIPROT:P30018; UNIPARC:UPI0000031A36; GB:BA000007; PIDN:BA035103.1

A;Experimental source: strain O157:H7, substrain RIMD 0509952

C;Genetics:

A;Gene: ECs1680

C;Superfamily: disulfide bond formation protein B (disulfide oxidoreductase B)

Query Match 51.9%; Score 41; DB 2; Length 176;
Best Local Similarity 60.0%; Pred. No. 9.6;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 EQQWNPAGIE 12

||:|:|:|:|

Db 132 EQQWDFLGL 141

RESULT 13

D82342 Probable cadaverine/lysine antiporter CadB VC0280 [imported] - Vibrio cholerae (strain N

C;Species: Vibrio cholerae

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004

C;Accession: D82342

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;

chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, R

l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-445 <HEI>

A;Cross-references: UNIPROT:Q9KV76; UNIPARC:UPI00000C2C57; GB:AE004116; GB:AE003852; NID

A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics:

A;Gene: VC0280

A;Map position: 1

C;Superfamily: ecotropic retrovirus receptor protein

Query Match 51.9%; Score 41; DB 2; Length 445;

Best Local Similarity 60.0%; Pred. No. 26;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 WNPAGIEAAA 15

||:|:|:|:|

Db 199 WSPFVGESAA 208

RESULT 14

E69435 hypothetical protein AF1486 - Archaeoglobus fulgidus

C;Species: Archaeoglobus fulgidus

C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Dec-2002

C;Accession: E69435

R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson

; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.P.; McDonald, L.

Nature 390, 364-370, 1997

A;Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.

Smith, H.O.; Woese, C.R.; Venter, J.C.

A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo

A;Reference number: A69250; MUID:98049343; PMID:9389475

A;Accession: E69435

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-471 <KLE>

A;Cross-references: UNIPARC:UPI0000056CF0; GB:AE001000; GB:AE000782; NID:g2689323; PIDN:

C;Superfamily: uncharacterized conserved protein

Query Match 51.9%; Score 41; DB 2; Length 471;

Best Local Similarity 61.5%; Pred. No. 28;

Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 EQQWNPAGIEAAA 15

||:|:|:|:|

Db 45 EQWDFEGKEADA 57

RESULT 15

H82256

hypothetical protein VC0978 [imported] - Vibrio cholerae (strain N16961 serogroup O1)

C;Species: Vibrio cholerae

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C;Accession: H82256

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.

chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers,

l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: H82256

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-38 <HEI>

A;Cross-references: UNIPROT:Q9KTC4; UNIPARC:UPI00000C2E40; GB:AE004179; GB:AE003852; NI

A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics:

A;Gene: VC0978

A;Map position: 1

Query Match 50.6%; Score 40; DB 2; Length 38;

Best Local Similarity 50.0%; Pred. No. 2.7;

Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MTEQWNPAGIEAAA 14

||:|:|:|:|

Db 18 MTLNOWNWIGVGVA 31

RESULT 16

AG2036

hypothetical protein alr1845 [imported] - Nostoc sp. (strain PCC 7120)

C;Species: Nostoc sp. PCC 7120

A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-May-2004

C;Accession: AG2036

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriquch

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,

DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic

A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AG2036

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-219 <KUR>

A;Cross-references: UNIPARC:UPI00000CE21F; GB:BA000019; PIDN:BA073544.1; PID:g17130935;

A;Experimental source: strain PCC 7120

C;Genetics:

A;Gene: alr1845

C;Superfamily: tRNA (guanine-N(7)-)-methyltransferase

Query Match 49.4%; Score 39; DB 2; Length 219;

Best Local Similarity 60.0%; Pred. No. 27;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 EQQWNPAGIE 12

||:|:|:|:|

Db 63 EPNNWFLGLE 72

RESULT 17

A70145

prolipoprotein diacylglycerol transferase (lgt) homolog - Lyme disease spirochete

C;Species: Borrelia burgdorferi (Lyme disease spirochete)

C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004

C;Accession: A70145

R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Whit

son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt

```
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:98065943; PMID:9403685
A:Accession: A70145
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-328 <ML>
A:Cross-references: UNIPROT:O51337; UNIPARC:UPI0000057453; GB:AE001142; GB:AE000783; NID
A:Experimental source: strain B31

Query Match 49.4%; Score 39; DB 2; Length 328;
Best Local Similarity 46.2%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 3 EQWNPAGIEAAA 15
   : ||| | | | |
Db 96 DQWNTGPRGMA 108

RESULT 18
AH2150
hypothetical protein alr2759 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 16-Aug-2004
C:Accession: AH2150
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriiguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
A:Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AH2150
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-393 <KUR>
A:Cross-references: UNIPROT:Q8YTF8; UNIPARC:UPI00000CE556; GB:BA000019; FIDN:BA874458.1;
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr2759
C:Superfamily: Aldehyde reductase

Query Match 49.4%; Score 39; DB 2; Length 393;
Best Local Similarity 70.0%; Pred. No. 51;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 QWNPAGIEAA 14
   : ||| | | | |
Db 185 QWNPAGIEAA 194

RESULT 19
T01762
hypothetical protein A_IG002P16.6 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 09-Jul-2004
C:Accession: T01762
R:Miller, N.; Beck, C.; Kramer, J.
submitted to the EMBL Data Library, June 1997
A:Description: The sequence of A. thaliana IG002P16.
A:Reference number: Z14421
A:Accession: T01762
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-482 <ML>
A:Cross-references: UNIPROT:O04629; UNIPARC:UPI00000A2ABB; EMBL:AF007270; NID:G2191157;
C:Genetics:
A:Gene: AtSP:A_IG002P16.6
A:Map position: 5
A:Introns: 15/2; 86/3; 108/1; 179/3; 238/3; 263/3; 301/1; 396/2; 433/3

Query Match 49.4%; Score 39; DB 2; Length 482;
```

```
Best Local Similarity 53.3%; Pred. No. 64;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 MTEQWNPAGIEAAA 15
   : ||| | | | |
Db 118 LVEQLMFWFAPSAIA 132

RESULT 20
G86844
hypothetical protein glpP [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C:Species: Lactococcus lactis subsp. lactis
C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C:Accession: G86844
R:Bohlooli, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlich,
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: G86844
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-714 <STO>
A:Cross-references: UNIPROT:Q9CE85; UNIPARC:UPI00000D44A5; GB:AE005176; PID:G12724781; F
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: glpP

Query Match 49.4%; Score 39; DB 2; Length 714;
Best Local Similarity 60.0%; Pred. No. 98;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 QWNPAGIEAA 14
   : ||| | | | |
Db 302 KWNFIGFOAA 311

RESULT 21
D83093
secretion protein SecA PA4403 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 05-Oct-2004
C:Accession: D83093
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: D83093
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-916 <STO>
A:Cross-references: UNIPROT:Q9LCT3; UNIPARC:UPI00000C4ED9; GB:AE004856; GB:AE004091; NI
A:Experimental source: strain PA01
C:Genetics:
A:Gene: secA; PA4403
C:Superfamily: preprotein translocase, subunit SecA

Query Match 49.4%; Score 39; DB 2; Length 916;
Best Local Similarity 54.5%; Pred. No. 1.3e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 QWNPAGIEAA 14
   : ||| | | | |
Db 699 EQWDIEGLEAA 709

RESULT 22
AB87572
aminotransferase, class V [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 05-Oct-2004
C:Accession: AB87572
```

R.Nierman, W.C.; Feildblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolonitsky, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A;Title: Complete Genome Sequence of *Caulobacter crescentus*.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: A87572
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-392 <STO>
A;Cross-references: UNIPROT:Q9A560; UNIPARC:UPI00000C77A0; GB:AE005673; MID:g13424177; F;1-26/Domain: signal sequence #status predicted <SIG>
C;Genetics:
A;Gene: CC2604
C;Superfamily: serine-pyruvate/aspartate aminotransferase

Query Match 48.7%; Score 38.5; DB 2; Length 392;
Best Local Similarity 45.0%; Pred. No. 62;
Matches 9; Conservative 2; Mismatches 2; Indels 7; Gaps 1;

QY 2 TEQWNF-----AGIEAA 14
| : : : : :
45 TQNRWTFITDGTSPAGIEAA 64

Db

RESULT 23
PC1140
cellulase (EC 3.2.1.4) celCCE precursor - Clostridium cellulolyticum (fragment)
N;Alternate names: endo-1,4-beta-glucanase
C;Species: Clostridium cellulolyticum
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: PC1140
R;Bagnara-Tardif, C.; Gaudin, C.; Belaich, A.; Hoesst, P.; Citard, T.; Belaich, J.P. Gene 119, 17-18, 1992
A;Title: Sequence analysis of a gene cluster encoding cellulases from Clostridium cellulolyticum
A;Reference number: JC1299; MUID:93012971; PMID:1398087
A;Accession: PC1140
A;Molecule type: DNA
A;Residues: 1-252 <BAG>
A;Cross-references: UNIPROT:Q46002; UNIPARC:UPI000017ACE8; GB:M87018
C;Genetics:
A;Gene: celCCE
C;Function:
A;Description: hydrolysis of 1,4-beta-D-glucosidic linkages in beta-D-glucans such as cellobiose
A;Pathway: cellulose degradation
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-252/Product: cellulase celCCE #status predicted <MAT>

Query Match 48.1%; Score 38; DB 2; Length 252;
Best Local Similarity 60.0%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 QQWNFAGIEA 13
| : : : : :
135 QQWNFLELQA 144

Db

RESULT 24
E82868
hypotheoretical protein XFA0062 [imported] - *Xylella fastidiosa* (strain 9a5c)
C;Species: *Xylella fastidiosa*
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: E82868
R;Anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequencing
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: E82868
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-284 <SIM>
A;Cross-references: UNIPROT:Q9PHE6; UNIPARC:UPI00000C2278; GB:AE003851; NID:g9112238; PT

A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Canargo, L.E.A.; Carraro, D.M.; Carrer, I.; as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froh, J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laus, chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasa, A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XFA0062
A;Genome: plasmid
A;Note: plasmid pXF5.1

Query Match 48.1%; Score 38; DB 2; Length 284;
Best Local Similarity 63.6%; Pred. No. 53;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 QQWNFAGIEAA 14
| : : : : :
260 QQWNFAGIEAA 270

Db

RESULT 25
AD2851
cytochrome c1 fbcC [imported] - *Agrobacterium tumefaciens* (strain C58, Dupont)
C;Species: *Agrobacterium tumefaciens*
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AD2851
R;Wood, D.W.; Secubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McCle Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AD2851
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-297 <KUR>
A;Cross-references: UNIPROT:Q0UD90; UNIPARC:UPI00001646D7; GB:AE008688; PIDN:AAL43226.1
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: fbcC
A;Map position: circular chromosome
C;Superfamily: cytochrome c1 heme protein; cytochrome c1 heme protein homology
C;Keywords: chromoprotein; heme; iron; metalloprotein
F;80/83/Binding site: heme (Cys) (covalent) #status predicted
F;84/Binding site: heme iron (His) (axial ligand) #status predicted

Query Match 48.1%; Score 38; DB 2; Length 297;
Best Local Similarity 75.0%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 EQQWNFAG 10
| : : : : :
52 EQQWNFAG 59

Db

RESULT 26
H75285
probable phosphotesterase (EC 3.1.-.-) DR2345 [similarity] - *Deinococcus radiodurans* (strain ATCC 29210)
C;Species: *Deinococcus radiodurans*
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 05-Oct-2004
C;Accession: H75285
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioreistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: H75285
A:Molecule type: DNA
A:Residues: 1-305 <WHI>
A:Cross-references: UNIPROT:Q9RRY7; UNIPARC:UPI0000013BA83; GB:AE002065; GB:AE000513; NID
A:Experimental source: strain R1
A:Comment: This sequence has motifs characteristic of a variety of phosphoesterases.
C:Genetics:
A:Gene: DR2345
A:Map position: 1
C:Superfamily: phosphoesterase, YkuE type; phosphoesterase core homology
C:Keywords: hydrolase
F:62-139/Domain: phosphoesterase core homology <PEC>

Query Match 48.1%; Score 38; DB 1; Length 305;
Best Local Similarity 45.5%; Pred. No. 58;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MTEQWNPAGI 11
Db 47 VTREQNVLVGL 57
:|:|:|:|:
:|:|:|:|:

RESULT 27
B97628
cytochrome c1 (AF109172) [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C:Accession: B97628
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollan, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: B97628
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-319 <KUR>
A:Cross-references: UNIPROT:Q8UD90; UNIPARC:UPI00000DIE1E; GB:AE007869; PIDN:AAK87979.1
C:Genetics:
A:Gene: AGR_C_4072
A:Map position: circular chromosome
C:Superfamily: cytochrome c1 heme protein; cytochrome c1 heme protein homology
C:Keywords: chromoprotein; heme; iron; metalloprotein
F:102/105/Binding site: heme (Cys) (covalent) #status predicted
F:106/Binding site: heme iron (His) (axial ligand) #status predicted

Query Match 48.1%; Score 38; DB 2; Length 319;
Best Local Similarity 75.0%; Pred. No. 61;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 EQQWNPAG 10
Db 74 EQQWSPAG 81
:|:|:|:|:
:|:|:|:|:

RESULT 28
AE0826
probable cadaverine/lysine antiporter [imported] - Salmonella enterica subsp. enterica s
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: This species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 05-Oct-2004
C:Accession: AE0826
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AE0826
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-443 <PAR>
A:Cross-references: UNIPARC:UPI0000059A81; GB:AL513382; PIDN:CAD02761.1; PID:G16503771;
C:Genetics:
A:Gene: STY2805
C:Superfamily: ecotropic retrovirus receptor protein

Query Match 48.1%; Score 38; DB 2; Length 443;
Best Local Similarity 60.0%; Pred. No. 87;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 WNFAGIEAAA 15
Db 198 WAFVGVESAA 207
:|:|:|:|:
:|:|:|:|:

RESULT 29
H86108
transport of lysine/cadaverine [imported] - Escherichia coli (strain O157:H7, substrain
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C:Accession: H86108
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: H86108
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-444 <STO>
A:Cross-references: UNIPARC:UPI00001659E5; GB:AE005174; NID:G12519112; PIDN:AAG59332.1;
A:Experimental source: strain O157:H7, substrain EDU933
C:Genetics:
A:Gene: cadB
C:Superfamily: ecotropic retrovirus receptor protein

Query Match 48.1%; Score 38; DB 2; Length 444;
Best Local Similarity 60.0%; Pred. No. 87;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 WNFAGIEAAA 15
Db 198 WAFVGVESAA 207
:|:|:|:|:
:|:|:|:|:

RESULT 30
A1842
lysine/cadaverine antiporter membrane protein cadB - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Oct-2004
C:Accession: A41842; B41968; S56361; C65223
R:Meng, S.Y.; Bennett, G.N.
J. Bacteriol. 174, 2659-2669, 1992
A:Title: Nucleotide sequence of the Escherichia coli cad operon: a system for neutraliz
A:Reference number: A41842; MUID:92210511; PMID:1556085
A:Accession: A41842
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-444 <MEN>
A:Cross-references: UNIPROT:P23891; UNIPARC:UPI0000001701; GB:M76411; NID:G145455; PIDN
R:Watson, N.; Dnyyak, D.S.; Rosey, E.L.; Slonczewski, J.L.; Olson, E.R.
J. Bacteriol. 174, 530-540, 1992
A:Title: Identification of elements involved in transcriptional regulation of the Esche
A:Reference number: A41968; MUID:92105022; PMID:11370290
A:Accession: B41968
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-444 <WAT>
A:Cross-references: UNIPARC:UPI0000001701; GB:M67452; NID:G145451; PIDN:AAA23532.1; PID

A;Note: sequence extracted from NCBI backbone (NCBIN:75631, NCBI:P:75633)
R;Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
Nucleic Acids Res. 23, 2105-2119, 1995
A;Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.
A;Reference number: S56314; MUID:95334362; PMID:7610040
A;Accession: S56361
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-444 <BUR>
A;Cross-references: UNIPARC:UPI0000001701; EMBL:U14003; NID:g1263172; PIDN:AAA97032.1; B
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Ferna, N.T.; Burland, V.; Riley, M.; C
.A.; Rose, B.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: C65223
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-444 <BLAT>
A;Cross-references: UNIPARC:UPI0000001701; GB:AE000486; GB:U00096; NID:g1790574; PIDN:AA
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: cadB
C;Superfamily: ecotropic retrovirus receptor protein
C;Keywords: membrane protein

Query Match 48.1%; Score 38; DB 2; Length 444;
Best Local Similarity 60.0%; Pred. No. 87;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 WNFAGTAA 15
| | | | |
Db 198 WAFVGVESAA 207

RESULT 31
B91268
transport protein of lysine/cadaverine ECs5114 [imported] - Escherichia coli (strain O15
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004
C;Accession: B91268
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
sasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: B91268
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-444 <HAY>
A;Cross-references: UNIPARC:UPI0000001701; GB:BA000007; PIDN:BA838537.1;
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs5114
C;Superfamily: ecotropic retrovirus receptor protein

Query Match 48.1%; Score 38; DB 2; Length 444;
Best Local Similarity 60.0%; Pred. No. 87;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 WNFAGTAA 15
| | | | |
Db 198 WAFVGVESAA 207

RESULT 32
I51213
drebrin - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 21-Jul-2000
C;Accession: I51213
R;Kojima, N.; Shirao, T.; Obata, K.

Brain Res. Mol. Brain Res. 19, 101-114, 1993
A;Title: Molecular cloning of a developmentally regulated brain protein, chicken drebrin
A;Reference number: I51212; MUID:93368392; PMID:8361332
A;Accession: I51213
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-593 <KOJ>
A;Cross-references: UNIPARC:UPI0000171477; GB:S65296; NID:g410604; PIDN:AAB28012.1; PID
C;Genetics:
A;Introns: 26/3; 51/3; 100/3; 126/3; 177/2; 198/3; 218/3; 257/1; 303/1; 346/1; 536/3; 5;
Query Match 48.1%; Score 38; DB 2; Length 593;
Best Local Similarity 57.1%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 TEQWNFAGTAA 15
| | | | |
Db 360 TEQWPFPGPEDKA 373

RESULT 33
A43776
drebrin E2 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 01-Dec-1992 #sequence_revision 30-Jan-1993 #text_change 09-Jul-2004
C;Accession: A43776; B43776; I51212; I50221
R;Kojima, N.; Kato, Y.; Shirao, T.; Obata, K.
Brain Res. Mol. Brain Res. 4, 207-215, 1988
A;Title: Nucleotide sequences of two embryonic drebrins, developmentally regulated brai
A;Reference number: A43776
A;Accession: A43776
A;Molecule type: mRNA
A;Residues: 1-607 <KOJ>
A;Cross-references: UNIPARC:UPI0000171308; GB:M36961; NID:g211725; PID:
A;Accession: B43776
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-315,359-607 <KO2>
A;Cross-references: UNIPARC:UPI000017C002
R;Kojima, N.; Shirao, T.; Obata, K.
Brain Res. Mol. Brain Res. 19, 101-114, 1993
A;Title: Molecular cloning of a developmentally regulated brain protein, chicken drebrin
A;Reference number: I51212; MUID:93368392; PMID:8361332
A;Accession: I51212
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-132 <KO3>
A;Cross-references: UNIPARC:UPI0000171475; GB:S65230; NID:g410591; PIDN:AAB28010.1; PID

Query Match 48.1%; Score 38; DB 2; Length 607;
Best Local Similarity 57.1%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 TEQWNFAGTAA 15
| | | | |
Db 373 TEQWPFPGPEDKA 386

RESULT 34
E86084
hypothetical protein Z5491 [imported] - Escherichia coli (strain O157:H7, substrain EDL
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: E86084
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: E86084
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-61 <STO>

A:Cross-references: UNIPROT:Q8X302; UNIPARC:UPI000000ED4; GB:AE005174; NID:gl2518848; H
A:Experimental source: strain O157:H7, substrain EDL33
C:Genetics:
A:Gene: Z5491

Query Match 46.8%; Score 37; DB 2; Length 61;
Best Local Similarity 60.0%; Pred. No. 15;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 QOWNFAGIEA 13
|||:|:|
Db 9 QOWSFVGSKA 18

RESULT 35

S75273
hypothetical protein sll1300 - Synecocystis sp. (strain PCC 6803)
C:Species: Synecocystis sp.
A:Variety: PCC 6803
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-May-2004
C:Accession: S75273
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O. K.; Okumura, S.; Shimpō, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis
s.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S75273
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-192 <KAN>
A:Cross-references: UNIPARC:UPI0000164C3E; EMBL:D90904; GB:AB001339; NID:gl652225; PIDN:
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996.
C:Genetics:
A:Start codon: GTG
A:Superfamily: tRNA (guanine-N(7)-)-methyltransferase

Query Match 46.8%; Score 37; DB 1; Length 192;
Best Local Similarity 50.0%; Pred. No. 52;
Matches 7; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 MTEQ--QOWNFAGIE 12
|||:|:|
Db 33 MAQQHPDNFLGVE 46

RESULT 36

D90002
hypothetical protein SA1897 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: D90002
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: D90002
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-229 <KUR>
A:Cross-references: UNIPROT:Q99SG3; UNIPARC:UPI00000D76DB; GB:BA000018; PID:gl3701889; H
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA1897

Query Match 46.8%; Score 37; DB 2; Length 229;
Best Local Similarity 60.0%; Pred. No. 63;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MTEQOWNFAG 10
|||:|:|

Db 216 MTEQWEFGG 225

RESULT 37

C81816
hypothetical protein NMA1888 [imported] - Neisseria meningitidis (strain Z2491 serogroup
C)Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C:Accession: C81816
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; More,
.; Holroyd, S.; Jagsels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: A81775; MUID:20222556; PMID:10761919
A:Accession: C81816
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-251 <PAR>
A:Cross-references: UNIPROT:Q9JTB7; UNIPARC:UPI00000C4CBE; GB:AL162757; GB:AL157959; NII
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA1888

Query Match 46.8%; Score 37; DB 2; Length 251;
Best Local Similarity 46.2%; Pred. No. 70;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 TEQOWNFAGIEA 14
|||:|:|
Db 128 TIDEWEPAGLASA 140

RESULT 38

AD1115
hypothetical protein lmo0323 [imported] - Listeria monocytogenes (strain EGD-e)
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AD1115
R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauguet, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Krefte, J.; Kuhn, M.; Kunet, F.; Kurapkat, G.; Madieno, E.; Maitournam, A.; M
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AD1115
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-236 <GLA>
A:Cross-references: UNIPROT:Q9YAA1; UNIPARC:UPI00000550A2; GB:NC_003210; PIDN:CAD000850
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo0323

Query Match 46.8%; Score 37; DB 2; Length 256;
Best Local Similarity 41.7%; Pred. No. 71;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MTEQOWNFAGIE 12
|||:|:|
Db 32 LDKYQWDFMGVE 43

RESULT 39

AE1476
hypothetical protein homolog lin0348 [imported] - Listeria innocua (strain Clp11262)
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AE1476
R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauguet, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tietze, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of *Listeria* species
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AB1476
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-257 <GLA>
A;Cross-references: UNIPROT:Q92EWO; UNIPARC:UPI00000CC1D2; GB:AL592023; PIDN:CAC95581.1;
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin0348

Query Match 46.8%; Score 37; DB 2; Length 257;
Best Local Similarity 41.7%; Pred. No. 71;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MTEQWNFAGIE 12
: ||| :
Db 32 LDKYQWDFMGVE 43

RESULT 40
S22090
N;Alternate names: catechol-O-methyltransferase (EC 2.1.1.6) - rat
C;Species: *Rattus norvegicus* (Norway rat)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S22090; JQ0787; F52356
R;Tenhunen, J.; Salminen, M.; Jalanko, A.; Ukkonen, S.; Ulmanen, I.
submitted to the EMBL Data Library, June 1992
A;Description: Structure of the rat catechol-O-methyltransferase gene: Separate promoter
A;Reference number: S22090
A;Accession: S22090
A;Molecule type: DNA
A;Residues: 1-264 <YEN>
A;Cross-references: UNIPROT:P22734; UNIPARC:UPI0000127EAA; EMBL:Z12651; NID:955889; PIDN
R;Salminen, M.; Lundstroem, K.; Tilgmann, C.; Savolainen, R.; Kalkkinen, N.; Ulmanen, I.
Gene 93, 241-247, 1990
A;Title: Molecular cloning and characterization of rat liver catechol-O-methyltransferase
A;Reference number: JQ0787; MUID:91033034; PMID:2227437
A;Accession: JQ0787
A;Molecule type: mRNA
A;Residues: 44-264 <SAL>
A;Cross-references: UNIPARC:UPI0000112023; GB:M60753; NID:9203336; PIDN:AAA40881.1; PID
A;Experimental source: liver
R;Tenhunen, J.; Ulmanen, I.
Biochem. J. 296, 595-600, 1993
A;Title: Production of rat soluble and membrane-bound catechol O-methyltransferase forms
A;Reference number: F52356; MUID:94107221; PMID:8280056
A;Accession: F52356
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-264 <RES>
A;Cross-references: UNIPARC:UPI0000127EAA; EMBL:Z12651; NID:955889; PIDN:CAA78276.1; PID
C;Comment: This enzyme catalyzes the transfer of a methyl group from S-adenosyl-L-methio
C;Genetics:
A;Gene: COMT
C;Superfamily: caffeoyl-CoA 3-O-methyltransferase
C;Keywords: methyltransferase; S-adenosylmethionine; transmembrane protein

Query Match 46.8%; Score 37; DB 2; Length 264;
Best Local Similarity 50.0%; Pred. No. 74;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTEQWNFAGIE 12
: ||| :
Db 141 ITQWMLNFAGLQ 152

RESULT 41
AB7404

ribosomal protein L3 [imported] - *Caulobacter crescentus*
C;Species: *Caulobacter crescentus*
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: AB7404
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolo
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete genome sequence of *Caulobacter crescentus*.
A;Reference number: AB7249; MUID:21173698; PMID:11259647
A;Accession: AB7404
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-267 <STO>
A;Cross-references: UNIPROT:Q9ABV3; UNIPARC:UPI00000C730D; GB:AB005673; NID:913422579;
C;Genetics:
A;Gene: CC1248
C;Superfamily: *Escherichia coli* ribosomal protein L3

Query Match 46.8%; Score 37; DB 2; Length 267;
Best Local Similarity 50.0%; Pred. No. 74;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 QOWNFAGIEA 13
: ||| :
Db 141 KRWNFGLRA 150

RESULT 42

I41220
glyceralddehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - *Escherichia*;
C;Species: *Escherichia blattae*
C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C;Accession: I41220; I41223; I41226
R;Lawrence, J.G.; Ochman, H.; Hartl, D.L.
J. Gen. Microbiol. 137, 1911-1921, 1991
A;Title: Molecular and evolutionary relationships among enteric bacteria.
A;Reference number: I40701; MUID:92065252; PMID:1955870
A;Accession: I41220
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-294 <RES>
A;Cross-references: UNIPROT:P24749; UNIPARC:UPI000012AEAA; GB:M63358; NID:9146076; PIDN
A;Accession: I41223
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-294 <RE2>
A;Cross-references: UNIPARC:UPI000012AEAA; GB:M63359; NID:9146108; PIDN:AAA23852.1; PID
A;Experimental source: ATCC 33429
A;Accession: I41226
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-294 <RE3>
A;Cross-references: UNIPARC:UPI000012AEAA; GB:M63360; NID:9146114; PIDN:AAA23855.1; PID
A;Experimental source: ATCC 33430
C;Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C;Keywords: oxidoreductase

Query Match 46.8%; Score 37; DB 2; Length 294;
Best Local Similarity 54.5%; Pred. No. 83;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 QOWNFAGIEAAA 15
: ||| :
Db 69 KRWNFAGVEVVA 79

RESULT 43

A41862
C-S lyase (ORF326) - *Corynebacterium glutamicum*
C;Species: *Corynebacterium glutamicum*
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
C;Accession: A41862

R.Rossol, I.; Puhler, A.
J. Bacteriol. 174, 2968-2977, 1992
A:Title: The Corynebacterium glutamicum aecD gene encodes a C-S lyase with alpha, beta-e
A:Reference number: A41862; MUID:92234956; PMID:1569026
A:Accession: A41862
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-326 <ROS>
A:Cross-references: UNIPARC:UPI00017AD33
A>Note: sequence extracted from NCBI backbone (NCBIN:97385, NCBIP:97386)

Query Match 46.8%; Score 37; DB 2; Length 326;
Best Local Similarity 46.2%; Pred. No. 92;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 TEQOWNFAGIEAA 14
DB 176 TSKAMTAGLKCA 188
		:				
:						
:						
:						

RESULT 44
T39033
hypothetical protein SPAC6C3.09 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T39033
R:Devlin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, February 1996
A:Reference number: Z21750
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Accession: T39033
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-335 <DEV>
A:Cross-references: UNIPROT:Q10312; UNIPARC:UPI000013A870; EMBL:Z69731; PIDN:CAB40281.1;
A:Experimental source: strain 972h-; cosmid C6C3
C:Genetics:
A:Gene: SPDB:SPAC6C3.09
A:Map position: 1
A:Introns: 31/3; 81/1; 100/1; 286/2
A:Superfamily: Schizosaccharomyces pombe hypothetical protein SPAC6C3.09

Query Match 46.8%; Score 37; DB 2; Length 335;
Best Local Similarity 62.5%; Pred. No. 95;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 WNPAGIEA 13
DB 290 WNFIVGES 297

RESULT 45
A12475
hypothetical protein alr5361 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A>Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: A12475
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriiguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: A12475
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-348 <KUR>
A:Cross-references: UNIPROT:Q8YLE1; UNIPARC:UPI00000CEE58; GB:BA000019; PIDN:BA077060.1;
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr5361

Query Match 46.8%; Score 37; DB 2; Length 348;
Best Local Similarity 50.0%; Pred. No. 99;

Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MTEQOWNFAGIE 12
DB 53 ITDOAWNQSGYE 64
		:				
	:					
	:					
	:					

RESULT 46
G90508
GMP synthase, PP-ATPase domain (guaA) [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: G90508
R:She, Q.; Singh, R. K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, I.
arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.
submitted to Genbank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A59139
A:Accession: G90508
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-367 <KUR>
A:Cross-references: UNIPROT:Q97T28; UNIPARC:UPI00000649D2; GB:AE006641; NID:g13816676;
C:Genetics:
A:Gene: guaA

Query Match 46.8%; Score 37; DB 2; Length 367;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 TEQOWNFAGIEAAA 15
DB 154 TEKENGFTLIEPLA 167
		:				
	:					
	:					
	:					

RESULT 47
C70626
hypothetical protein RV1048c - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: C70626
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: C70626
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-371 <COL>
A:Cross-references: UNIPROT:P96353; UNIPARC:UPI00000D11B4; GB:Z92539; GB:AL123456; NID:
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: RV1048c
C:Superfamily: Mycobacterium tuberculosis hypothetical protein RV1048c

Query Match 46.8%; Score 37; DB 2; Length 371;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 QQWNPAGIEAAA 15
DB 259 QLWDAAGLEWAA 270
		:				
	:					
	:					
	:					

RESULT 48
AF1022
probable amino acid permease STY4493 [imported] - Salmonella enterica subsp. enterica s
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A>Note: this species has also been called Salmonella typhi

1

C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 05-Oct-2004
C;Accession: AF1022
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AF1022
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-445 <PAR>
A;Cross-references: UNIPARC:UPI00005A86C; GB:AL513382; PIDN:CAD09279.1; PID:gl6505283;
C;Genetics:
A;Gene: STY4493
C;Superfamily: ecotropic retrovirus receptor protein
Query Match 46.8%; Score 37; DB 2; Length 445;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 6 WNFAGIEAAA 15
|:|:|:|:
Db 202 WSPIGVESAS 211

RESULT 49

B65221
probable amino acid/amine transport protein [similarity] - Escherichia coli (strain K-12
N;Alternate names: hypothetical protein f326a
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
C;Accession: B65221; S56344
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: B65221
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-445 <BLAT>
A;Cross-references: UNIPROT:P60061; UNIPARC:UPI000013B545; GB:AE000484; GB:U00096; NID:S
A;Experimental source: strain K-12, substrain MG1655
R;Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
Nucleic Acids Res. 23, 2105-2119, 1995
A;Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.
A;Reference number: S56314; MUID:95334362; PMID:7610040
A;Accession: S56344
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-321, 'SQWR', 326 <BUR>
A;Cross-references: UNIPARC:UPI000016F6C5; EMBL:U14003; NID:gl263172; PIDN:AAA97015.1; B
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
C;Superfamily: ecotropic retrovirus receptor protein

Query Match 46.8%; Score 37; DB 2; Length 445;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 6 WNFAGIEAAA 15
|:|:|:|:
Db 202 WSPIGVESAS 211

RESULT 50

A91266
probable amino acid/amine transport protein ECs5097 [imported] - Escherichia coli (strain
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004
C;Accession: A91266
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.

gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: A91266
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-445 <HAY>
A;Cross-references: UNIPROT:P60063; UNIPARC:UPI000013B545; GB:BA000007; PIDN:BA038520.1
A;Experimental source: strain O157:H7, substrain RMD 0509952
C;Genetics:
A;Gene: ECs5097
C;Superfamily: ecotropic retrovirus receptor protein
Query Match 46.8%; Score 37; DB 2; Length 445;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 6 WNFAGIEAAA 15
|:|:|:|:
Db 202 WSPIGVESAS 211
Search completed: May 4, 2006, 15:17:57
Job time : 39 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 14:59:41 ; Search time 322 Seconds
(without alignments)
20.468 Million cell updates/sec

Title: US-09-830-839-1

Perfect score: 79

Sequence: 1 MTEQWNFAGIEAAA 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

A_Geneseq_21:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*
9: Geneseq2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	100.0	15	3	AAY94590 Mycobacte
2	79	100.0	15	5	ABG30951 Mycobacte
3	79	100.0	15	5	AAO17432 Early sec
4	79	100.0	15	8	ADI33341 Mycobacte
5	79	100.0	15	9	ABE45086 M. tuberc
6	79	100.0	17	3	AAY88581 Antigenic
7	79	100.0	19	2	AAY85548 ESAT-6 an
8	79	100.0	20	9	ABE44911 Mycobacte
9	79	100.0	20	9	ABE45107 M. tuberc
10	79	100.0	51	2	AAW32339 Mycobacte
11	79	100.0	51	2	AAW32466 Mycobacte
12	79	100.0	51	2	AAW64334 Mycobacte
13	79	100.0	51	2	AAW81701 M. tuberc
14	79	100.0	51	2	AAI38988 M. tuberc
15	79	100.0	51	2	AAI39131 M. tuberc
16	79	100.0	51	4	AAU01897 Mycobacte
17	79	100.0	51	5	AAE29716 Mycobacte
18	79	100.0	51	5	AAE17580 Mycobacte
19	79	100.0	95	2	AAW11494 ESAT6. 3/
20	79	100.0	95	2	AAI29788 Mycobacte
21	79	100.0	95	2	AAI29890 Mycobacte
22	79	100.0	95	4	AAI35219 M tubercu
23	79	100.0	95	5	ABG30968 Mycobacte
24	79	100.0	95	5	AAW50740 Mycobacte

25	79	100.0	95	7	ADB28550	Mycobacte
26	79	100.0	95	8	ADI33376	Mycobacte
27	79	100.0	95	8	ADN36323	Mycobacte
28	79	100.0	95	9	ABE45084	M. tuberc
29	79	100.0	142	7	ADB28541	Human/Myc
30	79	100.0	145	7	ADB28543	Human/Myc
31	79	100.0	146	7	ADB28545	Human/Myc
32	79	100.0	146	7	ADB28547	Human/Myc
33	79	100.0	196	2	AAW29888	Mycobacte
34	79	100.0	403	2	AAW72943	Mycobacte
35	79	100.0	403	2	AAW21963	Amino aci
36	79	100.0	404	2	AAW72942	Mycobacte
37	79	100.0	404	2	AAW21962	Amino aci
38	69	87.3	13	8	ADK00561	Immunogen
39	69	87.3	13	9	ABE44918	M. tuberc
40	69	87.3	13	9	ABE44912	Mycobacte
41	59	74.7	15	9	ABE45087	M. tuberc
42	59	74.7	20	4	AAE12275	Mycobacte
43	58	73.4	10	9	ABE45115	M. tuberc
44	54	68.4	10	9	ABE45116	M. tuberc
45	54	68.4	15	3	AAV94595	Mycobacte
46	54	68.4	15	5	ABG30952	Mycobacte
47	54	68.4	15	5	AAO17433	Early sec
48	54	68.4	15	8	ADI33342	Mycobacte
49	52	65.8	10	2	AAW70180	N-termina
50	52	65.8	10	6	ABO43500	M. tuberc
51	52	65.8	10	6	ABO43500	M. tuberc
52	52	65.8	10	7	ADP12072	Mycobacte
53	50	63.3	9	9	ABE44913	Mycobacte
54	48	60.8	893	6	ABU41797	Protein e
55	43	54.4	13	4	AAE12274	Mycobacte
56	43	54.4	16	7	ADL34423	MHC/HLA p
57	43	54.4	20	4	AAE12276	Mycobacte
58	43	54.4	247	7	ADC01171	Enterohae
59	43	54.4	911	6	ABU23441	Protein e
60	42	53.2	409	2	AAV35136	Chlamydia
61	42	53.2	413	2	AAW41058	Phytoene
62	42	53.2	539	8	ADS27740	Bacterial
63	41	51.9	176	3	AAV84601	Amino aci
64	41	51.9	445	6	ABU49075	Protein e
65	40	50.6	235	4	AAW79230	Corynebac
66	40	50.6	295	4	AAW91028	C glucami
67	40	50.6	317	4	ABG03344	Novel hum
68	40	50.6	939	6	ABU40087	Protein e
69	39	49.4	68	6	ABM66077	Propionib
70	39	49.4	81	4	AAU42989	Propionib
71	39	49.4	81	6	ABM39508	Propionib
72	39	49.4	169	3	AAW10430	Arabidops
73	39	49.4	212	3	AAW10429	Arabidops
74	39	49.4	243	4	AAW65891	Amino aci
75	39	49.4	253	4	AAW23550	Human EST
76	39	49.4	288	8	ADN25376	Bacterial
77	39	49.4	320	3	AAW10428	Arabidops
78	39	49.4	371	3	AAW09603	Arabidops
79	39	49.4	498	7	ADY06890	Plant ful
80	39	49.4	538	8	ABO69280	Pseudomon
81	39	49.4	576	5	ABW93606	Herbicida
82	39	49.4	599	5	ABP30263	Streptoco
83	39	49.4	599	8	ADV89677	Streptoco
84	39	49.4	599	8	ADV83078	Streptoco
85	39	49.4	599	8	ADV80930	Streptoco
86	39	49.4	610	8	ADI36901	Human tNO
87	39	49.4	621	5	ABP26041	Streptoco
88	39	49.4	714	5	ABW55108	Lactococc
89	39	49.4	804	4	AAW69038	Chimeric
90	39	49.4	858	4	AAW64427	Chimeric
91	39	49.4	916	6	ABU36413	Pseudomon
92	39	49.4	916	6	ABU38720	Protein e
93	39	49.4	928	7	ABO75454	Pseudomon
94	38.5	48.7	372	8	ADR21283	Mesorhizo
95	38	48.1	86	5	ABG60190	Human DIT
96	38	48.1	118	3	AAV93243	An Escher
97	38	48.1	123	4	ABW15055	Human ner

98	38	48.1	155	3	AAy81425	Clostridi
99	38	48.1	160	8	ADx94748	Plant ful
100	38	48.1	251	4	AAU343858	Propionib
101	38	48.1	251	6	ABM40377	Propionib
102	38	48.1	251	6	ABM65838	Propionib
103	38	48.1	297	9	ABEA1515	L. pneumo
104	38	48.1	301	4	AGAG93126	C. glutami
105	38	48.1	301	7	ADU13701	C. glutam
106	38	48.1	314	4	ABB065918	Micromono
107	38	48.1	317	9	ABE38228	L. pneumo
108	38	48.1	320	8	ADY13825	Plant ful
109	38	48.1	339	7	ABM89415	Rice abio
110	38	48.1	339	8	ADG65502	Novel hum
111	38	48.1	346	6	ABP99211	Orthosomy
112	38	48.1	349	7	ABO67061	Klebsiell
113	38	48.1	400	8	ADSA3420	Bacterial
114	38	48.1	410	2	RAW41057	Phytoene
115	38	48.1	410	2	RAW41059	Phytoene
116	38	48.1	410	2	RAW41060	Phytoene
117	38	48.1	410	5	AAW51842	Nicotiana
118	38	48.1	425	6	ADU51578	Protein e
119	38	48.1	438	7	ABE37556	Neural th
120	38	48.1	438	8	ADG93165	Sarcoglyc
121	38	48.1	443	6	ADU47132	Protein e
122	38	48.1	443	6	AGU47865	Protein e
123	38	48.1	444	6	ADU44922	Protein e
124	38	48.1	444	6	ABU31889	Human pro
125	38	48.1	455	7	ADMO5643	Human pro
126	38	48.1	508	8	ADM98865	HMG-CoA r
127	38	48.1	633	8	ADP99030	C. albica
128	38	48.1	650	7	ADB65482	Human pro
129	38	48.1	741	7	ABM88485	Rice abio
130	38	48.1	795	7	ABO81889	Pseudomon
131	38	48.1	1997	7	ADJ69207	Human hea
132	38	48.1	2293	3	ADJ69197	Amino aci
133	37	46.8	50	4	ABG14371	Novel hum
134	37	46.8	136	4	ABM86268	Human imm
135	37	46.8	186	3	AAW75008	Neisseria
136	37	46.8	186	3	AAW75009	Neisseria
137	37	46.8	186	3	AAW75010	Neisseria
138	37	46.8	221	2	RAU13542	Rat catec
139	37	46.8	223	3	AGLO4943	Arabidops
140	37	46.8	229	6	ABU36798	Staphyloc
141	37	46.8	229	6	ABU16090	Protein e
142	37	46.8	229	6	ABW17827	Staphyloc
143	37	46.8	240	8	ADN27215	Bacterial
144	37	46.8	251	3	AAW75012	Neisseria
145	37	46.8	251	3	AAW75011	Neisseria
146	37	46.8	251	3	AAW75013	Neisseria
147	37	46.8	251	6	ABP77888	N. gonorr
148	37	46.8	256	5	ABE48338	Listeria
149	37	46.8	264	7	ABE59233	Rat Prote
150	37	46.8	285	3	AGAO4942	Arabidops
151	37	46.8	285	7	ADJ31029	Plant vie
152	37	46.8	285	7	ADJ31022	Plant tra
153	37	46.8	285	8	ADJ34325	Bacterial
154	37	46.8	299	8	ADU27131	Bacterial
155	37	46.8	303	8	ADU26363	Bacterial
156	37	46.8	304	8	ADU71331	Plant ful
157	37	46.8	306	3	ADU71331	Plant ful
158	37	46.8	312	4	ABE59582	Drosophill
159	37	46.8	312	9	ADZ75728	Xanthomon
160	37	46.8	323	5	ABU11054	Yeast sel
161	37	46.8	325	4	AAU71864	C. glutam
162	37	46.8	325	4	AAU792281	C. glutam
163	37	46.8	331	7	ABO63122	Klebsiell
164	37	46.8	335	4	ABG28518	Novel hum
165	37	46.8	342	6	AAU49617	Propionib
166	37	46.8	342	6	ABM46136	Propionib
167	37	46.8	368	7	ADU13679	C. glutam
168	37	46.8	369	5	ABG70792	C. glutam
169	37	46.8	377	3	AAW75615	Neisseria
170	37	46.8	435	7	ABO74474	Pseudomon

171	37	46.8	490	5	AB955389
172	37	46.8	493	8	ADJ04434
173	37	46.8	496	5	AB955385
174	37	46.8	498	5	ABU11357
175	37	46.8	536	8	ADJ77741
176	37	46.8	536	8	ADX93527
177	37	46.8	574	3	ADG35879
178	37	46.8	585	6	ABP78315
179	37	46.8	597	8	ADY11463
180	37	46.8	620	3	ADG35878
181	37	46.8	640	3	ADG35877
182	37	46.8	640	3	AB991512
183	37	46.8	643	6	ABM67172
184	37	46.8	643	6	ABM67172
185	37	46.8	820	7	ADH88552
186	37	46.8	820	7	ADH88553
187	36.5	46.2	955	5	ABP66533
188	36.5	46.2	955	5	ABP66533
189	36.5	46.2	994	7	ABM87489
190	36.5	46.2	994	7	ABM87489
191	36.5	46.2	934	2	ADZ04447
192	36	45.6	55	4	AAW07637
193	36	45.6	88	3	AA901321
194	36	45.6	88	3	ABY58034
195	36	45.6	102	5	ABU05740
196	36	45.6	102	5	ABU05740
197	36	45.6	109	4	ABE70234
198	36	45.6	138	4	ABY01319
199	36	45.6	140	8	ABM41828
200	36	45.6	147	8	ADG76819
201	36	45.6	149	8	ADG76819
202	36	45.6	149	8	ADG76819
203	36	45.6	172	3	ADG54692
204	36	45.6	172	3	ADG54692
205	36	45.6	175	7	ADG57228
206	36	45.6	175	7	ADG57228
207	36	45.6	175	7	ADG57228
208	36	45.6	175	7	ADG57228
209	36	45.6	187	8	ADK41802
210	36	45.6	195	8	ADG67066
211	36	45.6	197	3	ADG21465
212	36	45.6	212	3	ADG21465
213	36	45.6	221	3	AAV91434
214	36	45.6	221	3	ADG34566
215	36	45.6	229	6	ADG34566
216	36	45.6	238	3	ADG52769
217	36	45.6	255	6	ABM70718
218	36	45.6	272	8	ADG05513
219	36	45.6	274	3	ADG31165
220	36	45.6	282	7	ADG52768
221	36	45.6	285	3	ADG52767
222	36	45.6	291	3	ADG21463
223	36	45.6	316	3	ADG21463
224	36	45.6	321	6	ADG19613
225	36	45.6	324	5	ABP69059
226	36	45.6	325	8	ADN13610
227	36	45.6	326	8	ADN13610
228	36	45.6	338	8	ADT250033
229	36	45.6	342	4	ABH11919
230	36	45.6	342	4	ABH11919
231	36	45.6	371	8	ADW79442
232	36	45.6	376	3	ABM28404
233	36	45.6	383	6	ADT59805
234	36	45.6	395	3	ABU25869
235	36	45.6	459	4	ADG62646
236	36	45.6	459	4	ADG62646
237	36	45.6	459	7	ADJ37943
238	36	45.6	470	9	ABJ38985
239	36	45.6	489	8	ADN19859
240	36	45.6	563	4	ADG08370
241	36	45.6	602	2	AAW93825
242	36	45.6	602	2	AAW93820
243	36	45.6	602	2	AAW93822

Abb55389	Lactococcus
Adl04434	M. catarrhalis
Adb55385	Lactococcus
Abj11357	Yeast
Abj77741	Plant full
Adx93527	Plant full
Aag55879	Arabidopsis
Abj78315	N. gonorrhoeae
Ady11463	Plant full
Aag55878	Arabidopsis
Aag55877	Arabidopsis
Abb59152	Herbicidal
Abm67172	Phototrophic
Adh88552	Enterococcus
Adh56833	Bifidobacterium
Abm87489	Rice
Abm87409	Brassica
Adi21293	Ralstonia
Adi21285	Burkholderia
Adi04447	Medicago
Aaw07637	P. suis
Aae01321	Human genome
Aay58034	Maize
Aaq21157	Zea mays
Abm05740	M. tuberculosis
Abm05564	M. tuberculosis
Abu70234	Drosophila
Aae01319	Human genome
Abu14828	Human genome
Adx76819	Plant full
Abb62446	Klebsiella
Adl67173	Lactobacillus
Aag54692	Arabidopsis
Adh57228	Rat protease
Adh57216	Rat protease
Adh57220	Rat protease
Adh57224	Rat protease
Abb90005	Human polio
Adk41802	R. equi
Adx67066	Plant full
Aag21465	Arabidopsis
Aag21464	Arabidopsis
Aay91434	Human secretase
Abu43566	Protein e
Adh52769	Arabidopsis
Abm70718	Phototrophic
Adg65513	Novel human
Aag31165	Arabidopsis
Aag52768	Arabidopsis
Adel2782	L. rhamnosus
Aag52767	Arabidopsis
Aag31164	Arabidopsis
Aag21463	Arabidopsis
Aae019613	Human nuclear
Abp69069	Human protease
Abm78458	Human protease
Adi13610	Human betaine
Ady25003	Plant full
Abb11319	Human cytochrome
Aam79442	Human protease
Adi56805	Plant protease
Abb28404	Staphylococcus
Abb28405	Protein e
Abb28406	Protein e
Aag31163	Arabidopsis
Abb62646	Drosophila
Adj37943	D. melanogaster
Abb38985	Protein e
Abm90697	M. xanthus
Adm19859	Bacterial
Abg08370	Novel human
Aaw93825	Bacillus
Aaw93820	Bacillus
Aaw93822	Bacillus

244	36	45.6	602	2	AAW93826	Aaw93826	Bacillus	317	35.5	44.9	593	4	AAW59224	Aab59224	SHP-2 act
245	36	45.6	602	3	AAW28402	Aab28402	Staphyloc	318	35.5	44.9	593	4	AAW59221	Aab59221	SHP-2 act
246	36	45.6	604	3	AAW18201	Aab18201	Staphyloc	319	35.5	44.9	593	4	AAW59214	Aab59214	SHP-2 mut
247	36	45.6	612	3	AAW18186	Aab18186	Gibberell	320	35.5	44.9	593	4	AAW59219	Aab59219	SHP-2 act
248	36	45.6	615	3	AAW28408	Aab28408	Codon-opt	321	35.5	44.9	593	4	AAW86321	Aab86321	Human PTP
249	36	45.6	618	2	AAW93821	Aab93821	Bacillus	322	35.5	44.9	593	7	AAW86372	Aab86372	Human PTP
250	36	45.6	654	3	AAW99662	Aay99662	Human GRP	323	35.5	44.9	593	7	AAW86374	Aab86374	Human PTP
251	36	45.6	654	3	AAW92621	Aab92621	Human pro	324	35.5	44.9	593	7	AAW86355	Aab86355	Human PTP
252	36	45.6	654	5	AAW97197	Aab97197	Novel hum	325	35.5	44.9	593	7	AAW86358	Aab86358	Human PTP
253	36	45.6	654	8	AAW80608	Abm80608	Tumour-as	326	35.5	44.9	593	7	AAW86369	Aab86369	Human PTP
254	36	45.6	658	4	AAW67806	Aag67806	Human bet	327	35.5	44.9	593	7	AAW86364	Aab86364	Human PTP
255	36	45.6	666	4	AAW66873	Abs66873	Drosophil	328	35.5	44.9	593	7	AAW86363	Aab86363	Human PTP
256	36	45.6	674	6	AAW58867	Abs58867	Drosophil	329	35.5	44.9	593	7	AAW86371	Aab86371	Human PTP
257	36	45.6	702	6	AAW53104	Abs53104	Human put	330	35.5	44.9	593	7	AAW86379	Aab86379	Human PTP
258	36	45.6	702	6	AAW96018	Adc96018	E. faeciu	331	35.5	44.9	593	7	AAW86361	Aab86361	Human PTP
259	36	45.6	743	5	AAW49311	Aab49311	Listeria	332	35.5	44.9	593	7	AAW86377	Aab86377	Human PTP
260	36	45.6	753	4	AAW95726	Aab95726	Human pro	333	35.5	44.9	593	7	AAW86378	Aab86378	Human PTP
261	36	45.6	753	4	AAW95109	Aab95109	Human pro	334	35.5	44.9	593	7	AAW86375	Aab86375	Human PTP
262	36	45.6	753	8	AAW4299	Adt4299	PRO polyP	335	35.5	44.9	593	7	AAW86362	Aab86362	Human PTP
263	36	45.6	823	8	AAW5725	Adt5725	Haemophil	336	35.5	44.9	593	7	AAW86375	Aab86375	Human PTP
264	36	45.6	864	6	AAW19580	Abu19580	Protein e	337	35.5	44.9	593	7	AAW86381	Aab86381	Human PTP
265	36	45.6	901	4	AAW35555	Aau35555	Haemophil	338	35.5	44.9	593	7	AAW86380	Aab86380	Human PTP
266	36	45.6	901	6	AAW30423	Abu30423	Protein e	339	35.5	44.9	593	7	AAW86356	Aab86356	Human PTP
267	36	45.6	1018	8	AAW23210	Ady23210	Plant ful	340	35.5	44.9	593	7	AAW86357	Aab86357	Human PTP
268	36	45.6	1188	2	AAW94622	Aar94622	HIV-1 gpl	341	35.5	44.9	593	7	AAW86359	Aab86359	Human PTP
269	36	45.6	1487	8	AAW47746	Adp47746	Human inf	342	35.5	44.9	593	7	AAW86368	Aab86368	Human PTP
270	36	45.6	1658	8	AAW95774	Adx95774	Plant ful	343	35.5	44.9	593	7	AAW86376	Aab86376	Human PTP
271	36	45.6	1866	8	AAW47905	Adp47905	Human inf	344	35.5	44.9	593	7	AAW86366	Aab86366	Human PTP
272	36	45.6	1866	8	AAW12959	Adp12959	Protein e	345	35.5	44.9	593	7	AAW86373	Aab86373	Human PTP
273	36	45.6	1866	9	AAW44759	Adv44759	Human nuc	346	35.5	44.9	593	7	AAW86365	Aab86365	Human PTP
274	36	45.6	3070	5	AAW17359	Aao17359	Human lam	347	35.5	44.9	593	7	AAW86373	Aab86373	Human PTP
275	36	45.6	3084	3	AAW19796	Aab19796	Mouse lam	348	35.5	44.9	593	7	AAW86376	Aab86376	Human PTP
276	36	45.6	3084	8	AAW17493	Adi17493	Amino aci	349	35.5	44.9	593	7	AAW86373	Aab86373	Human PTP
277	36	45.6	3084	8	AAW97662	Adr97662	Marine la	350	35.5	44.9	593	7	AAW16167	Adl16167	Rat prote
278	36	45.6	3084	9	AAW44474	Adw44474	Marine la	351	35.5	44.9	593	7	AAW16183	Adl16183	Human pro
279	36	45.6	3084	9	AAW55708	Ady55708	Mouse lam	352	35.5	44.9	593	7	AAW16177	Adl16177	Human pro
280	36	45.6	3084	9	AAW32462	Ady32462	Mouse lam	353	35.5	44.9	593	7	AAW16181	Adl16181	Human pro
281	36	45.6	3084	9	AAW56262	Aeb56262	Event seq	354	35.5	44.9	593	8	AAW66621	Adj66621	SHP2 prot
282	36	45.6	3084	3	AAW19794	Aab19794	Human lam	355	35.5	44.9	593	8	AAW75964	Adn75964	Human sig
283	36	45.6	3089	3	AAW19792	Aab19792	Human lam	356	35.5	44.9	593	8	AAW75966	Adn75966	Human sig
284	36	45.6	3106	3	AAW19795	Aab19795	Mouse lam	357	35.5	44.9	593	8	AAW14045	Ado14045	Human pro
285	36	45.6	3106	7	AAW61792	Ade61792	Rat Prote	358	35.5	44.9	593	8	AAW84843	Abu84843	Human can
286	36	45.6	3110	2	AAW171730	Aar171730	Merostin m	359	35.5	44.9	593	9	AAW37018	Ady37018	Protein t
287	36	45.6	3110	2	AAW15460	Aay15460	Human lam	360	35.5	44.9	593	9	AAW37016	Ady37016	Protein t
288	36	45.6	3110	3	AAW19793	Aab19793	Human lam	361	35.5	44.9	593	9	AAW37020	Ady37020	Protein t
289	36	45.6	3110	3	AAW19791	Aab19791	Human lam	362	35.5	44.9	597	2	AAW13475	Aay13475	Peptide S
290	36	45.6	3110	5	AAW84345	Aau84345	Protein L	363	35.5	44.9	597	5	AAW69480	Abg69480	Human bai
291	36	45.6	3122	7	AAW61794	Ade61794	Human pro	364	35.5	44.9	597	9	AAW16165	Adl16165	Mouse pro
292	36	45.6	3122	8	AAW17881	Adq17881	Human sof	365	35.5	44.9	597	9	AAW37028	Ady37028	Protein t
293	36	45.6	3150	4	AAW30414	Abg30414	Novel hum	366	35.5	44.9	611	8	AAW04956	Abg04956	Novel hum
294	36	45.6	6879	8	AAW36918	Adn36918	X. albili	367	35.5	44.9	616	8	AAW84842	Abu84842	Marine ca
295	35.5	44.9	104	4	AAW59243	Aab59243	Partial S	368	35	44.3	23	8	AAW84090	Adr84090	S. pyogen
296	35.5	44.9	112	2	AAW03988	Aaw03988	SH2 domai	369	35	44.3	67	4	AAW09111	Aao09111	Human pol
297	35.5	44.9	112	2	AAW02126	Aaw02126	Human SH-	370	35	44.3	69	8	AAW87751	Adv87751	Streptoco
298	35.5	44.9	112	2	AAW02126	Aaw02126	Human SH-	371	35	44.3	69	8	AAW79004	Adv79004	Streptoco
299	35.5	44.9	460	7	AAW11427	Adk11427	Human Shp	372	35	44.3	74	4	AAW60129	Abb60129	Drosophil
300	35.5	44.9	460	7	AAW11429	Adk11429	Human Shp	373	35	44.3	77	4	AAW65226	Aau65226	Propionib
301	35.5	44.9	524	8	AAW59240	Aab59240	SHP-2 pro	374	35	44.3	77	6	AAW61745	Abm61745	Propionib
302	35.5	44.9	561	8	AAW4083	Ado14083	Human pro	375	35	44.3	81	8	AAW57719	Abu57719	Human gen
303	35.5	44.9	583	9	AAW37030	Ady37030	Protein t	376	35	44.3	83	8	AAW56997	Abu56997	Human gen
304	35.5	44.9	584	9	AAW37032	Ady37032	Protein t	377	35	44.3	87	5	AAW06127	Abp06127	Human ORF
305	35.5	44.9	592	7	AAW66367	Ade66367	Human PTP	378	35	44.3	94	1	AAW70567	Aap70567	Product o
306	35.5	44.9	593	2	AAW52991	Aar52991	Human pro	379	35	44.3	98	7	AAW49417	Ada49417	Multi-epi
307	35.5	44.9	593	2	AAW13476	Aay13476	Peptide S	380	35	44.3	98	8	AAW24095	Ado24095	HCV, PC3 m
308	35.5	44.9	593	4	AAW59218	Aab59218	SHP-2 act	381	35	44.3	98	9	AAW25628	Abp25628	Streptoco
309	35.5	44.9	593	4	AAW59223	Aab59223	SHP-2 act	382	35	44.3	107	5	AAW81208	Abv81208	Streptoco
310	35.5	44.9	593	4	AAW59226	Aab59226	SHP-2 act	383	35	44.3	107	8	AAW40064	Aau40064	Propionib
311	35.5	44.9	593	4	AAW59220	Aab59220	SHP-2 act	384	35	44.3	146	6	AAW36583	Abm36583	Propionib
312	35.5	44.9	593	4	AAW59225	Aab59225	SHP-2 act	385	35	44.3	146	6	AAW36583	Abm36583	Propionib
313	35.5	44.9	593	4	AAW59222	Aab59222	SHP-2 act	386	35	44.3	153	3	AAW43922	Aab43922	Human can
314	35.5	44.9	593	4	AAW59227	Aab59227	SHP-2 act	387	35	44.3	153	9	AAW217687	Adz17687	Human h25
315	35.5	44.9	593	4	AAW59213	Aab59213	SHP-2 mut	388	35	44.3	169	4	AAW23505	Aau23505	Novel hum
316	35.5	44.9	593	4	AAW59215	Aab59215	SHP-2 pro	389	35	44.3	191	3	AAW21338	Aag21338	Arabidops

390	35	44.3	194	7	ABO67548	Abob67548 Klebsiell	463	35	44.3	301	6	ADA85100	Ada85100 Novel hum
391	35	44.3	198	6	ABU50484	Abu50484 Protein e	464	35	44.3	301	6	ADA84548	Ada84548 Novel hum
392	35	44.3	204	5	ABP29144	Abp29144 Streptoco	465	35	44.3	301	6	ADB29804	ADB29804 Human PRO
393	35	44.3	204	5	ABP29144	Abp29144 Streptoco	466	35	44.3	301	6	ADA80332	Ada80332 Human PRO
394	35	44.3	204	8	ADR86534	Adr86534 Aspergill	467	35	44.3	301	6	ADA75574	Ada75574 Human PRO
395	35	44.3	204	8	ADR86534	Adr86534 Aspergill	468	35	44.3	301	6	ADA45799	Ada45799 Human PRO
396	35	44.3	205	7	ABO74714	Abp74714 Pseudomon	469	35	44.3	301	6	ADB25095	Adb25095 Human PRO
397	35	44.3	210	5	ABP29141	Abp29141 Streptoco	470	35	44.3	301	6	ADA93271	Ada93271 Human PRO
398	35	44.3	210	5	ABP29141	Abp29141 Streptoco	471	35	44.3	301	6	ADB26621	Adb26621 Human PRO
399	35	44.3	210	8	ADR83903	Adr83903 S. pyogen	472	35	44.3	301	6	ADA60836	Ada60836 Homo sapi
400	35	44.3	214	5	ABU05967	Abu05967 M. tuberc	473	35	44.3	301	6	ADA96312	Ada96312 Human PRO
401	35	44.3	221	5	ABP53935	Abp53935 Lactococc	474	35	44.3	301	6	ADA95760	Ada95760 Human PRO
402	35	44.3	222	7	ABO77898	Abp77898 Pseudomon	475	35	44.3	301	6	ADA80884	Ada80884 Human PRO
403	35	44.3	224	3	AAAG6396	Aag6396 Arabidops	476	35	44.3	301	6	ADB26069	Adb26069 Human PRO
404	35	44.3	224	3	AAAG52839	Aag52839 Arabidops	477	35	44.3	301	6	ADA87560	Ada87560 Human PRO
405	35	44.3	232	5	ABP53266	Abp53266 Human MDD	478	35	44.3	301	6	ADB21554	Adb21554 Novel hum
406	35	44.3	232	7	ADI21261	Adi21261 Novel hum	479	35	44.3	301	6	ADA77333	Ada77333 Human PRO
407	35	44.3	232	6	ABR41716	Abp41716 Human DT	480	35	44.3	301	7	ADB18073	Adb18073 Human PRO
408	35	44.3	237	6	ABR41716	Abp41716 Human DT	481	35	44.3	301	7	ADA86756	Ada86756 Novel hum
409	35	44.3	242	5	ADA21133	Ada21133 Human sec	482	35	44.3	301	7	ADA87859	Ada87859 Novel hum
410	35	44.3	249	5	ABG96498	Abg96498 PRRS viru	483	35	44.3	301	7	ADA46247	Ada46247 Novel hum
411	35	44.3	251	6	ABR41666	Abp41666 Human DT	484	35	44.3	301	7	ADB28277	Adb28277 Human PRO
412	35	44.3	265	9	ABR93827	Abp93827 M. xanthu	485	35	44.3	301	7	ADB28829	Adb28829 Human PRO
413	35	44.3	284	8	ADI36894	Adi36894 Arabidops	486	35	44.3	301	7	ADA76781	Ada76781 Human PRO
414	35	44.3	292	3	AAAG52838	Aag52838 Arabidops	487	35	44.3	301	7	ADA89411	Ada89411 Novel hum
415	35	44.3	292	3	AAAG66395	Aag66395 Arabidops	488	35	44.3	301	7	ADA89411	Ada89411 Novel hum
416	35	44.3	292	7	ADB31937	Adb31937 Plant (A.	489	35	44.3	301	7	ADB27173	Adb27173 Human PRO
417	35	44.3	292	8	ADO02349	Ado02349 Thalecres	490	35	44.3	301	7	ADB22106	Adb22106 Novel hum
418	35	44.3	292	8	ADN72805	Adn72805 Thale cre	491	35	44.3	301	7	ADB22106	Adb22106 Novel hum
419	35	44.3	293	6	ABM68111	Abm68111 Photorhab	492	35	44.3	301	7	ADB22658	Adb22658 Human PRO
420	35	44.3	296	6	AAU49283	Aau49283 Protein e	493	35	44.3	301	7	ADA92153	Ada92153 Novel hum
421	35	44.3	301	3	AAU73329	Aau73329 HTRM clon	494	35	44.3	301	7	ADB15216	Adb15216 Human PRO
422	35	44.3	301	4	AAU88414	Aau88414 Human mem	495	35	44.3	301	7	ADB91558	Adb91558 Human sec
423	35	44.3	301	4	AAU88414	Aau88414 Human mem	496	35	44.3	301	7	ADB38468	Adb38468 Novel hum
424	35	44.3	301	4	AAU88414	Aau88414 Human mem	497	35	44.3	301	7	ADB38468	Adb38468 Novel hum
425	35	44.3	301	4	AAU88414	Aau88414 Human mem	498	35	44.3	301	7	ADB38468	Adb38468 Novel hum
426	35	44.3	301	6	ABO17703	Abp17703 Novel hum	499	35	44.3	301	7	ADB37916	Adb37916 Novel hum
427	35	44.3	301	6	ABU56979	Abu56979 Human sec	500	35	44.3	301	7	ADB66388	Adb66388 Novel hum
428	35	44.3	301	6	ABU60957	Abu60957 Human PRO	501	35	44.3	301	7	ADB89468	Adb89468 Human PRO
429	35	44.3	301	6	ABU66657	Abu66657 Human PRO	502	35	44.3	301	7	ADB90200	Adb90200 Human PRO
430	35	44.3	301	6	ADA40830	Ada40830 Human sec	503	35	44.3	301	7	ADB39301	Adb39301 Novel hum
431	35	44.3	301	6	ABR47774	Abp47774 Human sec	504	35	44.3	301	7	ADB46924	Adb46924 Novel hum
432	35	44.3	301	6	ABU59738	Abu59738 Novel sec	505	35	44.3	301	7	ADB86531	Adb86531 Human PRO
433	35	44.3	301	6	ABO24928	Abp24928 Human sec	506	35	44.3	301	7	ADB77136	Adb77136 Novel hum
434	35	44.3	301	6	ABR00089	Abp00089 Human gen	507	35	44.3	301	7	ADB34293	Adb34293 Human PRO
435	35	44.3	301	6	ABU66657	Abu66657 Human sec	508	35	44.3	301	7	ADB33741	Adb33741 Human PRO
436	35	44.3	301	6	ADA45695	Ada45695 Novel hum	509	35	44.3	301	7	ADB34845	Adb34845 Human PRO
437	35	44.3	301	6	ADA76126	Ada76126 Human PRO	510	35	44.3	301	7	ADB35949	Adb35949 Human PRO
438	35	44.3	301	6	ADA18776	Ada18776 Human PRO	511	35	44.3	301	7	ADB34845	Adb34845 Human PRO
439	35	44.3	301	6	ADA61399	Ada61399 Homo sapi	512	35	44.3	301	7	ADB35949	Adb35949 Human PRO
440	35	44.3	301	6	ADB19184	Adb19184 Novel hum	513	35	44.3	301	7	ADC50217	Adc50217 Novel hum
441	35	44.3	301	6	ADA67349	Ada67349 Human PRO	514	35	44.3	301	7	ADC71764	Adc71764 Novel hum
442	35	44.3	301	6	ADA66204	Ada66204 Novel hum	515	35	44.3	301	7	ADC52750	Adc52750 Novel hum
443	35	44.3	301	6	ADB15768	Adb15768 Human PRO	516	35	44.3	301	7	ADC52750	Adc52750 Novel hum
444	35	44.3	301	6	ADA47554	Ada47554 Human PRO	517	35	44.3	301	7	ADC57104	Adc57104 Novel hum
445	35	44.3	301	6	ADA67349	Ada67349 Human PRO	518	35	44.3	301	7	ADC60295	Adc60295 Novel hum
446	35	44.3	301	6	ADB30356	Adb30356 Human PRO	519	35	44.3	301	7	ADC50770	Adc50770 Novel hum
447	35	44.3	301	6	ADA85652	Ada85652 Novel hum	520	35	44.3	301	7	ADC65297	Adc65297 Human PRO
448	35	44.3	301	6	ADA96864	Ada96864 Human PRO	521	35	44.3	301	7	ADC54395	Adc54395 Novel hum
449	35	44.3	301	6	ADA79168	Ada79168 Human PRO	522	35	44.3	301	7	ADC53356	Adc53356 Novel hum
450	35	44.3	301	6	ADA87307	Ada87307 Novel hum	523	35	44.3	301	7	ADC58879	Adc58879 Novel hum
451	35	44.3	301	6	ADB16509	Adb16509 Human PRO	524	35	44.3	301	7	ADC55757	Adc55757 Novel hum
452	35	44.3	301	6	ADA91601	Ada91601 Novel hum	525	35	44.3	301	7	ADC58327	Adc58327 Novel hum
453	35	44.3	301	6	ADB14664	Adb14664 Human PRO	526	35	44.3	301	7	ADC74163	Adc74163 Human sec
454	35	44.3	301	6	ADB18625	Adb18625 Novel hum	527	35	44.3	301	7	ADD03001	Add03001 Novel hum
455	35	44.3	301	6	ADA93840	Ada93840 Human PRO	528	35	44.3	301	7	ADC89993	Adc89993 Novel hum
456	35	44.3	301	6	ADB19736	Adb19736 Novel hum	529	35	44.3	301	7	ADC69412	Adc69412 Human PRO
457	35	44.3	301	6	ADB13048	Adb13048 Human PRO	530	35	44.3	301	7	ADC48301	Adc48301 Human PRO
458	35	44.3	301	6	ABO43236	Abp43236 Novel hum	531	35	44.3	301	7	ADC09830	Adc09830 Human PRO
459	35	44.3	301	6	ADA74302	Ada74302 Human PRO	532	35	44.3	301	7	ADD04405	Add04405 Novel hum
460	35	44.3	301	6	ADB24535	Adb24535 Human PRO	533	35	44.3	301	7	ADC80361	Adc80361 Novel hum
461	35	44.3	301	6	ADA82059	Ada82059 Human PRO	534	35	44.3	301	7	ADD10868	Add10868 Human PRO
462	35	44.3	301	6	ADA75022	Ada75022 Human PRO	535	35	44.3	301	7	ADC47749	Adc47749 Human PRO

536	301	7	ADC79809	Adc79809	Novel	hum	609	35	44.3	301	8	ADG02092	Adg02092	Human	PRO
537	301	7	ADD09278	Add09278	Human	hum	610	35	44.3	301	8	ADG21878	Adg21878	Novel	hum
538	301	7	ADD04091	Add04091	Novel	hum	611	35	44.3	301	8	ADG19948	Adg19948	Human	PRO
539	301	7	ADD52130	Add52130	Human	PRO	612	35	44.3	301	8	ADG97854	Adg97854	Human	PRO
540	301	7	ADD52870	Add52870	Human	PRO	613	35	44.3	301	8	ADG24071	Adg24071	Novel	hum
541	301	7	ADD53422	Add53422	Novel	hum	614	35	44.3	301	8	ADG98425	Adg98425	Human	PRO
542	301	7	ADD51578	Add51578	Human	PRO	615	35	44.3	301	8	ADG03256	Adg03256	Human	PRO
543	301	7	ADD02377	Add02377	Human	PRO	616	35	44.3	301	8	ADG98977	Adg98977	Human	PRO
544	301	7	ADD01811	Add01811	Human	PRO	617	35	44.3	301	8	ADG16562	Adg16562	Human	PRO
545	301	7	ADD53993	Add53993	Novel	hum	618	35	44.3	301	8	ADG05021	Adg05021	Human	PRO
546	301	7	ADD92310	Add92310	Human	PRO	619	35	44.3	301	8	ADG19288	Adg19288	Human	PRO
547	301	7	ADD91206	Add91206	Human	PRO	620	35	44.3	301	8	ADG13125	Adg13125	Human	PRO
548	301	7	ADG03820	Adg03820	Human	PRO	621	35	44.3	301	8	ADG08182	Adg08182	Novel	hum
549	301	7	ADG32117	Adg32117	Novel	hum	622	35	44.3	301	8	ADG15352	Adg15352	Human	PRO
550	301	7	ADG22049	Adg22049	Human	PRO	623	35	44.3	301	8	ADG96750	Adg96750	Human	PRO
551	301	7	ADG22017	Adg22017	Human	PRO	624	35	44.3	301	8	ADG05935	Adg05935	Human	PRO
552	301	7	ADG79273	Adg79273	Human	PRO	625	35	44.3	301	8	ADG23519	Adg23519	Novel	hum
553	301	7	ADG41809	Adg41809	Human	PRO	626	35	44.3	301	8	ADG03808	Adg03808	Human	PRO
554	301	7	ADG17626	Adg17626	Human	PRO	627	35	44.3	301	8	ADG24709	Adg24709	Novel	hum
555	301	7	ADD91758	Add91758	Human	PRO	628	35	44.3	301	8	ADG07006	Adg07006	Novel	hum
556	301	7	ADG33773	Adg33773	Novel	hum	629	35	44.3	301	8	ADG07558	Adg07558	Novel	hum
557	301	7	ADG79825	Adg79825	Human	PRO	630	35	44.3	301	8	ADG55053	Adg55053	Novel	hum
558	301	7	ADD92862	Add92862	Human	PRO	631	35	44.3	301	8	ADG60717	Adg60717	Novel	hum
559	301	7	ADG19282	Adg19282	Human	PRO	632	35	44.3	301	8	ADG61821	Adg61821	Novel	hum
560	301	7	ADG18730	Adg18730	Human	PRO	633	35	44.3	301	8	ADG82022	Adg82022	Human	PRO
561	301	7	ADG42926	Adg42926	Human	PRO	634	35	44.3	301	8	ADG57261	Adg57261	Novel	hum
562	301	7	ADG95715	Adg95715	Human	PRO	635	35	44.3	301	8	ADG56709	Adg56709	Novel	hum
563	301	7	ADG22601	Adg22601	Human	PRO	636	35	44.3	301	8	ADG58365	Adg58365	Novel	hum
564	301	7	ADD78719	Add78719	Human	PRO	637	35	44.3	301	8	ADG58365	Adg58365	Novel	hum
565	301	7	ADG32669	Adg32669	Novel	hum	638	35	44.3	301	8	ADG70731	Adg70731	Novel	hum
566	301	7	ADG42361	Adg42361	Human	PRO	639	35	44.3	301	8	ADG57813	Adg57813	Novel	hum
567	301	7	ADG80377	Adg80377	Human	PRO	640	35	44.3	301	8	ADG53397	Adg53397	Novel	hum
568	301	7	ADG89405	Adg89405	Human	PRO	641	35	44.3	301	8	ADG71283	Adg71283	Novel	hum
569	301	7	ADG40689	Adg40689	Human	PRO	642	35	44.3	301	8	ADG81470	Adg81470	Human	PRO
570	301	7	ADG04488	Adg04488	Human	PRO	643	35	44.3	301	8	ADH30432	Adh30432	Human	PRO
571	301	7	ADG21326	Adg21326	Novel	hum	644	35	44.3	301	8	ADH11799	Adh11799	Novel	hum
572	301	7	ADG31326	Adg31326	Novel	hum	645	35	44.3	301	8	ADG52221	Adg52221	Novel	hum
573	301	7	ADG22967	Adg22967	Novel	hum	646	35	44.3	301	8	ADG53949	Adg53949	Novel	hum
574	301	7	ADG97302	Adg97302	Human	PRO	647	35	44.3	301	8	ADG80918	Adg80918	Human	PRO
575	301	7	ADG80366	Adg80366	Human	PRO	648	35	44.3	301	8	ADG56157	Adg56157	Novel	hum
576	301	7	ADG79814	Adg79814	Human	PRO	649	35	44.3	301	8	ADH12423	Adh12423	Novel	hum
577	301	7	ADH55106	Adh55106	Novel	hum	650	35	44.3	301	8	ADG61269	Adg61269	Novel	hum
578	301	7	ADH55658	Adh55658	Novel	hum	651	35	44.3	301	8	ADH28356	Adh28356	Human	PRO
579	301	7	ADI63877	Adi63877	Novel	hum	652	35	44.3	301	8	ADG54501	Adg54501	Novel	hum
580	301	7	ADI64826	Adi64826	Novel	hum	653	35	44.3	301	8	ADG59541	Adg59541	Human	PRO
581	301	7	ADH81739	Adh81739	Novel	hum	654	35	44.3	301	8	ADH80965	Adh80965	Human	PRO
582	301	7	ADH81187	Adh81187	Novel	hum	655	35	44.3	301	8	ADG09708	Adg09708	Novel	hum
583	301	7	ADM82356	Adm82356	Novel	hum	656	35	44.3	301	8	ADH15179	Adh15179	Novel	hum
584	301	7	ADN15755	Adn15755	Novel	hum	657	35	44.3	301	8	ADG09056	Adg09056	Novel	hum
585	301	7	ADN16384	Adn16384	Novel	hum	658	35	44.3	301	8	ADH14511	Adh14511	Novel	hum
586	301	7	ADN15203	Adn15203	Novel	hum	659	35	44.3	301	8	ADH18106	Adh18106	Novel	hum
587	301	7	ADN14651	Adn14651	Novel	hum	660	35	44.3	301	8	ADJ63387	Adj63387	Novel	hum
588	301	7	ADI63325	Adi63325	Novel	hum	661	35	44.3	301	8	ADJ77282	Adj77282	Human	PRO
589	301	7	ADC80913	Adc80913	Novel	hum	662	35	44.3	301	8	ADJ65404	Adj65404	Human	PRO
590	301	8	ADD76361	Add76361	Human	PRO	663	35	44.3	301	8	ADJ77282	Adj77282	Human	PRO
591	301	8	ADD87725	Add87725	Human	PRO	664	35	44.3	301	8	ADJ63387	Adj63387	Novel	hum
592	301	8	ADD86129	Add86129	Human	PRO	665	35	44.3	301	8	ADJ65404	Adj65404	Human	PRO
593	301	8	ADG75577	Adg75577	Human	PRO	666	35	44.3	301	8	ADJ65404	Adj65404	Human	PRO
594	301	8	ADG23153	Adg23153	Human	PRO	667	35	44.3	301	8	ADJ65404	Adj65404	Human	PRO
595	301	8	ADG23705	Adg23705	Human	PRO	668	35	44.3	301	8	ADJ65404	Adj65404	Human	PRO
596	301	8	ADG24348	Adg24348	Human	PRO	669	35	44.3	301	8	ADJ65404	Adj65404	Human	PRO
597	301	8	ADG87173	Adg87173	Human	PRO	670	35	44.3	301	8	ADJ63387	Adj63387	Novel	hum
598	301	8	ADG89039	Adg89039	Human	PRO	671	35	44.3	301	8	ADJ63387	Adj63387	Novel	hum
599	301	8	ADG18178	Adg18178	Human	PRO	672	35	44.3	301	8	ADJ63387	Adj63387	Novel	hum
600	301	8	ADG88487	Adg88487	Human	PRO	673	35	44.3	301	8	ADJ63387	Adj63387	Novel	hum
601	301	8	ADG94507	Adg94507	Human	PRO	674	35	44.3	301	8	ADJ63387	Adj63387	Novel	hum
602	301	8	ADG90918	Adg90918	Human	PRO	675	35	44.3	301	8	ADJ63387	Adj63387	Novel	hum
603	301	8	ADG95059	Adg95059	Human	PRO	676	35	44.3	301	8	ADJ63387	Adj63387	Novel	hum
604	301	8	ADG93169	Adg93169	Human	PRO	677	35	44.3	301	8	ADJ63387	Adj63387	Novel	hum
605	301	8	ADF34750	Adf34750	Human	PRO	678	35	44.3	301	8	ADJ63387	Adj63387	Novel	hum
606	301	8	ADG2065	Adg2065	Novel	hum	679	35	44.3	301	8	ADJ63387	Adj63387	Novel	hum
607	301	8	ADG90366	Adg90366	Human	PRO	680	35	44.3	301	8	ADJ63387	Adj63387	Novel	hum
608	301	8	ADG91513	Adg91513	Novel	hum	681	35	44.3	301	8	ADJ63387	Adj63387	Novel	hum

682	35	44.3	308	9	AD240601	Adz40601 HCV.2431(755	35	44.3	603	2	AAW93827	AAW93827 E. coli G
683	35	44.3	328	8	ADY25081	Ady25081 Plant ful	756	35	44.3	603	2	AAW93824	AAW93824 Human GUS
684	35	44.3	335	3	AGS2837	AgS2837 Arabidops	757	35	44.3	603	3	AAE28431	AAE28431 Human bet
685	35	44.3	336	3	AGG06394	AgG06394 Arabidops	758	35	44.3	603	5	ABB84108	ABB84108 GUS prote
686	35	44.3	360	3	AYG69157	AYG69157 PeptideA	759	35	44.3	603	6	ABP96657	ABP96657 E. coli b
687	35	44.3	360	3	AD217689	Ad217689 Human h25	760	35	44.3	603	6	ABJ19649	ABJ19649 Artificia
688	35	44.3	384	7	ADF06059	AdF06059 Bacterial	761	35	44.3	603	6	ADN18189	ADN18189 Bacterial
689	35	44.3	391	8	ADT136893	AdT136893 Human tru	762	35	44.3	603	9	ABB18200	ABB18200 Escherich
690	35	44.3	392	8	ADN21393	AdN21393 Bacterial	763	35	44.3	604	7	ADD27986	ADD27986 Beta-gluc
691	35	44.3	399	4	AAU28394	AAU28394 Novel hum	764	35	44.3	604	7	ADS54300	ADS54300 Beta-gluc
692	35	44.3	404	8	ADX91164	ADX91164 Plant ful	765	35	44.3	607	4	ABE26258	ABE26258 Bacterial
693	35	44.3	404	9	AE991634	AE991634 Microbial	766	35	44.3	610	4	ABE68350	ABE68350 Human NAD
694	35	44.3	407	3	AGG10932	AgG10932 Arabidops	767	35	44.3	610	8	ADT136892	ADT136892 Human cNO
695	35	44.3	407	3	AGG39068	AgG39068 Arabidops	768	35	44.3	610	8	ADT136896	ADT136896 Human cNO
696	35	44.3	410	7	ABO82428	ABO82428 Pseudomon	769	35	44.3	610	8	ADT136900	ADT136900 Human cNO
697	35	44.3	415	6	ADA33362	AdA33362 Acinetoba	770	35	44.3	610	8	ADT136895	ADT136895 Human cNO
698	35	44.3	422	3	AGG36771	AgG36771 Arabidops	771	35	44.3	610	8	ADT136851	ADT136851 Human cNO
699	35	44.3	422	8	ADN73955	AdN73955 Thale cre	772	35	44.3	610	8	ADT136899	ADT136899 Human cNO
700	35	44.3	422	8	ADT56474	AdT56474 Plant pol	773	35	44.3	610	8	ADT136897	ADT136897 Human cNO
701	35	44.3	423	5	ABP65312	ABP65312 Bifidobac	774	35	44.3	610	8	ADT136897	ADT136897 Human cNO
702	35	44.3	423	5	ABP65667	ABP65667 Bifidobac	775	35	44.3	610	8	ADT136897	ADT136897 Human cNO
703	35	44.3	445	3	AGG39067	AgG39067 Arabidops	776	35	44.3	610	8	ADT136897	ADT136897 Human cNO
704	35	44.3	445	3	AGG10931	AgG10931 Arabidops	777	35	44.3	621	6	ABU16576	ABU16576 Protein e
705	35	44.3	448	7	ADP06960	AdP06960 Bacterial	778	35	44.3	637	8	ADS26569	ADS26569 Bacterial
706	35	44.3	448	8	ADG96358	AdG96358 T cell ac	779	35	44.3	637	8	ABB67755	ABB67755 Drosophil
707	35	44.3	448	8	ADG96356	AdG96356 T cell ac	780	35	44.3	659	7	ADD27989	ADD27989 Oleosin/b
708	35	44.3	450	7	ADL01578	AdL01578 Int-c/GUS	781	35	44.3	659	8	ADS54303	ADS54303 Oleosin/b
709	35	44.3	454	7	ABO81267	ABO81267 Pseudomon	782	35	44.3	665	8	ADN72687	ADN72687 Thale cre
710	35	44.3	456	3	AGS20758	AgS20758 Arabidops	783	35	44.3	665	4	AAW93423	AAW93423 Human pol
711	35	44.3	456	3	AGS50449	AgS50449 Arabidops	784	35	44.3	669	8	ADL31013	ADL31013 Human pro
712	35	44.3	459	3	AGG20638	AgG20638 Arabidops	785	35	44.3	669	8	ADG96360	ADG96360 T cell ac
713	35	44.3	461	3	AGG20637	AgG20637 Arabidops	786	35	44.3	669	8	ABM82132	ABM82132 Tumour-ag
714	35	44.3	465	7	ADG50886	AdG50886 V. parado	787	35	44.3	669	8	ADP24430	ADP24430 PRO polyP
715	35	44.3	466	3	AGG39066	AgG39066 Arabidops	788	35	44.3	673	7	ABE62848	ABE62848 Drosophil
716	35	44.3	466	3	AGG10930	AgG10930 Arabidops	789	35	44.3	686	7	ADU69739	ADU69739 Human hea
717	35	44.3	468	8	ADS44861	AdS44861 Bacterial	790	35	44.3	686	8	ADU96362	ADU96362 T cell ac
718	35	44.3	472	4	AAU35231	AAU35231 Enterococ	791	35	44.3	686	8	ADU96362	ADU96362 T cell ac
719	35	44.3	472	6	ABU14656	ABU14656 Protein e	792	35	44.3	711	6	ABR83626	ABR83626 SUMO-beta
720	35	44.3	472	6	AAU35231	AAU35231 Enterococ	793	35	44.3	711	6	ADN17946	ADN17946 Bacterial
721	35	44.3	477	4	AAW93894	AAW93894 Human pol	794	35	44.3	736	4	ABE63170	ABE63170 Drosophil
722	35	44.3	477	8	ADL31996	AdL31996 Human pro	795	35	44.3	739	7	ABR62849	ABR62849 Drosophil
723	35	44.3	478	7	ADH87658	AdH87658 Enterococ	796	35	44.3	739	7	ABR62849	ABR62849 Drosophil
724	35	44.3	481	3	AGS50448	AgS50448 Arabidops	797	35	44.3	764	6	ABU38393	ABU38393 Protein e
725	35	44.3	483	3	ABO80822	ABO80822 A. mammali	798	35	44.3	791	5	ABE93713	ABE93713 Herbicida
726	35	44.3	484	5	ABP43984	ABP43984 Acetylchol	799	35	44.3	791	1	ADT56021	ADT56021 Plant pol
727	35	44.3	485	6	ADA14400	AdA14400 Mouse spe	800	35	44.3	819	1	AAW92011	AAW92011 Antitbody/
728	35	44.3	485	6	ADL14400	AdL14400 Mouse spe	801	35	44.3	832	2	AAW04302	AAW04302 Antitbody/
729	35	44.3	496	8	ADX88393	ADX88393 Drosophil	802	35	44.3	839	6	ABU20406	ABU20406 Protein e
730	35	44.3	498	4	ABE63363	ABE63363 Drosophil	803	35	44.3	850	7	ADD27991	ADD27991 Caleosin/
731	35	44.3	504	4	ABE66372	ABE66372 Drosophil	804	35	44.3	850	7	ADS54305	ADS54305 Caleosin/
732	35	44.3	512	3	AGG20636	AgG20636 Plant pol	805	35	44.3	850	8	ADU93779	ADU93779 Maidenhai
733	35	44.3	513	3	ADT56580	AdT56580 Plant pol	806	35	44.3	873	6	ABM98978	ABM98978 Diterpene
734	35	44.3	514	5	AAE22914	AAE22914 Human tra	807	35	44.3	873	6	ADP81142	ADP81142 Sequence
735	35	44.3	516	6	ABW70141	ABW70141 Photorhab	808	35	44.3	881	1	AAW93129	AAW93129 Protein e
736	35	44.3	517	5	ADH22134	ADH22134 Human cho	809	35	44.3	931	6	ADL05129	ADL05129 M. catarr
737	35	44.3	517	8	ABM83681	ABM83681 Human dia	810	35	44.3	963	8	AAW68840	AAW68840 Fuslon pr
738	35	44.3	520	7	ADBE64077	ADBE64077 Human Pro	811	35	44.3	1010	3	AAW68840	AAW68840 Fuslon pr
739	35	44.3	520	8	ADQ14359	AdQ14359 Human nlc	812	35	44.3	1056	2	AAW68840	AAW68840 Fuslon pr
740	35	44.3	520	8	ADL1740	AdL1740 Human cho	813	35	44.3	1067	7	ABO81780	ABO81780 Pseudomon
741	35	44.3	520	8	ADS14333	AdS14333 Human cho	814	35	44.3	1082	4	ABE65972	ABE65972 Drosophil
742	35	44.3	520	9	ABE77820	ABE77820 Human cho	815	35	44.3	1223	8	ABE64058	ABE64058 Bacterial
743	35	44.3	533	8	ADQ66775	AdQ66775 Novel hum	816	35	44.3	1242	5	ABE81108	ABE81108 LUC-U3'-U
744	35	44.3	542	4	ABE66844	ABE66844 Drosophil	817	35	44.3	1242	6	ABE84637	ABE84637 LUC-U3'-U
745	35	44.3	548	3	AGS50447	AgS50447 Arabidops	818	35	44.3	1572	5	ABP65360	ABP65360 Bifidobac
746	35	44.3	548	3	AGG20756	AgG20756 Arabidops	819	35	44.3	449	4	AAW95636	AAW95636 Human pro
747	35	44.3	550	4	AAW69049	AAW69049 Hordeum v	820	35	44.3	526	2	AAW25222	AAW25222 Yeast his
748	35	44.3	551	2	AAW61643	AAW61643 Nicotian	821	35	44.3	572	5	ABP63661	ABP63661 Human pol
749	35	44.3	561	7	ABO78021	ABO78021 Pseudomon	822	35	44.3	1030	5	ABE91346	ABE91346 Herbicida
750	35	44.3	579	8	ADN20597	AdN20597 Bacterial	823	35	44.3	42	4	AAE02660	AAE02660 Modified
751	35	44.3	602	1	AAW62848	AAW62848 Beta-gluc	824	35	44.3	42	4	AAE00450	AAE00450 Modified
752	35	44.3	602	2	AAW43387	AAW43387 Beta-gluc	825	35	44.3	55	5	ABP31209	ABP31209 Human hyd
753	35	44.3	602	2	AAW42429	AAW42429 Escherich	826	35	44.3	76	4	ABB16208	ABB16208 Human ner
754	35	44.3	602	3	AAE28409	AAE28409 Salmonell	827	35	44.3	79	4	AAU56084	AAU56084 Propionib

828	34	43.0	79	6	ABM52603	Abm52603 Propionib	901	34	43.0	433	2	AAW05389	Aaw05389 Mouse SH3
829	34	43.0	82	8	ADQ75910	ADQ75910 Lysine de	902	34	43.0	438	5	ABP73856	Abp73856 Candida a
830	34	43.0	96	4	ABB64664	Abb64664 Drosophil	903	34	43.0	440	8	Adx77815	Adx77815 Plant ful
831	34	43.0	141	2	AAR67917	Aar67917 (1-3)-bet	904	34	43.0	445	6	ABJ25545	Abj25545 Aspergill
832	34	43.0	147	7	ADB64403	Adb64403 Human pro	905	34	43.0	457	3	ABJ43259	Abj43259 Human ORF
833	34	43.0	156	4	AAU20178	Aau20178 Human nov	906	34	43.0	461	4	AAU43079	Aau43079 Propionib
834	34	43.0	158	7	ADF05708	Adf05708 Bacterial	907	34	43.0	461	6	ABM39598	Abm39598 Propionib
835	34	43.0	187	4	AAU41383	Aau41383 Propionib	908	34	43.0	466	8	ADU33990	Adu33990 Protein e
836	34	43.0	187	6	ABM37902	Abm37902 Propionib	909	34	43.0	466	8	ADS27504	Ads27504 Bacterial
837	34	43.0	187	9	ABM40706	Abm40706 L. pneumo	910	34	43.0	469	4	ABG12495	Abg12495 Novel hum
838	34	43.0	196	9	ABM37388	Abm37388 L. pneumo	911	34	43.0	470	6	ADA35386	Ada35386 Acinetoba
839	34	43.0	201	2	AAW79540	Aaw79540 Adenoviru	912	34	43.0	474	6	ABU30004	Abu30004 Protein e
840	34	43.0	201	3	AAAB63213	Aab63213 Gene 38 h	913	34	43.0	475	6	ABU29756	Abu29756 Protein e
841	34	43.0	201	3	AAU67374	Aau67374 Propionib	914	34	43.0	476	7	ABO78332	Ab078332 Pseudomon
842	34	43.0	225	6	ABM63893	Abm63893 Propionib	915	34	43.0	478	7	ADG97241	Adg97241 E. faeciu
843	34	43.0	225	6	ABM63893	Abm63893 Propionib	916	34	43.0	479	7	ADG33826	Adg33826 Actinomyc
844	34	43.0	220	6	ABM65059	Abm65059 Propionib	917	34	43.0	487	8	ADS28228	Ads28228 Bacterial
845	34	43.0	245	8	ADS21212	Ads21212 Bacterial	918	34	43.0	488	2	AAW89248	Aaw89248 Human SAD
846	34	43.0	247	6	ABM66054	Abm66054 Propionib	919	34	43.0	488	7	ADG38351	Adg38351 Human pro
847	34	43.0	261	6	AAO23118	Aao23118 Human mo	920	34	43.0	491	4	ABR79425	AbR79425 Corynebac
848	34	43.0	262	8	ADY13514	Ady13514 plant ful	921	34	43.0	492	7	ADC97318	Adc97318 E. faeciu
849	34	43.0	280	6	ABP96395	Abp96395 Nostoc pu	922	34	43.0	500	6	ABU29319	Abu29319 Protein e
850	34	43.0	288	7	ADD19156	Add19156 Nostoc pu	923	34	43.0	504	8	ADM32776	Adm32776 Amino aci
851	34	43.0	289	4	AAAG91771	Aag91771 C glutami	924	34	43.0	504	7	ABO67399	Ab067399 Klebsiell
852	34	43.0	290	4	AAAB87519	Aab87519 B thuring	925	34	43.0	512	4	ABG60925	Abg60925 Drosophil
853	34	43.0	290	8	ADN01739	Adn01739 Toxin pro	926	34	43.0	512	8	ABU24030	Abu24030 Plant ful
854	34	43.0	290	8	ADQ16186	Adq16186 Bacillus	927	34	43.0	525	4	ABG06254	Abg06254 Novel hum
855	34	43.0	292	8	ADN20991	Adn20991 Bacterial	928	34	43.0	526	7	ADH88831	Adh88831 Enterococ
856	34	43.0	314	7	ABO78871	Ab078871 Pseudomon	929	34	43.0	526	6	ABP80112	Abp80112 N. gonorr
857	34	43.0	317	2	AAR26061	Aar26061 Growth Fa	930	34	43.0	526	8	ADP08268	Adp08268 Neisseria
858	34	43.0	319	4	AAAM15093	Aam15093 Peptide #	931	34	43.0	528	6	ABU22840	Abu22840 Protein e
859	34	43.0	319	4	AAAM27542	Aam27542 Peptide #	932	34	43.0	528	6	ABU31836	Abu31836 Protein e
860	34	43.0	319	4	ABB28910	Abb28910 Peptide #	933	34	43.0	549	6	ABU45163	Abu45163 Protein e
861	34	43.0	319	4	ABB19521	Abb19521 Protein #	934	34	43.0	552	4	ABR71495	AbR71495 Drosophil
862	34	43.0	319	4	AAAM67249	Aam67249 Human bon	935	34	43.0	552	7	ABR71493	AbR71493 Drosophil
863	34	43.0	319	4	AAAM54868	Aam54868 Human bra	936	34	43.0	555	4	ADJ24919	Adj24919 Xanthomon
864	34	43.0	319	4	ABGA48912	Abg48912 Human liv	937	34	43.0	557	4	AAU38414	Aau38414 Salmonell
865	34	43.0	319	4	AAAM02830	Aam02830 Peptide #	938	34	43.0	557	4	AAU34521	Aau34521 E. coli c
866	34	43.0	319	5	ABG36900	Abg36900 Human pep	939	34	43.0	557	6	ABU14912	Abu14912 Protein e
867	34	43.0	321	4	ABBS9947	Abbs9947 Drosophil	940	34	43.0	557	6	ABU47312	Abu47312 Protein e
868	34	43.0	323	4	ABG06500	Abg06500 Novel hum	941	34	43.0	557	6	ABU50079	Abu50079 Protein e
869	34	43.0	323	4	ABG06510	Abg06510 Novel hum	942	34	43.0	557	6	ABU40533	Abu40533 Protein e
870	34	43.0	323	7	ABO67390	Ab067390 Klebsiell	943	34	43.0	557	6	ABU48047	Abu48047 Protein e
871	34	43.0	338	3	AAG10548	Aag10548 Arabidops	944	34	43.0	560	7	ABO65610	Ab065610 Klebsiell
872	34	43.0	338	6	ADA35864	Ada35864 Acinetoba	945	34	43.0	563	6	ABM68942	Abm68942 Phototrab
873	34	43.0	342	6	AAAG10547	Aag10547 Arabidops	946	34	43.0	564	7	ADF04986	Adf04986 Bacterial
874	34	43.0	345	6	ABP56672	Abp56672 Human ade	947	34	43.0	574	8	ADS41628	Ads41628 Bacterial
875	34	43.0	347	7	AAU36087	Aau36087 Klebsiell	948	34	43.0	585	5	ABP64725	Abp64725 Human pro
876	34	43.0	353	7	ABO68926	Ab068926 Pseudomon	949	34	43.0	588	8	ABO60329	Ab060329 Human gen
877	34	43.0	354	8	ADY13065	Ady13065 Plant ful	950	34	43.0	590	3	ABM56641	Abm56641 Human pro
878	34	43.0	363	5	ABP73896	Abp73896 Candida a	951	34	43.0	592	8	ADN99266	Adn99266 Novel hum
879	34	43.0	376	8	ADN17901	Adn17901 Bacterial	952	34	43.0	593	8	ADN05235	Adn05235 Antipsori
880	34	43.0	379	5	ABG93171	Abg93171 S. cerevi	953	34	43.0	608	4	ABG08671	Abg08671 Novel hum
881	34	43.0	380	8	ADN19527	Adn19527 Bacterial	954	34	43.0	612	2	AAR91947	Aar91947 Brevibact
882	34	43.0	387	3	AAAB36484	Aab36484 Bacillus	955	34	43.0	612	3	AAAB10681	Aab10681 C. glutam
883	34	43.0	387	4	AAAB7515	Aab7515 B thuring	956	34	43.0	613	3	AAAB10035	Aab10035 C. glutam
884	34	43.0	387	8	ADN01731	Adn01731 Toxin pro	957	34	43.0	613	4	AAAG91145	Aag91145 C glutami
885	34	43.0	387	8	ADQ16178	Adq16178 Bacillus	958	34	43.0	620	6	ABU34746	Abu34746 Protein e
886	34	43.0	398	4	ABM64093	Abm64093 Drosophil	959	34	43.0	630	4	ABM79424	Abm79424 Corynebac
887	34	43.0	404	3	AAG10546	Aag10546 Arabidops	960	34	43.0	639	6	ABU36687	Abu36687 Protein e
888	34	43.0	409	2	AAR85868	Aar85868 WD-40 dom	961	34	43.0	653	6	ABU33972	Abu33972 Protein e
889	34	43.0	409	2	AAR70002	Aar70002 OPDE 45 k	962	34	43.0	656	6	ABU35973	Abu35973 Protein e
890	34	43.0	409	7	ADES6488	Ade6488 Rat Prote	963	34	43.0	673	2	AAAR67915	Aar67915 (1-3)-bet
891	34	43.0	409	7	ADEB3492	Ade83492 Rat Prote	964	34	43.0	673	6	ABR57645	AbR57645 Alpha sub
892	34	43.0	409	7	ADES4235	Ade54235 Human Pro	965	34	43.0	729	4	ABM64294	Abm64294 Drosophil
893	34	43.0	409	7	ADES4233	Ade54233 Rat Prote	966	34	43.0	730	4	AAAB18000	Aab18000 Amino aci
894	34	43.0	409	8	ADR99123	Adr99123 Platelet-	967	34	43.0	736	5	ABBS2568	Abbs2568 Herbicida
895	34	43.0	410	2	AAR70005	Aar70005 OPDE 45 k	968	34	43.0	739	5	ABBS2567	Abbs2567 Herbicida
896	34	43.0	410	8	ADN04527	Adn04527 Antipsori	969	34	43.0	790	9	ADM18282	Adm18282 Eucalyptu
897	34	43.0	410	9	ADN05924	Adn05924 Cyclin-de	970	34	43.0	803	5	ABBS2885	Abbs2885 Herbicida
898	34	43.0	423	6	ABU15234	Abu15234 Protein e	971	34	43.0	811	8	ADX93417	Adx93417 Plant ful
899	34	43.0	428	4	ABG17824	Abg17824 Novel hum	972	34	43.0	811	8	ADY23684	Ady23684 Plant ful
900	34	43.0	432	6	ABM67605	Abm67605 Phototrab	973	34	43.0	813	6	ABU24411	Abu24411 Protein e

974 34 43.0 814 6 ABUL18161
975 34 43.0 828 7 AD6262562
976 34 43.0 828 7 ADD48013
977 34 43.0 828 7 AD6262566
978 34 43.0 828 7 ADD48015
979 34 43.0 828 7 ADD48023
980 34 43.0 828 7 ADD48023
981 34 43.0 836 4 AAG92051
982 34 43.0 892 6 ABUL17889
983 34 43.0 902 4 ABG17042
984 34 43.0 909 6 ABM68642
985 34 43.0 927 4 ABG14898
986 34 43.0 934 4 ABG15516
987 34 43.0 934 4 ABG15516
988 34 43.0 950 4 ABG12699
989 34 43.0 950 4 ABG04340
990 34 43.0 968 2 AAW79538
991 34 43.0 981 9 ABM90649
992 34 43.0 991 4 ABM58156
993 34 43.0 1145 7 ADD25137
994 34 43.0 1145 8 ADN61152
995 34 43.0 1223 8 ADJ48692
996 34 43.0 1266 2 ADW25157
997 34 43.0 1266 3 ABG07754
998 34 43.0 1314 5 ABBS2290
999 34 43.0 1321 6 ADAZ2697
1000 34 43.0 1520 4 ABB64314

ALIGNMENTS

RESULT 1
AA94590
ID AA94590 standard; peptide; 15 AA.
AC AA94590;
XX
XX
XX 28-NOV-2000 (first entry)
XX
XX Mycobacterium tuberculosis ESAT-6 peptide ES1.
XX
XX Tuberculosis; infection diagnosis; ESAT-6.
XX
XX Mycobacterium tuberculosis.
XX
XX WO200026248-A2.
XX
XX 11-MAY-2000.
XX
XX 03-NOV-1999; 99WO-GB003635.
XX
XX 04-NOV-1998; 98GB-00024213.
XX
XX 04-NOV-1998; 98US-0107004P.
XX
XX (ISIS-) ISIS INNOVATION LTD.
XX
XX Lalvani A, Pathan AA;
XX
XX WPI, 2000-365579/31.
XX
XX Novel method of diagnosing infection, or exposure of a host, to a
XX mycobacterium comprising contacting T cells from the host with ESAT-6
XX derived peptides.
XX
XX Claim 1; Page 3; 33pp; English.
XX
XX The present sequence is the peptide ES1 derived from the Mycobacterium
XX tuberculosis ESAT-6 gene. This sequence is one of eleven peptides derived
XX from the ESAT-6 gene (see AA94590 to AA94600). The peptides are
XX recognised, to varying degrees, by the T cells of patients with
XX tuberculosis. When the peptides are combined together as a panel they
XX provide a high specificity and sensitivity diagnostic test for

CC M.tuberculosis infection. This test has the advantage that it does not
CC give false positives for patients who have been vaccinated with BCG
XX
XX Sequence 15 AA;
XX
XX Query Match 100.0%; Score 79; DB 3; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 3e-06; 0; Indels 0; Gaps 0;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MTEQQWNPAGIEAAA 15
XX
XX 1 MTEQQWNPAGIEAAA 15
XX
XX
XX RESULT 2
XX ABG30951
XX ID ABG30951 standard; peptide; 15 AA.
XX
XX AC ABG30951;
XX
XX 21-OCT-2002 (first entry)
XX
XX Mycobacterium tuberculosis ESAT-6 residues 1-15.
XX
XX ESAT-6; mycobacterial infection; tuberculosis; pulmonary tuberculosis;
XX tuberculosis lymphadenitis; extrapulmonary tuberculosis.
XX
XX Mycobacterium tuberculosis.
XX
XX WO200254072-A2.
XX
XX 11-JUL-2002.
XX
XX 08-JAN-2002; 2002WO-GB0000055.
XX
XX 08-JAN-2001; 2001GB-00000432.
XX
XX 08-JAN-2001; 2001US-0259868P.
XX
XX (ISIS-) ISIS INNOVATION LTD.
XX
XX Lalvani A;
XX
XX WPI, 2002-583633/62.
XX
XX Determining the progress of a mycobacterial infection, by direct ex vivo
XX quantitation of ESAT-6-specific T cells.
XX
XX Example 2; Page 40; 53pp; English.
XX
XX The invention describes a method of determining the efficacy of treatment
XX for mycobacterial infection (such as pulmonary tuberculosis, tuberculosis
XX lymphadenitis and extrapulmonary tuberculosis). The method involves
XX determining the level of T cells specific for a mycobacterial antigen
XX that has decreased after the treatment and therefore determining the
XX efficacy of the treatment. The method is useful for determining the
XX efficacy of treatment for mycobacterial infection, the mycobacterial
XX infection is Mycobacterium tuberculosis or M.bovis infection. The
XX invention also describes a method useful for determining the presence of T
XX cells specific for a mycobacterial antigen. Also described in a method
XX for determining the effect of an intervention on a mycobacterial
XX infection in an individual an a method for treating an individual
XX infected by a mycobacterium. This sequence represents a peptide of
XX Mycobacterium tuberculosis ESAT-6, the mycobacterial antigen measured in
XX the invention
XX
XX Sequence 15 AA;
XX
XX Query Match 100.0%; Score 79; DB 5; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 3e-06; 0; Indels 0;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MTEQQWNPAGIEAAA 15
XX

```

DB      1 MTEQOWNFAGIEAAA 15
|||||
RESULT 3
AAO17432
ID      AAO17432 standard; peptide; 15 AA.
XX
AC      AAO17432;
XX
DT      11-JUL-2002 (first entry)
XX
DE      Early secreted antigenic target 6 T cell epitope #1.
XX
KW      Tuberculosis; TB; vaccination; vaccine; CD4+ T cell immune response;
KW      poxvirus vector; HIV; malaria; Helicobacter pylori; influenza; hepatitis;
KW      viral infection; leprosy; protozoan parasite; cancer; tuberculostatic;
KW      anti-HIV; protozoicide; antibacterial; virucide; hepatotropic;
KW      antiinflammatory; antileprotic; cytostatic; epitope.
XX
OS      Mycobacterium tuberculosis.
XX
PN      WO200224224-A2.
XX
PD      28-MAR-2002.
XX
PF      13-SEP-2001; 2001WO-GB004116.
XX
PR      21-SEP-2000; 2000GB-00023203.
XX
PA      (OXO-) OXON PHARMACINES LTD.
XX
PI      Hill AVS, Mcshane H, Gilbert S, Reece W, Schneider J;
XX
DR      WPI; 2002-394098/42.
XX
PT      Inducing CD4+ T-cell response against target antigen by administering a
PT      composition comprising a source of CD4+ epitopes which is a non-
PT      replicating or replication impaired recombinant poxvirus vector.
XX
PS      Example 1; Page 21; 50pp; English.
XX
CC      The present invention relates to a method of inducing a CD4+ T-cell
CC      response against a target antigen, by administering two different
CC      compositions comprising a source of CD4+ T-cell epitope(s) of the target
CC      antigen, where the second composition further includes an epitope which
CC      is same as the epitope of the first composition, where the source of the
CC      epitopes for the compositions is a non-replicating or replication
CC      impaired recombinant poxvirus vector. The methods are useful for inducing
CC      CD4+ T-cell immune responses against diseases such as tuberculosis, human
CC      immunodeficiency virus (HIV) (persistent viral infection), malaria,
CC      Helicobacter pylori, influenza, hepatitis (chronic hepatitis B and C),
CC      cytomegalovirus (CMV), viral infection, herpes virus-induced disease,
CC      leprosy and diseases caused by non-malarial protozoan parasite such as
CC      toxoplasma and cancer. The present sequence is an epitope from
CC      Mycobacterium tuberculosis useful in the method of the invention
XX
SQ      Sequence 15 AA;

Query Match      100.0%; Score 79; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MTEQOWNFAGIEAAA 15
|||||
DB      1 MTEQOWNFAGIEAAA 15
|||||

RESULT 4
ADI33341
ID      ADI33341 standard; peptide; 15 AA.
XX
AC      ADI33341;
XX

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XX      22-APR-2004 (first entry)
XX      Mycobacterium tuberculosis ESAT-6 peptide epitope #1.
XX
DE      pathogen; vaccine; cellular response; HPV; HIV; HCV; chlamydia; HBV;
DE      EBV; CMV; VZV; HSV; Legionella; Leishmaniasis; influenza;
KW      foot and mouth virus; Toxoplasma; Brucella; Cryptococcus; Candida;
KW      Aspergillus; Mycobacterium; T cell; ESAT-6; CFP10; virucide; protozoicide;
KW      antibacterial; fungicide; epitope.
XX
OS      Mycobacterium tuberculosis.
XX
PN      WO2004005925-A2.
XX
PD      15-JAN-2004.
XX
PF      07-JUL-2003; 2003WO-GB002936.
XX
PR      05-JUL-2002; 2002GB-00015710.
XX
PA      (ISIS-) ISIS INNOVATION LTD.
XX
PI      Lalvani A, Ewer K;
XX
DR      WPI; 2004-143006/14.
XX
PT      Diagnosing in an individual recent exposure to an agent, useful in
PT      treating a disease caused by a pathogen, by determining in vitro or in
PT      vivo whether the T cells of recognize a protein having at least 30 amino
PT      acids.
XX
PS      Claim 16; Page 33; 48pp; English.
XX
CC      The invention relates to a novel method for diagnosing in an individual
CC      recent exposure to an agent which is a pathogen, vaccine or any other
CC      moiety, which induces a cellular response. The pathogen can include: HPV,
CC      HIV, SIV, HCV, chlamydia species, HBV, EBV, CMV, VZV, HSV, Legionella, S.
CC      typhi, P. falciparum, Leishmaniasis, M. leprae, influenza virus, foot and
CC      mouth virus, a Toxoplasma species, a Brucella species, a Cryptococcus
CC      species, a Candida species, an Aspergillus species, or Mycobacterium
CC      tuberculosis. The invention also provides a vaccine against any of the
CC      above pathogens. The method comprises determining in vitro or in vivo
CC      whether the T cells of the individual recognize a protein from the agent
CC      having a length of at least 30 amino acids. The invention also comprises
CC      a protein or epitope peptide which is from ESAT-6 or CFP10. The vaccines
CC      of the invention have: virucide, protozoicide, antibacterial, and fungicide
CC      activity. The method is useful in diagnosing in an individual recent
CC      exposure to an agent which is a pathogen, vaccine or any other moiety
CC      which induces a cellular response. The protein described above, the
CC      product which prevents or treats a condition caused by a pathogen or the
CC      antigen or its analogue is useful in the manufacturing of a medicament
CC      for diagnosing and treating an individual recently exposed to a pathogen.
CC      This sequence represents a peptide epitope of the invention for
CC      recognition by a T cell relating to the invention.
XX
SQ      Sequence 15 AA;

Query Match      100.0%; Score 79; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MTEQOWNFAGIEAAA 15
|||||
DB      1 MTEQOWNFAGIEAAA 15
|||||

RESULT 5
AEB45086
ID      AEB45086 standard; peptide; 15 AA.
XX
AC      AEB45086;
XX

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DT 06-OCT-2005 (first entry)
XX M. tuberculosis ESAT6 peptide fragment SEQ ID NO 216.
DE
XX immunogenicity; viral infection; infection; bacterial infection; cancer;
KW neoplasm; autoimmune disease; immune disorder; inflammation; allergy;
KW Antibacterial; Virucide; Fungicide; Anti-HIV; Hepatotropic;
KW Antiparasitic; Cytostatic; immunosuppressive; antiarthritic;
KW antineoplastic; neuroprotective; antidiabetic; gastrointestinal-Gen.;
KW antiinflammatory; antiulcer; antipsoriatic; dermatological;
KW antiasthmatic; antiallergic; immunomodulator.
XX
XX Mycobacterium tuberculosis.
OS
XX
XX WO2005070959-A2.
XX
XX 04-AUG-2005.
XX
XX 24-JAN-2005; 2005WO-US002251.
XX
XX 23-JAN-2004; 2004US-0538713P.
XX
XX 06-OCT-2004; 2004US-0616855P.
XX
XX (VIEV-) VIEVAX CORP.
XX
XX Mahairas GG;
XX
XX WPI; 2005-542270/55.
XX
XX Immune response altering agent useful for treating autoimmune diseases,
PT comprises first domain having T/B cell epitopes or Toll-like receptor-
PT binding proteins, and second domain having heterologous target molecule.
PT
XX
XX Claim 65; SEQ ID NO 216; 130pp; English.
XX
XX The invention relates to an immune response altering agent (I) which
CC comprises a first domain having one or more components chosen from T cell
CC epitopes, B cell epitopes, and Toll-like receptor (TLR)-binding proteins
CC or its TLR-binding domains, and a second domain having heterologous
CC target molecule against which an immune response is desired. (I) is
CC useful for altering or inducing an immune response to a target. (I) is
CC also useful for treating viral infections (e.g., HIV and hepatitis C
CC virus), bacterial infections (e.g., Staphylococcus and Pseudomonas),
CC parasites (e.g., Leishmania), fungal infections (e.g., Candida), cancer
CC (e.g., non-Hodgkin's lymphoma, Hodgkin's disease and leukemia), and
CC autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,
CC insulin dependent diabetes, Addison's disease, celiac disease,
CC inflammatory bowel disease, ulcerative colitis, Crohn's disease, systemic
CC lupus erythematosus, psoriasis, Sjogren's syndrome, etc. (I) is useful
CC for treating inflammatory and hyperproliferative skin diseases, and
CC allergic reactions such as asthma, bronchitis, allergic rhinitis etc. (I)
CC alters an immune response generated against the heterologous target
CC molecule. (I) can be applied to wide range of species such as humans, non
CC -human primates, horses, etc. The present sequence represents the amino
CC acid sequence of a M. tuberculosis early secretory antigenic target 6,
CC ESAT6, peptide fragment.
XX
XX Sequence 15 AA;
SQ
Query Match 100.0%; Score 79; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTEQWNPAGIEAAA 15
Db 1 MTEQWNPAGIEAAA 15
RESULT 6
AAY88581
ID AAY88581 standard; peptide; 17 AA.
XX
XX AAY88581;
AC

XX 11-AUG-2000 (first entry)
DT
XX Antigenic N-terminal sequence of ESAT-6.
DE
XX
XX Ligand presenting assembly; early secreted antigen target 6; ESAT-6;
KW bacteria; detect; diagnosis; allergen; cancer; vaccine; immune response;
KW neurotropic factor; autoimmune-system related compound; LPA; fungi;
KW parasite; cell-adhesion molecule.
XX
XX Mycobacterium tuberculosis.
OS
XX
XX Key Location/Qualifiers
FH 17
XX Cross-links
FT /note= "Ala at position 17 is linked via a linker to Ala
FT at position 17 of an identical peptide, where the linker
FT is COCH2-CH(NH-Lys)-CH2CO, and the Lys residue contained
FT in the linker is also linked to another peptide (see
FT AAY88579)"
XX
XX WO200018791-A1.
XX
XX 06-APR-2000.
XX
XX 29-SEP-1999; 99WO-DK000510.
XX
XX 29-SEP-1998; 98DK-00001233.
XX
XX (STAT-) STATENS SERUM INST.
XX (HOLM/) HOLM A.
XX Holm A, Jorgensen RM, Ostergaard S, Theisen M;
XX WPI; 2000-303438/26.
XX
XX New ligand presenting assemblies useful for diagnosis, treatment and
PT prevention of diseases caused by e.g. viruses, bacteria, toxins,
PT allergens, autoimmune system-related compounds, cancer-related compounds,
PT cell adhesion molecules.
XX
XX Claim 34; Page 81; 100pp; English.
XX
XX This sequence represents an antigenic N-terminal sequence from the
CC Mycobacterium tuberculosis early secreted antigenic target 6 (ESAT-6)
CC protein. The peptide is presented on the new ligand presenting assembly
CC of the invention. The invention relates to method for preparing ligand
CC presenting assemblies (LPAs) comprising: (a) providing by solid phase
CC synthesis or fragment coupling, ligands comprising desired sequences
CC (e.g. the present sequence), the ligands being attached to a solid phase;
CC (b) if necessary, deprotecting any N-terminal amino groups while the
CC ligands are still attached to the solid phase; (c) reacting the ligands
CC having unprotected N-terminal amino groups with an achiral di-, tri- or
CC tetracarboxylic acid, to provide a construct having a ring structure; and
CC (d) cleaving the construct from the solid phase, to provide an LPA
CC comprising ligands having free C-terminal groups. The LPAs can be used in
CC for raising an immune response in an animal. They can also be used in
CC vaccines and for generating antibodies in an animal. Alternatively they
CC can be used for the treatment, alleviation, detection, diagnosis, or
CC prophylaxis of diseases caused by viruses, bacteria, toxins, allergens,
CC autoimmune system-related compounds, cancer related compounds, cell
CC adhesion molecules, neurotropic factors, fungi or parasites. Use of the
CC method enables the preparation of very long ring systems interconnected
CC by reaction with the achiral di-, tri- or tetracarboxylic acid. The ring
CC structure formed between desired sequences further enables additional
CC presentation of desired sequences and chemical moieties. The LPAs provide
CC very flexible systems for polyfunctional constructs, and furthermore,
CC products of high purity are obtained
XX
XX Sequence 17 AA;
SQ

Query Match 100.0%; Score 79; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTEQOWNFAGIEAAA 15
|||||
Db 1 MTEQOWNFAGIEAAA 15

RESULT 7
AAW35548
ID AAW35548 standard; peptide; 19 AA.

AC AAW35548;
XX
XX 25-MAR-2003 (revised)
DT 22-APR-1998 (first entry)
XX
DE BSAT-6 antigen SEQ ID NO:120 from WO9738011.
XX
XX T-cell stimulatory peptide; immunogen; non-dendritic; carrier; tumour;
KW scaffold; inhibition; metastasis; wound healing; solid phase.
XX
XX Synthetic.

OS
XX WO9738011-A1.
XX
XX 16-OCT-1997.

XX
XX 03-APR-1997; 97WO-DK000146.
XX
XX 03-APR-1996; 96DK-00000398.

XX (PEPR-) PEPRESEARCH AS.
XX
XX Heegaard PMH, Jakobsen PH;

XX WPI; 1997-512645/47.
XX
XX

PT Non-dendritic peptide carrier linked to a solid phase - useful as a
PT diagnostic agent and as a scaffold for production of chemical
PT derivatives.

XX Example 32; Page 156; 262pp; English.

CC A non-dendritic peptide carrier (A) has been developed which is coupled
CC through a linker to a solid phase, forming a complex of (A)-solid phase.
CC Where (A) comprises 10-50 amino acids capable of forming a secondary
CC structure in a benign buffer after liberation from the solid phase, and
CC further the (A)-solid phase complex comprises an immunogenic substance
CC and/or an immune mediator coupled on (A). The present sequence represents
CC a peptide used in an example from the present invention. An (A)-solid
CC phase complex can be used as a scaffold for the production of chemical
CC derivatives, characterised by covalently attaching molecules at
CC attachment points. Alternatively (A) is used as a scaffold-peptide for
CC the incorporation into an immunostimulating complex (Iscom), resulting an
CC (A)-Iscom complex which is used for the chemical coupling of antigenic
CC substances in an aqueous solution by conjugation. (A) derivatised with
CC one or more peptides having fibronectin-, laminin- or vitronectin-like
CC binding activities can be used for the promotion of cell-attachment to
CC plastic surfaces, in particular to inhibit tumour growth and metastasis,
CC and for promotion of wound healing. Also a derivatised (A) can be used
CC for the selection of specifically-binding aptamers or as a diagnostic
CC agent. Such diagnostic-(A) molecules could be used to detect molecules
CC derived from or indicative of pregnancy or of a disease, such as an
CC infectious, autoimmune or cancerous disease. (Updated on 25-MAR-2003 to
CC correct PF field.)
XX

XX Sequence 19 AA;

Query Match 100.0%; Score 79; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTEQOWNFAGIEAAA 15
|||||

Db 1 MTEQOWNFAGIEAAA 15

RESULT 8

AEBA4911
ID AEB44911 standard; peptide; 20 AA.

XX
AC AEB44911;

XX
DT 06-OCT-2005 (first entry)

XX
DE Mycobacterium ESAT6 T cell epitope SEQ ID NO 41.

XX
KW immunogenicity; viral infection; infection; bacterial infection; cancer;
KW neoplasm; autoimmune disease; immune disorder; inflammation; allergy;
KW Antibacterial; Virucide; Fungicide; Anti-HIV; Hepatotropic;
KW Antiparasitic; Cytostatic; immunosuppressive; antiarthritic;
KW antirheumatic; neuroprotective; antidiabetic; gastrointestinal-Gen.;
KW antiinflammatory; antitumor; antipsoriatic; dermatological;
KW antiasthmatic; antiallergic; immunomodulator.

XX
OS Mycobacterium tuberculosis.
OS Mycobacterium bovis.

XX WO2005070959-A2.

XX 04-AUG-2005.

XX 24-JAN-2005; 2005WO-US002251.

XX 23-JAN-2004; 2004US-0538713P.

XX 06-OCT-2004; 2004US-0616855P.

XX (VIEW-) VIEVAX CORP.

XX Mahairas GG;

XX WPI; 2005-542270/55.

XX
PT Immune response altering agent useful for treating autoimmune diseases,
PT comprises first domain having T/B cell epitopes or Toll-like receptor-
PT binding proteins, and second domain having heterologous target molecule.

XX Disclosure; SEQ ID NO 41; 130pp; English.

XX The invention relates to an immune response altering agent (I) which
CC comprises a first domain having one or more components chosen from T cell
CC epitopes, B cell epitopes, and Toll-like receptor (TLR)-binding proteins
CC or its TLR-binding domains, and a second domain having heterologous
CC target molecule against which an immune response is desired. (I) is
CC useful for altering or inducing an immune response to a target. (I) is
CC also useful for treating viral infections (e.g., HIV and hepatitis C
CC virus), bacterial infections (e.g., Staphylococcus and Pseudomonas),
CC parasites (e.g., Leishmania), fungal infections (e.g., Candida), cancer
CC (e.g., non-Hodgkin's lymphoma, Hodgkin's disease and leukemia), and
CC autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,
CC insulin dependent diabetes, Addison's disease, celiac disease,
CC inflammatory bowel disease, ulcerative colitis, Crohn's disease,
CC lupus erythematosus, psoriasis, Sjogren's syndrome, etc. (I) is useful
CC for treating inflammatory and hyperproliferative skin diseases, and
CC allergic reactions such as asthma, bronchitis, allergic rhinitis etc. (I)
CC alters an immune response generated against the heterologous target
CC molecule. (I) can be applied to wide range of species such as humans, non
CC -human primates, horses, etc. The present sequence represents the amino
CC acid sequence of a T-cell epitope used to illustrate the present
CC invention.

XX
-SQ Sequence 20 AA;

Query Match 100.0%; Score 79; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQWNFAGIEAAA 15
|||||
DB 1 MTEQWNFAGIEAAA 15

RESULT 9
AEB45107
ID AEB45107 standard; peptide; 20 AA.

XX AC AEB45107;
XX DT 06-OCT-2005 (first entry)
XX DE M. tuberculosis ESAT6 peptide fragment SEQ ID NO 237.
XX KW immunogenicity; viral infection; infection; bacterial infection; cancer;
KW neoplasm; autoimmune disease; immune disorder; inflammation; allergy;
KW Antibacterial; Virucide; Fungicide; Anti-HIV; Hepatotropic;
KW Antiparasitic; Cytostatic; Immunosuppressive; Antiarthritic;
KW antiRheumatic; neuroprotective; antidiabetic; gastrointestinal-Gen.;
KW antiinflammatory; atulcer; antipsoriatic; dermatological;
KW antiasthmatic; antiallergic; Immunomodulator.

XX OS Mycobacterium tuberculosis.
XX PN WO2005070959-A2.

XX PD 04-AUG-2005.
XX PF 24-JAN-2005; 2005WO-US002251.

XX PR 23-JAN-2004; 2004US-0538713P.
XX PR 06-OCT-2004; 2004US-0616855P.

XX PA (VIEW-) VIEWAX CORP.

XX PI Mahairas GG;

XX DR WPI; 2005-542270/55.

XX PT Immune response altering agent useful for treating autoimmune diseases,
PT comprises first domain having T/B cell epitopes or Toll-like receptor-
PT binding proteins, and second domain having heterologous target molecule.

XX PS Claim 65; SEQ ID NO 237; 130pp; English.

XX CC The invention relates to an immune response altering agent (I) which
CC comprises a first domain having one or more components chosen from T cell
CC epitopes, B cell epitopes, and Toll-like receptor (TLR)-binding proteins
CC or its TLR-binding domains, and a second domain having heterologous
CC target molecule against which an immune response is desired. (I) is
CC useful for altering or inducing an immune response to a target. (I) is
CC also useful for treating viral infections (e.g., HIV and hepatitis C
CC virus), bacterial infections (e.g., Staphylococcus and Pseudomonas),
CC parasites (e.g., Leishmania), fungal infections (e.g., Candida), cancer
CC (e.g., non-Hodgkin's lymphoma, Hodgkin's disease and leukemia), and
CC autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,
CC insulin dependent diabetes, Addison's disease, celiac disease,
CC inflammatory bowel disease, ulcerative colitis, Crohn's disease, systemic
CC lupus erythematosus, psoriasis, Sjogren's syndrome, etc. (I) is useful
CC for treating inflammatory and hyperproliferative skin diseases. (I)
CC allergic reactions such as asthma, bronchitis, allergic rhinitis etc. (I)
CC alters an immune response generated against the heterologous target
CC molecule. (I) can be applied to wide range of species such as humans, non
CC -human primates, horses, etc. The present sequence represents the amino
CC acid sequence of a M. tuberculosis early secretory antigenic target 6,
CC ESAT6, peptide fragment.

XX SQ Sequence 20 AA;

Query Match 100.0%; Score 79; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQWNFAGIEAAA 15
|||||
DB 1 MTEQWNFAGIEAAA 15

RESULT 10
AAW32339
ID AAW32339 standard; protein; 51 AA.

XX AC AAW32339;
XX DT 13-JAN-1998 (first entry)
XX DE Mycobacterium tuberculosis antigen ESAT-6.

XX KW Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant;
KW skin testing; M.tuberculosis.

XX OS Mycobacterium tuberculosis.

XX PN WO9709429-A2.

XX PD 13-MAR-1997.

XX PF 30-AUG-1996; 96WO-US014675.

XX PR 01-SEP-1995; 95US-00523435.

XX PR 22-SEP-1995; 95US-00532136.

XX PR 22-MAR-1996; 96US-00620280.

XX PR 05-JUN-1996; 96US-00658800.

XX PR 12-JUL-1996; 96US-00680573.

XX PA (CORI-) CORIXA CORP.

XX PI Reed SG, Skeiky YAM, Dillon DC, Campos-Neto A, Houghton R;

XX PT Vedvick TH, Twardzik DR;

XX DR WPI; 1997-192904/17.

XX DR N-PSDB; AAT91463.

XX PT New immunogenic polypeptide(s) from soluble M. tuberculosis antigens -
PT useful for diagnosis of M. tuberculosis infection.

XX PS Claim 43; Page 147; 190pp; English.

XX CC A new immunogenic polypeptide has been developed comprising an
CC immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its
CC variant differing only in conservative substitutions and/or
CC modifications). The present sequence represents a specifically claimed
CC sequence of the ESAT-6 M.tuberculosis antigen. The immunogenic
CC polypeptide can be used to diagnose M.tuberculosis infection by forming
CC complexes with specific antibodies in the sample. Fragments of DNA
CC encoding the immunogenic polypeptide can be used as diagnostic primers or
CC probes and agents that bind to the antigen, especially monoclonal
CC antibodies or equivalent polyclonal antibodies, are also used for
CC diagnosis

XX SQ Sequence 51 AA;

Query Match 100.0%; Score 79; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQWNFAGIEAAA 15
|||||
DB 1 MTEQWNFAGIEAAA 15

RESULT 11
AAW32466
ID AAW32466 standard; protein; 51 AA.

XX

AC AAW32466;
 XX
 DT 09-JAN-1998 (first entry)
 XX
 DE Mycobacterium tuberculosis antigen ESAT-6.
 XX
 KW Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant;
 KW skin testing; M.tuberculosis.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN WO9709428-A2.
 XX
 PD 13-MAR-1997.
 XX
 XX 30-AUG-1996; 96WO-US014674.
 XX
 PR 01-SEP-1995; 95US-00523436.
 PR 22-SEP-1995; 95US-00533634.
 PR 22-MAR-1996; 96US-00620874.
 PR 05-JUN-1996; 96US-00659683.
 PR 12-JUL-1996; 96US-00680574.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Reed SG, Skeiky YA, Dillon DC, Campos-Neto A, Houghton R;
 PI Vedvick TH, Twardzik DR;
 XX
 XX WPI; 1997-192903/17.
 DR N-PSDB; AAT91529.
 XX
 XX New immunogenic polypeptide(s) from Mycobacterium tuberculosis - are
 PT useful in vaccines for prevention or treatment of tuberculosis, also for
 PT diagnosis.
 XX
 PS Disclosure; Page 135; 168pp; English.
 XX
 CC A new immunogenic polypeptide has been developed comprising an
 CC immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its
 CC variant differing only in conservative substitutions and/or
 CC modifications). The present sequence represents a M.tuberculosis antigen,
 CC ESAT-6. The immunogenic protein, and fusion proteins containing one or
 CC more of the proteins or one of the proteins plus ESAT-6, are useful in
 CC vaccines, preferably when formulated with a non-specific adjuvant, to
 CC induce an immune response against M.tuberculosis (for treatment or
 CC prevention)
 XX
 SQ Sequence 51 AA;
 Query Match 100.0%; Score 79; DB 2; Length 51;
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 MTEQQWNFAGIEAAA 15
 DB 1 MTEQQWNFAGIEAAA 15
 |||||
 RESULT 12
 AAW64334
 ID AAW64334 standard; protein; 51 AA.
 XX
 AC AAW64334;
 XX
 XX 09-NOV-1998 (first entry)
 DT
 DE Mycobacterium tuberculosis antigen ESAT-6.
 XX
 KW Tuberculosis; infection; diagnosis; antigen; ESAT-6.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN WO9816645-A2.

XX 23-APR-1998.
 PD
 XX 07-OCT-1997; 97WO-US018214.
 PF
 XX 11-OCT-1996; 96US-00729622.
 PR
 XX 13-MAR-1997; 97US-00818111.
 PR
 XX (CORI-) CORIXA CORP.
 PA
 XX Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton R;
 PI Vedvick TS, Twardzik DR, Lodes MJ;
 XX
 XX WPI; 1998-251292/22.
 DR
 DR N-PSDB; AAV44393.
 XX
 XX New isolated Mycobacterium tuberculosis polypeptides and DNA - used to
 PT develop products for the detection of M. tuberculosis infection and
 PT diagnosis of tuberculosis.
 XX
 PS Disclosure; Page 130; 250pp; English.
 XX
 CC This polypeptide comprises an antigenic portion of Mycobacterium
 CC tuberculosis antigen ESAT-16. The invention relates to compositions and
 CC methods for diagnosing tuberculosis. It provides polypeptides (see
 CC AAW64291-W64379) comprising an antigenic portion of a soluble M.
 CC tuberculosis antigen, or an immunogenic portion of an M. tuberculosis
 CC antigen, as well as fusion proteins between these polypeptides and known
 CC antigens such as ESAT-6. Also claimed are methods and diagnostic kits for
 CC detecting M. tuberculosis infection in a patient using these
 CC polypeptides, antibodies, or oligonucleotide probes and primers
 XX
 SQ Sequence 51 AA;
 Query Match 100.0%; Score 79; DB 2; Length 51;
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 MTEQQWNFAGIEAAA 15
 DB 1 MTEQQWNFAGIEAAA 15
 |||||
 RESULT 13
 AAW81701
 ID AAW81701 standard; protein; 51 AA.
 XX
 AC AAW81701;
 XX
 DT 27-JAN-1999 (first entry)
 DT
 DE M. tuberculosis immunogenic polypeptide ESAT-6.
 XX
 KW Tuberculosis; immunogenic; soluble; antigen; protective immunity; TB;
 KW vaccine; pharmaceutical; infection; diagnosis.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN WO9816646-A2.
 XX
 PD 23-APR-1998.
 PD
 XX 07-OCT-1997; 97WO-US018293.
 PF
 XX 11-OCT-1996; 96US-00730510.
 PR
 XX 13-MAR-1997; 97US-00818112.
 PR
 XX (CORI-) CORIXA CORP.
 PA
 XX Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton R;
 PI Vedvick TS, Twardzik DR, Lodes MJ;
 XX
 XX WPI; 1998-261042/23.

DR N-PSDB; AAV64501.
XX Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - used to
PT develop products for the detection of M. tuberculosis infection and for
PT diagnosis, treatment and prevention of tuberculosis.
XX
XX Disclosure; Page 126; 230pp; English.
XX
XX This sequence represents an immunogenic portion of a soluble
CC Mycobacterium tuberculosis (MT) antigen which can be used in a method for
CC Mycobacterium tuberculosis (MT) antigen which can be used in a method for
CC be formulated into vaccines and/or pharmaceutical compositions for
CC immunising against M. tuberculosis infection or may be used for the
CC diagnosis of tuberculosis
XX
XX Sequence 51 AA;
SQ
Query Match 100.0%; Score 79; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTEQQWNFAGIEAAA 15
DB 1 MTEQQWNFAGIEAAA 15
RESULT 14
AAV38988
ID AAV38988 standard; protein; 51 AA.
XX
XX AAV38988;
AC
DT 05-NOV-1999 (first entry)
XX
XX M. tuberculosis recombinant antigen protein ESAT-6.
DE Antigen; diagnosis; detection; infection; antibody; immunisation;
XX vaccine; immunity.
KW
KW Mycobacterium tuberculosis.
OS
XX WO9942118-A2.
XX
XX 26-AUG-1999.
XX
XX 17-FEB-1999; 99WO-US003265.
XX
XX 18-FEB-1998; 98US-00024753.
PR 05-MAY-1998; 98US-00072596.
XX
XX (CORI-) CORIXA CORP.
XX
XX Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton R;
PI Vedvick TS, Twardzik DR, Lodes MJ, Hendrickson RC;
XX WPI; 1999-527416/44.
DR N-PSDB; AAZ19091.
XX
XX New polypeptide comprising antigenic portions of M. tuberculosis.
PT
XX Claim 51; Page 165; 323pp; English.
PS
XX This invention describes novel recombinant antigens and their encoding
CC nucleic acids derived from Mycobacterium tuberculosis. The novel
CC polypeptides are useful for detecting M. tuberculosis infection in a
CC biological sample by detecting antibodies which bind with the
CC polypeptides, and are useful as vaccines for immunizing against M.
CC tuberculosis infection. The new detection methods are needed as current
CC vaccination strategies do not provide 100% immunity
XX
XX Sequence 51 AA;
SQ
Query Match 100.0%; Score 79; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTEQQWNFAGIEAAA 15
DB 1 MTEQQWNFAGIEAAA 15
RESULT 16
AAU01897
ID AAU01897 standard; protein; 51 AA.
XX

Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTEQQWNFAGIEAAA 15
DB 1 MTEQQWNFAGIEAAA 15
RESULT 15
AAV39131
ID AAV39131 standard; protein; 51 AA.
XX
XX AAV39131;
AC
DT 05-NOV-1999 (first entry)
XX
XX M. tuberculosis ESAT-6 amino acid sequence.
DE
XX Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen;
KW immunotherapy; diagnosis; immunisation; vaccine; infection;
KW immune response; skin test.
XX
XX Mycobacterium tuberculosis.
OS
XX WO9942076-A2.
XX
XX 26-AUG-1999.
XX
XX 17-FEB-1999; 99WO-US003268.
XX
XX 18-FEB-1998; 98US-00025197.
PR 05-MAY-1998; 98US-00072967.
XX
XX (CORI-) CORIXA CORP.
XX
XX Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton R;
PI Vedvick TS, Twardzik DR, Lodes MJ, Hendrickson RC;
XX WPI; 1999-527409/44.
DR N-PSDB; AAZ19303.
XX
XX New antigens from Mycobacterium tuberculosis useful in diagnostic skin
PT tests and protective or therapeutic vaccines or compositions.
PT
XX Disclosure; Page 120; 299pp; English.
PS
XX The present invention describes polypeptides comprising an immunogenic
CC part of a Mycobacterium tuberculosis antigen (Ag). Also described are
CC vaccines and fusion protein containing M. tuberculosis Ag's. M.
CC tuberculosis Ag's, DNAs encoding them, derived fusion proteins and other
CC polypeptides fragments, can be used in pharmaceutical compositions or
CC vaccines to generate a protective or therapeutic immune response to M.
CC tuberculosis and as reagents in skin tests for diagnosis of tuberculosis.
CC Ag can induce proliferation of, or cytokine secretion by, T, B or natural
CC killer cells and/or macrophages in tuberculosis-immune subjects. AAZ19249
CC to AAZ19460 and AAV39083 to AAV39225 are used in the exemplification of
CC the present invention
XX
XX Sequence 51 AA;
SQ
Query Match 100.0%; Score 79; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTEQQWNFAGIEAAA 15
DB 1 MTEQQWNFAGIEAAA 15
RESULT 16
AAU01897
ID AAU01897 standard; protein; 51 AA.
XX

```

AC AAU01897;
XX
XX 29-AUG-2001 (first entry)
XX
XX Mycobacterium tuberculosis partial antigen ESAT-6.
DE
XX ESAT-6; antigen; vaccine; tuberculosis; AIDS;
XX acquired immunodeficiency disease.
KW
XX Mycobacterium tuberculosis.
OS
XX WO200124820-A1.
XX
XX 12-APR-2001.
XX
XX 10-OCT-2000; 2000WO-US028095.
XX
XX 07-OCT-1999; 99US-0158338P.
XX
XX 07-OCT-1999; 99US-0158425P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Skeiky Y, Reed S, Houghton RL, Mcneill PD, Dillon DC, Lodes ML;
PI
XX WPI; 2001-290576/30.
XX
XX N-PSDB; AAS03787.
XX
XX Vaccinating against Mycobacteria infections in mammals using fusion
PT proteins comprising combinations of heterologous antigens.
PT
XX
XX Disclosure; Page 164; 168pp; English.
XX
XX The sequence represents Mycobacterium tuberculosis ESAT-6 antigen.
XX Compositions comprising at least 2 heterologous antigens, as a fusion
CC protein, and vectors expressing the fusion proteins are used as vaccines
CC to prophylactically immunise mammals (especially humans) against
CC infection by Mycobacteria. The compositions contain at least 2
CC heterologous antigens that increase the serological sensitivity of
CC individuals infected with tuberculosis, a disease frequently affecting
CC patients with acquired immunodeficiency disease, AIDS
XX
XX Sequence 51 AA;
XX
XX Query Match 100.0%; Score 79; DB 4; Length 51;
XX Best Local Similarity 100.0%; Pred. No. 1.1e-05;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MTEQQWNFAGIEAAA 15
XX |||||
XX Db 1 MTEQQWNFAGIEAAA 15
XX
XX RESULT 17
XX AAE29716
XX ID AAE29716 standard; protein; 51 AA.
XX
XX AAE29716;
XX
XX 27-JAN-2003 (first entry)
XX
XX Mycobacterium tuberculosis ESAT-6 antigenic protein.
DE
XX Vaccine; immunity; diagnostic agent; gene therapy; ESAT-6 antigen.
XX
XX Mycobacterium tuberculosis.
XX
XX WO200272792-A2.
XX
XX 19-SEP-2002.
XX
XX 13-MAR-2002; 2002WO-US008223.
XX
XX 13-MAR-2001; 2001US-0275837P.
XX
XX
XX (CORI-) CORIXA CORP.
XX
XX Skeiky Y, Brannon M, Guderian J;
XX
XX WPI; 2002-759844/82.
XX
XX N-PSDB; AAD29716.
XX
XX New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF,
PT M15 or 6H polynucleotide, useful as vaccine to elicit protective immunity
PT against pathogenic microorganisms e.g. Leishmania and Mycobacterium
PT tuberculosis.
XX
XX Disclosure; Page 106; 155pp; English.
XX
XX The invention relates to a recombinant nucleic acid molecule encoding a
XX fusion polypeptide. The recombinant nucleic acid comprises a heterologous
CC polynucleotide sequence encoding an antigen or an antigenic fragment from
CC Mycobacterium sp. and a Leishmania polynucleotide sequence encoding a
CC polypeptide or its fragment. The Leishmania polynucleotide is selected
CC from TSA, LeIF, M15, and 6H polynucleotides. Sequences of the invention
CC are used in methods for eliciting immune response in mammals. They are
CC useful as vaccines to elicit protective immunity against pathogenic
CC microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion
CC polypeptides are used for enhancing the expression of polynucleotides, as
CC in vivo diagnostic agents and for raising antibodies in a non-human
CC animal. The invention is used in gene therapy. The present sequence is M.
CC tuberculosis ESAT-6 antigenic protein
XX
XX Sequence 51 AA;
XX
XX Query Match 100.0%; Score 79; DB 5; Length 51;
XX Best Local Similarity 100.0%; Pred. No. 1.1e-05;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MTEQQWNFAGIEAAA 15
XX |||||
XX Db 1 MTEQQWNFAGIEAAA 15
XX
XX RESULT 18
XX AAE17580
XX ID AAE17580 standard; protein; 51 AA.
XX
XX AAE17580;
XX
XX 22-APR-2002 (first entry)
XX
XX Mycobacterium species ESAT-6 protein.
XX
XX Fusion protein; antigen; serological sensitivity; immune response;
XX tuberculosis; infection; vaccine; ESAT-6 protein.
XX
XX Mycobacterium sp.
XX
XX WO200198460-A2.
XX
XX 27-DEC-2001.
XX
XX 20-JUN-2001; 2001WO-US019959.
XX
XX 20-JUN-2000; 2000US-00597796.
XX
XX 01-FEB-2001; 2001US-0265737P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Skeiky Y, Reed S, Alderson M;
XX
XX WPI; 2002-147798/19.
XX
XX N-PSDB; AAD28351.
XX
XX Composition comprising Mtb39 antigen and Mtb32A antigen from
PT Mycobacterium species, useful for eliciting immune response in a subject.
PT

```

XX Claim 9; Page 122; 136pp; English.

XX PS

CC The present invention relates to fusion proteins containing at least two

CC Mycobacterium species antigens, nucleotides encoding them and

CC compositions comprising such fusion proteins. The present invention

CC particularly relates to nucleic acids encoding fusion proteins that

CC include two or more individual M. tuberculosis antigens which increase

CC the serological sensitivity of sera from individuals infected with

CC tuberculosis and methods for their use in diagnosis, prevention and

CC treatment of tuberculosis infection. Sequences of the invention are

CC useful for eliciting an immune response in a mammal, e.g., human,

CC immunised with BCG. They are useful in the diagnosis, treatment and

CC prevention of Mycobacterium infection. The fusion proteins and the

CC polynucleotides are useful as diagnostic tools in patients infected with

CC Mycobacterium, in vitro and in vivo assays for detecting humoral

CC antibodies or cell-mediated immunity against M. tuberculosis, for the

CC diagnosis of an infection or monitoring of disease progression, as

CC immunogens to generate or elicit a protective immune response in a

CC patient and for raising anti-M. tuberculosis antibodies in a non-human

CC animal. Sequences of the invention are also used as vaccines. MT832A

CC fusion proteins of the invention are useful as in vivo diagnostic agents

CC for intradermal skin test. The present sequence is Mycobacterium species

CC ESAT-6 protein

XX Sequence 51 AA;

Query Match 100.0%; Score 79; DB 5; Length 51;
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQQWNFAGIEAAA 15
 |||||

Db 1 MTEQQWNFAGIEAAA 15

RESULT 19

AAW11494

ID AAW11494 standard; protein; 95 AA.

XX

AC AAW11494;

XX

DT 27-MAR-1997 (first entry)

XX

DE ESAT6.

XX

XX ESAT6; Mycobacterium tuberculosis; 6kDa antigen; tuberculosis complex;

KW HYB76-8 reactive antigen; interferon-gamma; memory T-lymphocyte; vaccine;

KW M. africanum; M. bovis; delayed-type hypersensitivity reaction; therapy.

XX

OS Mycobacterium tuberculosis.

XX

PN WO9501441-A1.

XX

PD 12-JAN-1995.

XX

PF 01-JUL-1994; 94WO-DK000273.

XX

PR 02-JUL-1993; 93DK-00000798.

XX

PA (STAT-) STATENS SERUMINSTITUT.

XX

PI Andersen P, Andersen AB, Haslov K, Sorensen A;

XX

DR WPI; 1995-061005/08.

DR N-PSDB; AAT51422.

XX

PT Vaccine for tuberculosis induces interferon-gamma release from T-

PT lymphocytes - comprises an antigen released from mycobacteria, for

PT immunisation of humans.

XX

PS Claim 5; Page 61-63; 101pp; English.

XX

CC This sequence represents the Mycobacterium tuberculosis ESAT6. ESAT6 is

CC also known as the 6kDa antigen, or the HYB76-8 reactive antigen. ESAT6 is

CC released from metabolising bacteria, and can be isolated from short term

CC filtrates grown as shaken cultures for 7 days. ESAT6 also induces a

CC release of interferon-gamma from reactivated memory T-lymphocytes. This

CC protein sequence is included in the vaccine of the invention. The vaccine

CC is for immunising an animal (including humans) against tuberculosis

CC caused by a Mycobacteria belonging to the tuberculosis complex. The

CC Mycobacteria of the tuberculosis complex are M. tuberculosis, M.

CC africanum, and M. bovis. The vaccine can evoke a protective immune

CC response against tuberculosis or a delayed-type hypersensitivity

CC reaction. The protein can also be included in a composition for

CC diagnosing tuberculosis. The composition is injected intradermally, and a

CC skin reaction is an indicator of tuberculosis

XX Sequence 95 AA;

Query Match 100.0%; Score 79; DB 2; Length 95;
 Best Local Similarity 100.0%; Pred. No. 2.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQQWNFAGIEAAA 15
 |||||

Db 1 MTEQQWNFAGIEAAA 15

RESULT 20

AAZ9788

ID AAZ9788 standard; protein; 95 AA.

XX

AC AAZ9788;

XX

DT 08-NOV-1999 (first entry)

XX

DE Mycobacterial tuberculosis ESAT-6 protein.

XX

KW Mycobacterial; ESAT-6; 6 kDa antigen; tuberculosis; infection;

KW immunological response; diagnosis; vaccine.

XX

OS Mycobacterium tuberculosis.

XX

PN US9595077-A.

XX

PD 21-SEP-1999.

XX

PF 05-JUN-1995; 95US-00465640.

XX

PR 20-SEP-1993; 93US-00123182.

PR 01-JUL-1994; 94WO-DK000273.

XX

PA (STAT-) STATENS SERUMINSTITUT.

XX

PI Andersen P, Haslov K, Sorensen AL, Andersen AB;

XX

DR WPI; 1999-539545/45.

DR N-PSDB; AAZ08877.

XX

PT Polypeptide secreted from Mycobacterium is useful as a vaccine against

PT tuberculosis.

XX

PS Claim 24; Fig 10C; 39pp; English.

XX

CC The present invention describes a purified or non-naturally occurring

CC polypeptide (I) released from a metabolising mycobacteria comprising an

CC ESAT6, also called the 6 kDa antigen. The present sequence represents

CC Mycobacterium tuberculosis ESAT-6 protein. Also described is a purified

CC or non-naturally occurring polypeptide (II) with the ability to elicit a

CC delayed type hypersensitivity reaction which comprises a T cell epitope

CC of (I). (II) can be used with a carrier or vehicle in a composition for

CC diagnosing tuberculosis caused by mycobacteria belonging to the

CC tuberculosis complex, i.e. Mycobacterium tuberculosis, M. bovis and M.

CC africanum. The composition can be used to detect microbial antibodies or

CC components of mycobacteria in samples or in animals through the use of

CC immunoassays. (II) can be used as a vaccine for immunising an animal,
 CC including humans against tuberculosis caused by mycobacteria of the
 CC tuberculosis-complex. (II) induce a release of IFN-gamma from reactivated
 CC T-lymphocytes evoking a protective immune response. Vaccine containing
 CC (II) has the same protective potency as the live BCG vaccine against
 CC tuberculosis

XX
 XX SQ Sequence 95 AA;

Query Match 100.0%; Score 79; DB 2; Length 95;
 Best Local Similarity 100.0%; Pred. No. 2.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQQWNFAGIEAAA 15
 |||||
 Db 1 MTEQQWNFAGIEAAA 15

RESULT 21

AAV29890
 ID AAV29890 standard; protein; 95 AA.

XX AC AAV29890;

XX DT 18-NOV-1999 (first entry)

XX DE Mycobacterium tuberculosis ESAT-6 protein sequence.

XX KW Mycobacterial; lactic acid bacterium; diagnosis; skin test; vaccine;
 KW delayed type hypersensitivity; DTH; ESAT-6 homodimer; tuberculosis;
 KW interferon-gamma release.

XX OS Mycobacterium tuberculosis.

XX PN WO9945119-A2.

XX PD 10-SEP-1999.

XX PF 05-MAR-1999; 99WO-DK000109.

XX PR 06-MAR-1998; 98DK-00000306.

XX PR 06-MAR-1998; 98US-0077105P.

XX PA (STAT-) STATENS SERUM INST.

XX PI Jensen CL, Folkersen J;

XX WPI; 1999-551043/46.

XX DR N-PSDB; AA221132.

XX PT New mycobacterial polypeptide produced in lactic acid bacteria, useful in
 XX tuberculosis diagnosis and vaccines.

XX PS Disclosure; Page 75-76; 76pp; English.

XX CC The present invention describes a bioactive polypeptide (or
 CC immunologically equivalent analogue) produced in lactic acid bacteria
 CC which reacts with lymphoid cells primed with Mycobacterium tuberculosis
 CC complex mycobacteria (M. tuberculosis, M. africanum or M. bovis). The
 CC polypeptide and ESAT-6 polypeptides are useful in compositions for
 CC diagnosis of and vaccination against tuberculosis caused by M.
 CC tuberculosis complex mycobacteria. The ESAT-6 polypeptide can be used to
 CC diagnose ongoing/previous sensitisation with these bacteria by detecting
 CC cytokine release when contacting blood samples with the polypeptide. The
 CC bioactive polypeptide may be used in diagnostic compositions and
 CC vaccines for mycobacteria other than of the M. tuberculosis complex, e.g.
 CC M. avium which infects poultry and occasionally humans, M. leprae; they
 CC are especially useful when they do not react with lymphoid cells
 CC previously primed with M. tuberculosis complex mycobacteria, and so do
 CC not give rise to a diagnostic reaction in individuals infected with these
 CC bacteria. The polypeptides may also be used in in vitro diagnostic tests
 CC e.g. stimulation of interferon-gamma release from lymphocytes. The
 CC polypeptide has similar or higher bioactivity as currently used

CC tuberculin reagent in the standard delayed type hypersensitivity (DTH)
 CC skin test for tuberculosis, but may have greater specificity, being
 CC better able to discriminate between lymphoid cells primed from
 CC tuberculosis and from previous vaccination. The present sequence
 CC represents M. tuberculosis ESAT-6 used in the exemplification of the
 CC present invention

XX SQ Sequence 95 AA;

Query Match 100.0%; Score 79; DB 2; Length 95;
 Best Local Similarity 100.0%; Pred. No. 2.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQQWNFAGIEAAA 15
 |||||
 Db 1 MTEQQWNFAGIEAAA 15

RESULT 22

AAB35219

ID AAB35219 standard; protein; 95 AA.

XX AC AAB35219;

XX DT 24-APR-2001 (first entry)

XX DE M tuberculosis Rv3875 protein.

XX KW Tuberculosis; TB; vaccine; esat-6 gene family; Rv0287; Rv1036c; Rv1037c;
 KW Rv2346c; Rv2348c; Rv2653c; Rv2854c; Rv3020c; Rv3444c; Rv3445c; Rv3890c;
 KW Rv3891c; Rv3904c; Rv3905c.

XX OS Mycobacterium tuberculosis.

XX PN WO200104151-A2.

XX PD 19-JAN-2001.

XX PF 13-JUL-2000; 2000WO-DK000398.

XX PR 13-JUL-1999; 99DK-00001020.

XX PR 15-JUL-1999; 99US-0144011P.

XX PA (STAT-) STATENS SERUM INST.

XX PI Andersen P, Skjot R;

XX WPI; 2001-091923/10.

XX PT New polypeptide encoded by a member of the esat-6 gene family for
 XX immunizing against and diagnosis of tuberculosis.

XX PS Example 2; Page 65; 80pp; English.

XX CC The present invention provides the protein and coding sequences for
 CC members of the esat-6 gene family from Mycobacterium tuberculosis. These
 CC proteins include Rv0287, Rv1037c, Rv2346c, Rv2348c, Rv2653c,
 CC Rv2654c, Rv3020c, Rv3444c, Rv3445c, Rv3890c, Rv3891c, Rv3904c and
 CC Rv3905c. These can be used to produce vaccines against, and in the
 CC diagnosis of, tuberculosis (TB) infection. The present sequence is one of
 CC the proteins of the invention

XX SQ Sequence 95 AA;

Query Match 100.0%; Score 79; DB 4; Length 95;
 Best Local Similarity 100.0%; Pred. No. 2.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQQWNFAGIEAAA 15
 |||||
 Db 1 MTEQQWNFAGIEAAA 15

RESULT 23
 ABC30968
 ID ABC30968 standard; protein; 95 AA.
 AC ABC30968;
 XX
 DT 21-OCT-2002 (first entry)
 DE Mycobacterium tuberculosis ESAT-6.
 XX
 KW ESAT-6; mycobacterial infection; tuberculosis; pulmonary tuberculosis;
 KW tuberculosis lymphadenitis; extrapulmonary tuberculosis.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN WO200254072-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 08-JAN-2002; 2002WO-GB000055.
 XX
 PR 08-JAN-2001; 2001GB-00000432.
 XX
 PR 08-JAN-2001; 2001US-0259868P.
 XX
 PA (ISIS-) ISIS INNOVATION LTD.
 XX
 PI Lalvani A;
 XX
 DR WPI; 2002-583633/62.
 XX
 DT Determining the progress of a mycobacterial infection, by direct ex vivo
 PT quantitation of ESAT-6-specific T cells.
 XX
 PS Disclosure; Page 42; 53pp; English.
 XX
 CC The invention describes a method of determining the efficacy of treatment
 CC for mycobacterial infection (such as pulmonary tuberculosis, tuberculosis
 CC lymphadenitis and extrapulmonary tuberculosis). The method involves
 CC determining the level of T cells specific for a mycobacterial antigen
 CC that has decreased after the treatment and therefore determining the
 CC efficacy of treatment. The method is useful for determining the
 CC infection is Mycobacterium tuberculosis or M.bovis infection. The
 CC invention also describes a method useful for determining the presence of
 CC a latent infection in a sample from the individual for the presence of T
 CC cells specific for a mycobacterial antigen. Also described in a method
 CC for determining the effect of an intervention on a mycobacterial
 CC infection in an individual an method for treating an individual
 CC infected by a mycobacterium. This is the amino acid sequence of
 CC Mycobacterium tuberculosis ESAT-6, the mycobacterial antigen measured in
 CC the invention
 XX
 SQ Sequence 95 AA;
 XX
 Query Match 100.0%; Score 79; DB 5; Length 95;
 Best Local Similarity 100.0%; Pred. No. 2.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 MTEQQWNFAGIEAAA 15
 DB 1 MTEQQWNFAGIEAAA 15
 XX
 RESULT 24
 AAM50740
 ID AAM50740 standard; protein; 95 AA.
 AC AAM50740;
 XX
 DT 18-APR-2002 (first entry)
 DE Mycobacterium tuberculosis immunodominant Mtb protein ESAT6.
 XX

KW Mtb; ESAT6; immunogen; mycobacteria; immunisation; vaccine.
 OS Mycobacterium tuberculosis.
 XX
 PN WO200204018-A2.
 XX
 PD 17-JAN-2002.
 XX
 PF 10-JUL-2001; 2001WO-US021717.
 XX
 PR 10-JUL-2000; 2000US-0217646P.
 XX
 PA (COLS) UNIV COLORADO STATE RES FOUND.
 XX
 PI Orme IM, Belisle JT;
 XX
 DR WPI; 2002-164602/21.
 XX
 PT Vaccine for boosting immunity to mycobacteria when administered in mid-
 PT life in a subject who has been vaccinated in childhood with bacillus
 PT Calmette-Guerrin, has purified proteins from mycobacterium tuberculosis.
 XX
 PS Claim 8; Page 18; 61pp; English.
 XX
 CC The present sequence is that of the Mycobacterium tuberculosis (Mtb)
 CC strain H37Rv gene Rv3875 product, designated ESAT6. This is one of 31
 CC immunodominant secreted or cytosolic Mtb proteins of strain H37Rv (see
 CC AAM50729-59) discovered through the use of 2-dimensional liquid phase
 CC electrophoresis coupled with an in vitro interferon-gamma assay and
 CC liquid chromatography-mass spectrometry. The immunogens stimulate a
 CC strong interferon-gamma response from T cells of M. tuberculosis infected
 CC mice. The invention provides vaccine compositions for boosting immunity
 CC to mycobacteria when administered in mid-life to a subject who has been
 CC vaccinated neonatally or in early childhood with BCG and in whom
 CC protective immunity has waned. The vaccine compositions comprise 1 or
 CC more of the 31 purified immunogenic proteins. When used as immunogens,
 CC the secreted Mtb proteins lack the secreted signal sequence. A preferred
 CC protein is Ag85A (see AAM50759), the secreted product of the Rv3084v gene
 XX
 SQ Sequence 95 AA;
 XX
 Query Match 100.0%; Score 79; DB 5; Length 95;
 Best Local Similarity 100.0%; Pred. No. 2.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 MTEQQWNFAGIEAAA 15
 DB 1 MTEQQWNFAGIEAAA 15
 XX
 RESULT 25
 ADE28550
 ID ADE28550 standard; protein; 95 AA.
 XX
 AC ADE28550;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Mycobacterium tuberculosis ESAT-6 protein.
 XX
 KW CD1 fusion protein; endosomal targeting; antibacterial; virucide;
 KW cytostatic; antidiabetic; antiinflammatory; dermatological;
 KW immunosuppressive; neuroprotective; immune response; microbial;
 KW viral infection; autoimmune disorder; diabetes; lupus;
 KW multiple sclerosis; cancer; gene therapy; vaccine; ESAT-6.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN WO2003066820-A2.
 XX
 PD 14-AUG-2003.
 XX
 PR 05-FEB-2003; 2003WO-US003550.
 PF

XX 05-FEB-2002; 2002US-0355432P.
 XX (REGC) UNIV CALIFORNIA.
 XX Modlin RL;
 XX
 XX WPI; 2003-748121/70.
 XX N-PSDB; ADE28549.
 XX
 XX New chimeric nucleic acid molecule encoding a CD1 fusion protein, useful
 XX for inducing an immune response against antigens associated with, e.g.
 XX microbial or viral infections, autoimmune disorders or cancer.
 XX
 XX Disclosure; Fig 9F; 114pp; English.
 XX
 XX The invention relates to a novel chimeric nucleic acid molecule
 XX consisting of a nucleotide sequence encoding a CD1 fusion protein
 XX comprising a CD1 endosomal targeting sequence or its fragment and an
 XX antigen of interest. The polynucleotide of the invention demonstrates
 XX antibacterial, virucide, cytostatic, antidiabetic, antiinflammatory,
 XX dermatological, immunosuppressive and neuroprotective activities whilst
 XX the composition and methods may be useful for inducing an immune response
 XX against antigens of interest which are associated with microbial or viral
 XX infections, autoimmune disorders including diabetes, lupus and multiple
 XX sclerosis and antigens associated with cancers. Furthermore, the
 XX composition may be utilised in gene therapy and vaccine development. The
 XX current sequence is that of the Mycobacterium tuberculosis ESAT-6 protein
 XX of the invention.
 XX
 XX Sequence 95 AA;
 XX
 XX Query Match 100.0%; Score 79; DB 7; Length 95;
 XX Best Local Similarity 100.0%; Pred. No. 2.1e-05;
 XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 MTEQQWNFAGIEAAA 15
 XX |||||
 XX Db 1 MTEQQWNFAGIEAAA 15
 XX |||||
 XX
 XX RESULT 26
 XX ADI33376
 XX ID ADI33376 standard; peptide; 95 AA.
 XX
 XX AC ADI33376;
 XX
 XX DT 22-APR-2004 (first entry)
 XX
 XX DE Mycobacterium tuberculosis ESAT-6 protein.
 XX
 XX KW pathogen; vaccine; cellular response; HPV; HIV; SIV; HCV; chlamydia; HBV;
 XX EBV; CMV; VZV; HSV; Legionella; Leishmaniasis; influenza;
 XX foot and mouth virus; Toxoplasma; Brucella; Cryptococcus; Candida;
 XX Aspergillus; Mycobacterium; T cell; ESAT-6; CFP10; virucide; protoazide;
 XX antibacterial; fungicide; epitope.
 XX
 XX OS Mycobacterium tuberculosis.
 XX
 XX PN WO2004005925-A2.
 XX
 XX PD 15-JAN-2004.
 XX
 XX PF 07-JUL-2003; 2003WO-GB002936.
 XX
 XX PR 05-JUL-2002; 2002GB-00015710.
 XX
 XX PA (ISIS-) ISIS INNOVATION LTD.
 XX
 XX PI Lalvani A, Ewer K;
 XX WPI; 2004-143006/14.
 XX
 XX PT New antibody single-chain variable region fragments capable of targeting

PT Diagnosing in an individual recent exposure to an agent, useful in
 PT treating a disease caused by a pathogen, by determining in vitro or in
 PT vivo whether the T cells of recognize a protein having at least 30 amino
 PT acids.
 XX
 XX Disclosure; Page 21-22; 48pp; English.
 XX
 XX The invention relates to a novel method for diagnosing in an individual
 XX recent exposure to an agent which is a pathogen, vaccine or any other
 XX moiety, which induces a cellular response. The pathogen can include: HPV,
 XX HIV, SIV, HCV, chlamydia species, HBV, EBV, CMV, VZV, HSV, Legionella, S.
 XX typhi, P. falciparum, Leishmaniasis, M. leprae, influenza virus, foot and
 XX mouth virus, a Toxoplasma species, a Brucella species, a Cryptococcus
 XX species, a Candida species, an Aspergillus species, or Mycobacterium
 XX tuberculosis. The invention also provides a vaccine against any of the
 XX above pathogens. The method comprises determining in vitro or in vivo
 XX whether the T cells of the individual recognize a protein from the agent
 XX having a length of at least 30 amino acids. The invention also comprises
 XX a protein or epitope peptide which is from ESAT-6 or CFP10. The vaccines
 XX of the invention have: virucide, protoazide, antibacterial, and fungicide
 XX activity. The method is useful in diagnosing in an individual recent
 XX exposure to an agent which is a pathogen, vaccine or any other moiety
 XX which induces a cellular response. The protein described above, the
 XX product which prevents or treats a condition caused by a pathogen or the
 XX antigen or its analogue is useful in the manufacturing of a medicament
 XX for diagnosing and treating an individual recently exposed to a pathogen.
 XX This sequence represents the Mycobacterium tuberculosis ESAT-6 protein
 XX used in the invention.
 XX
 XX Sequence 95 AA;
 XX

Query Match 100.0%; Score 79; DB 8; Length 95;
 Best Local Similarity 100.0%; Pred. No. 2.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTEQQWNFAGIEAAA 15
 |||||
 Db 1 MTEQQWNFAGIEAAA 15
 |||||
 RESULT 27
 ADN36323
 ID ADN36323 standard; protein; 95 AA.
 XX
 XX AC ADN36323;
 XX
 XX DT 15-JUL-2004 (first entry)
 XX
 XX DE Mycobacterium tuberculosis antigen ESAT-6.
 XX
 XX KW antibacterial; antiparasitic; virucide; immunosuppressive; cytostatic;
 XX gene therapy; vaccine; single-chain variable region fragment; scPv;
 XX antigen-presenting cell; dendritic cell; infectious disease;
 XX autoimmune disease; cancer; CD1lc.
 XX
 XX OS Mycobacterium tuberculosis.
 XX
 XX PN WO2004035619-A1.
 XX
 XX PD 29-APR-2004.
 XX
 XX PF 20-OCT-2003; 2003WO-AU001392.
 XX
 XX PR 18-OCT-2002; 2002US-0420232P.
 XX
 XX PA (CENT-) CENTENARY INST CANCER MEDICINE & CELL BI.
 XX
 XX PI Britton W, Demangel C;
 XX WPI; 2004-365152/34.
 XX N-PSDB; ADN36322.
 XX
 XX PT New antibody single-chain variable region fragments capable of targeting

PT antigen-presenting cells, useful for preventing or treating diseases,
 PT e.g. infectious diseases, autoimmune diseases or cancer.

XX Claim 20; SEQ ID NO 18; 82pp; English.

CC The invention relates to a single-chain variable region fragment (scFv)
 CC comprising a heavy chain variable region (VH) operably linked to a light
 CC chain variable region (VL), where the scFv is capable of specifically
 CC binding to a molecule on the surface of an antigen-presenting cell (APC).
 CC The composition and methods are useful for targeting antigens to antigen-
 CC presenting cells, such as dendritic cells. These may be used for
 CC preventing and/or treating diseases, such as infectious diseases,
 CC autoimmune diseases or cancer. This sequence corresponds to the
 CC Mycobacterium tuberculosis antigen ESAT-6. This sequence can be fused to
 CC a scFv protein sequence to form a fusion protein.

XX Sequence 95 AA;

Query Match 100.0%; Score 79; DB 8; Length 95;
 Best Local Similarity 100.0%; Pred. No. 2.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQQWNFAGIEAAA 15
 |||||
 Db 1 MTEQQWNFAGIEAAA 15

RESULT 28

AEB45084
 ID AEB45084 standard; protein; 95 AA.

XX AEB45084;

XX 06-OCT-2005 (first entry)

XX M. tuberculosis early secretory antigenic target 6, ESAT6.

XX immunogenicity; viral infection; infection; bacterial infection; cancer;
 KW neoplasm; autoimmune disease; immune disorder; inflammation; allergy;
 KW Antibacterial; Virucide; Fungicide; Anti-HIV; Hepatotropic;
 KW Antiparasitic; Cytostatic; immunosuppressive; antiarthritic;
 KW antirheumatic; neuroprotective; antidiabetic; gastrointestinal-Gen.;
 KW antiinflammatory; antiulcer; antipsoriatic; dermatological;
 KW antiasthmatic; antiallergic; Immunomodulator.

XX Mycobacterium tuberculosis.

XX WO2005070959-A2.

XX 04-AUG-2005.

XX 24-JAN-2005; 2005WO-US002251.

XX 23-JAN-2004; 2004US-0538713P.

XX 06-OCT-2004; 2004US-0616855P.

XX (VIEW-) VIEWAX CORP.

XX Mahairas GG;

XX WPI; 2005-542270/55.

XX Immune response altering agent useful for treating autoimmune diseases,
 PT comprises first domain having T/B cell epitopes or Toll-like receptor-
 PT binding proteins, and second domain having heterologous target molecule.

XX Claim 59; SEQ ID NO 214; 130pp; English.

XX The invention relates to an immune response altering agent (I) which
 CC comprises a first domain having one or more components chosen from T cell
 CC epitopes, B cell epitopes, and Toll-like receptor (TLR)-binding proteins
 CC or its TLR-binding domains, and a second domain having heterologous
 CC target molecule against which an immune response is desired. (I) is

CC useful for altering or inducing an immune response to a target. (I) is
 CC also useful for treating viral infections (e.g., HIV and hepatitis C
 CC virus), bacterial infections (e.g., Staphylococcus and Pseudomonas),
 CC parasites (e.g., Leishmania), fungal infections (e.g., Candida), cancer
 CC (e.g., non-Hodgkin's lymphoma, Hodgkin's disease and leukemia), and
 CC autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,
 CC insulin dependent diabetes, Addison's disease, celiac disease,
 CC inflammatory bowel disease, ulcerative colitis, Crohn's disease, systemic
 CC lupus erythematosus, psoriasis, Sjogren's syndrome, etc. (I) is useful
 CC for treating inflammatory and hyperproliferative skin diseases, and
 CC allergic reactions such as asthma, bronchitis, allergic rhinitis etc. (I)
 CC alters an immune response generated against the heterologous target
 CC molecule. (I) can be applied to wide range of species such as humans, non
 CC -human primates, horses, etc. The present sequence represents the amino
 CC acid sequence of the M. tuberculosis early secretory antigenic target 6,
 CC ESAT6.

XX Sequence 95 AA;

Query Match 100.0%; Score 79; DB 9; Length 95;
 Best Local Similarity 100.0%; Pred. No. 2.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQQWNFAGIEAAA 15
 |||||
 Db 1 MTEQQWNFAGIEAAA 15

RESULT 29

ADE28541

ID ADE28541 standard; protein; 142 AA.

XX ADE28541;

XX 29-JAN-2004 (first entry)

XX Human/Mycobacterium tuberculosis ESAT-6/CD1a fusion construct protein.

XX CDI fusion protein; endosomal targeting; antibacterial; virucide;
 KW cystostatic; antidiabetic; antinflammatory; dermatological;
 KW immunosuppressive; neuroprotective; immune response; microbial;
 KW viral infection; autoimmune disorder; diabetes; lupus;
 KW multiple sclerosis; cancer; gene therapy; vaccine; human; ESAT-6/CD1a;
 KW chimeric.

XX Chimeric.

XX Synthetic.

XX Homo sapiens.

XX Mycobacterium tuberculosis.

XX WO2003066820-A2.

XX 14-AUG-2003.

XX 05-FEB-2003; 2003WO-US003550.

XX 05-FEB-2002; 2002US-0355432P.

XX (REGC) UNIV CALIFORNIA.

XX Modlin RL;

XX WPI; 2003-748121/70.

XX N-PSDB; ADE28540.

XX New chimeric nucleic acid molecule encoding a CDI fusion protein, useful
 PT for inducing an immune response against antigens associated with, e.g.
 PT microbial or viral infections, autoimmune disorders or cancer.

XX Claim 26; Fig 9A; 114pp; English.

XX The invention relates to a novel chimeric nucleic acid molecule
 CC consisting of a nucleotide sequence encoding a CDI fusion protein

CC comprising a CD1 endosomal targeting sequence or its fragment and an
 CC antigen of interest. The polynucleotide of the invention demonstrates
 CC antibacterial, virucide, cytostatic, antidiabetic, antiinflammatory,
 CC dermatological, immunosuppressive and neuroprotective activities whilst
 CC the composition and methods may be useful for inducing an immune response
 CC against antigens of interest which are associated with microbial or viral
 CC infections, autoimmune disorders including diabetes, lupus and multiple
 CC sclerosis and antigens associated with cancers. Furthermore, the
 CC composition may be utilised in gene therapy and vaccine development. The
 CC current sequence is that of the human/Mycobacterium tuberculosis ESAT-
 CC 6/CD1a fusion construct protein of the invention.

XX Sequence 142 AA;

Query Match 100.0%; Score 79; DB 7; Length 142;
 Best Local Similarity 100.0%; Pred. No. 3.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQQWNFAGIEAAA 15
 |||||
 Db 20 MTEQQWNFAGIEAAA 34

RESULT 30
 ADE28543
 ID ADE28543 standard; protein; 145 AA.

AC ADE28543;

XX 29-JAN-2004 (first entry)

DE Human/Mycobacterium tuberculosis ESAT-6/CD1b fusion construct protein.

CC CD1 fusion protein; endosomal targeting; antibacterial; virucide;
 KW cytostatic; antidiabetic; antiinflammatory; dermatological;
 KW immunosuppressive; neuroprotective; immune response; microbial;
 KW viral infection; autoimmune disorder; diabetes; lupus;
 KW multiple sclerosis; cancer; gene therapy; vaccine; human; ESAT-6/CD1b;
 KW chimeric.

XX Chimeric.
 OS Synthetic.
 OS Homo sapiens.

OS Mycobacterium tuberculosis.

XX WO2003066820-A2.

XX 14-AUG-2003.

XX 05-FEB-2003; 2003WO-US003550.

XX 05-FEB-2002; 2002US-0355432P.

XX (REGC) UNIV CALIFORNIA.

XX Modlin RL;

XX WPI; 2003-748121/70.

XX N-PSDB; ADE28542.

XX New chimeric nucleic acid molecule encoding a CD1 fusion protein, useful
 PT for inducing an immune response against antigens associated with, e.g.
 PT microbial or viral infections, autoimmune disorders or cancer.

XX Example 1; Fig 9B; 114pp; English.

XX The invention relates to a novel chimeric nucleic acid molecule
 CC consisting of a nucleotide sequence encoding a CD1 fusion protein
 CC comprising a CD1 endosomal targeting sequence or its fragment and an
 CC antigen of interest. The polynucleotide of the invention demonstrates
 CC antibacterial, virucide, cytostatic, antidiabetic, antiinflammatory,
 CC dermatological, immunosuppressive and neuroprotective activities whilst
 CC the composition and methods may be useful for inducing an immune response

CC against antigens of interest which are associated with microbial or viral
 CC infections, autoimmune disorders including diabetes, lupus and multiple
 CC sclerosis and antigens associated with cancers. Furthermore, the
 CC composition may be utilised in gene therapy and vaccine development. The
 CC current sequence is that of the human/Mycobacterium tuberculosis ESAT-
 CC 6/CD1b fusion construct protein of the invention.

XX Sequence 145 AA;

Query Match 100.0%; Score 79; DB 7; Length 145;
 Best Local Similarity 100.0%; Pred. No. 3.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQQWNFAGIEAAA 15
 |||||
 Db 20 MTEQQWNFAGIEAAA 34

RESULT 31

ADE28545
 ID ADE28545 standard; protein; 146 AA.

AC ADE28545;

XX 29-JAN-2004 (first entry)

DE Human/Mycobacterium tuberculosis ESAT-6/CD1c fusion construct protein.

CC CD1 fusion protein; endosomal targeting; antibacterial; virucide;
 KW cytostatic; antidiabetic; antiinflammatory; dermatological;
 KW immunosuppressive; neuroprotective; immune response; microbial;
 KW viral infection; autoimmune disorder; diabetes; lupus;
 KW multiple sclerosis; cancer; gene therapy; vaccine; human; ESAT-6/CD1c;
 KW chimeric.

XX Chimeric.

OS Synthetic.

OS Homo sapiens.

OS Mycobacterium tuberculosis.

XX WO2003066820-A2.

XX 14-AUG-2003.

XX 05-FEB-2003; 2003WO-US003550.

XX 05-FEB-2002; 2002US-0355432P.

XX (REGC) UNIV CALIFORNIA.

XX Modlin RL;

XX WPI; 2003-748121/70.

XX N-PSDB; ADE28544.

XX New chimeric nucleic acid molecule encoding a CD1 fusion protein, useful
 PT for inducing an immune response against antigens associated with, e.g.
 PT microbial or viral infections, autoimmune disorders or cancer.

XX Example 1; Fig 9C; 114pp; English.

XX The invention relates to a novel chimeric nucleic acid molecule
 CC consisting of a nucleotide sequence encoding a CD1 fusion protein
 CC comprising a CD1 endosomal targeting sequence or its fragment and an
 CC antigen of interest. The polynucleotide of the invention demonstrates
 CC antibacterial, virucide, cytostatic, antidiabetic, antiinflammatory,
 CC dermatological, immunosuppressive and neuroprotective activities whilst
 CC the composition and methods may be useful for inducing an immune response
 CC against antigens of interest which are associated with microbial or viral
 CC infections, autoimmune disorders including diabetes, lupus and multiple
 CC sclerosis and antigens associated with cancers. Furthermore, the
 CC composition may be utilised in gene therapy and vaccine development. The
 CC current sequence is that of the human/Mycobacterium tuberculosis ESAT-

CC 6/CD1c fusion construct protein of the invention.

XX Sequence 146 AA;

Query Match 100.0%; Score 79; DB 7; Length 146;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQQNWFAGIEAAA 15
| | | | | | | | | | | | | | | |
DB 20 MTEQQNWFAGIEAAA 34

RESULT 32

AD28547
ID AD28547 standard; protein; 146 AA.

XX

AC AD28547;

XX 29-JAN-2004 (first entry)

XX Human/Mycobacterium tuberculosis ESAT-6/CD1d fusion construct protein.

XX CD1 fusion protein; endosomal targeting; antibacterial; virucide;

XX cytosolic; antidiabetic; antiinflammatory; dermatological;

XX immunosuppressive; neuroprotective; immune response; microbial;

XX viral infection; autoimmune disorder; diabetes; lupus;

XX multiple sclerosis; cancer; gene therapy; vaccine; human; ESAT-6/CD1d;

XX chimeric.

XX Chimeric.

XX Synthetic.

XX Homo sapiens.

XX Mycobacterium tuberculosis.

XX WO2003066820-A2.

XX 14-AUG-2003.

XX 05-FEB-2003; 2003WO-US003550.

XX 05-FEB-2002; 2002US-0355432P.

XX (BEGC) UNIV CALIFORNIA.

XX Modlin RL;

XX WPI; 2003-748121/70.

XX N-PSDB; AD28546.

XX New chimeric nucleic acid molecule encoding a CD1 fusion protein, useful

XX for inducing an immune response against antigens associated with, e.g.

XX microbial or viral infections, autoimmune disorders or cancer.

XX Example 1; Fig 9D; 114pp; English.

XX The invention relates to a novel chimeric nucleic acid molecule

XX consisting of a nucleotide sequence encoding a CD1 fusion protein

XX comprising a CD1 endosomal targeting sequence or its fragment and an

XX antigen of interest. The polynucleotide of the invention demonstrates

XX antibacterial, virucide, cytostatic, antidiabetic, antiinflammatory,

XX dermatological, immunosuppressive and neuroprotective activities whilst

XX the composition and methods may be useful for inducing an immune response

XX against antigens of interest which are associated with microbial or viral

XX infections, autoimmune disorders including diabetes, lupus and multiple

XX sclerosis and antigens associated with cancer. Furthermore, the

XX composition may be utilised in gene therapy and vaccine development. The

XX current sequence is that of the human/Mycobacterium tuberculosis ESAT-

XX 6/CD1d fusion construct protein of the invention.

XX Sequence 146 AA;

Query Match

100.0%; Score 79; DB 7; Length 146;

Best Local Similarity 100.0%; Pred. No. 3.3e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQQNWFAGIEAAA 15

| | | | | | | | | | | | | | | |

DB 20 MTEQQNWFAGIEAAA 34

RESULT 33

AAI29888
ID AAI29888 standard; protein; 196 AA.

XX

AC AAI29888;

XX 18-NOV-1999 (first entry)

XX Mycobacterium tuberculosis ESAT-6 protein sequence.

XX Mycobacterial; lactic acid bacterium; diagnosis; skin test; vaccine;

XX delayed type hypersensitivity; DTH; ESAT-6 homodimer; tuberculosis;

XX interferon-gamma release.

XX Mycobacterium tuberculosis.

XX WO9945119-A2.

XX 10-SEP-1999.

XX 05-MAR-1999; 99WO-DK000109.

XX 06-MAR-1998; 98DK-0000306.

XX 06-MAR-1998; 98US-0077105P.

XX (STAT-) STATENS SERUM INST.

XX Jensen CL, Folkersen J;

XX WPI; 1999-551043/46.

XX N-PSDB; AA221131.

XX New mycobacterial polypeptide produced in lactic acid bacteria, useful in

XX tuberculosis diagnosis and vaccines.

XX Disclosure; Page 74; 76pp; English.

XX The present invention describes a bioactive polypeptide (or

XX immunologically equivalent analogue) produced in lactic acid bacteria

XX which reacts with lymphoid cells primed with Mycobacterium tuberculosis

XX complex mycobacteria (M. tuberculosis, M. africanum or M. bovis). The

XX polypeptide and ESAT-6 polypeptides are useful in compositions for

XX diagnosis of and vaccination against tuberculosis caused by M.

XX tuberculosis complex mycobacteria. The ESAT-6 polypeptide can be used to

XX diagnose ongoing/previous sensitization with these bacteria by detecting

XX cytokine release when contacting blood samples with the polypeptide. The

XX bioactive polypeptide may be used in diagnostic compositions and

XX vaccines for mycobacteria other than of the M. tuberculosis complex, e.g.

XX M. avium which infects poultry and occasionally humans, M. leprae; they

XX are especially useful when they do not react with lymphoid cells

XX previously primed with M. tuberculosis complex mycobacteria, and so do

XX not give rise to a diagnostic reaction in individuals infected with these

XX bacteria. The polypeptides may also be used in in vitro diagnostic tests

XX e.g. stimulation of interferon-gamma release from lymphocytes. The

XX polypeptide has similar or higher bioactivity as currently used

XX tuberculin reagent in the standard delayed type hypersensitivity (DTH)

XX skin test for tuberculosis, but may have greater specificity, being

XX better able to discriminate between lymphoid cells primed from

XX tuberculosis and from previous vaccination. The present sequence

XX represents M. tuberculosis ESAT-6 used in the exemplification of the

XX present invention

XX Sequence 196 AA;

Query Match

100.0%; Score 79; DB 2; Length 196;

Best Local Similarity 100.0%; Pred. No. 4.4e-05; Indels 0; Gaps 0; Mismatches 0; Conservative 15; Matches 15;

QY 1 MTEQOWNFAGIEAAA 15
Db 5 MTEQOWNFAGIEAAA 19

RESULT 34
AAW72943
ID AAW72943 standard; protein; 403 AA.

XX AC AAW72943;
XX DT 21-JAN-1999 (first entry)

XX DE Mycobacterium tuberculosis antigen ESAT6-MPT59.
XX KW Mycobacterium tuberculosis; antigen; vaccine; immunological; immunogen; infection.

XX KW Mycobacterium tuberculosis.
XX OS Mycobacterium tuberculosis.

XX PN WO9844119-A1.
XX PD 08-OCT-1998.

XX PF 01-APR-1998; 98WO-DK000132.
XX PR 02-APR-1997; 97DK-00000376.

XX PR 18-APR-1997; 97US-0044624P.
XX PR 10-NOV-1997; 97DK-00001277.

XX PR 05-JAN-1998; 98US-0070488P.
XX PA (STAT-) STATENS SERUM INST.

XX PI Andersen P, Nielsen R, Rosenkrands I, Weldingh K, Rasmussen PB;
PI Oettinger T, Florio W;

XX DR WPI; 1998-542705/46.
XX PT New isolated mycobacteria polypeptides and nucleic acids - used for developing products for the diagnosis of or vaccination against mycobacterial infections, particularly tuberculosis.

XX PT Disclosure; Page 233-234; 163pp; English.
XX CC The present sequence represents a Mycobacterium tuberculosis protein.

XX CC Products from the present invention, which describes protein fragments and nucleic acid fragments derived from M.tuberculosis, can be used in the detection of and prevention of mycobacterial infections. In particular, the proteins and nucleic acids can be used for the diagnosis of or vaccination against tuberculosis caused by M. tuberculosis, M. africanum or M. bovis

XX SQ Sequence 403 AA;
Query Match 100.0%; Score 79; DB 2; Length 403;
Best Local Similarity 100.0%; Pred. No. 9.4e-05; Mismatches 0; Conservative 15; Matches 15; Indels 0; Gaps 0;

QY 1 MTEQOWNFAGIEAAA 15
Db 22 MTEQOWNFAGIEAAA 36

RESULT 35
AAW21963
ID AAY21963 standard; protein; 403 AA.

XX AC AAY21963;
XX DT 06-SEP-1999 (first entry)

XX DE Amino acid sequence of antigen ESAT-6.
XX KW Immunogenic; Mycobacterium tuberculosis; immune response; infection; tuberculosis; fusion polypeptide; T-cell epitope; ESAT-6; MPT59; TB;

XX KW pharmaceutical; vaccination; M. africanum; M. bovis; CFP7A; CFP30A; CFP7B; CFP19; CFP27; CFP30A; RD1-ORF; CFP10A; CFP16; CFP19; CFP23; CFP25A; CFP30B; CFP7B.

XX OS Mycobacterium tuberculosis.
XX PN WO9924577-A1.

XX PD 20-MAY-1999.
XX PF 08-OCT-1998; 98WO-DK000438.

XX PR 10-NOV-1997; 97DK-00001277.
XX PR 05-JAN-1998; 98US-0070488P.

XX PR 01-APR-1998; 98WO-DK000132.
XX PA (STAT-) STATENS SERUM INST.

XX PI Andersen P, Skjot R;
XX DR WPI; 1999-347282/29.

XX PT New immunogenic fragment of Mycobacterium tuberculosis.
XX PS Example; Page 250-251; 265pp; English.

XX CC The invention describes a substantially pure immunogenic polypeptide fragment (1) from Mycobacterium tuberculosis that is able to evoke a protective immune response against infections by mycobacteria belonging to the tuberculosis complex. The invention provides a (1) fusion polypeptide comprising at least one polypeptide fragment (1) and at least one fusion partner; (2) a fusion polypeptide fragment comprising a T-cell epitope from M. tuberculosis protein ESAT-6, or MPT59 and a second different amino acid sequence from M. tuberculosis, and/or including a sequence which protects the first amino acid sequence from in vivo degradation or post-translational processing; (3) a nucleic acid fragment that encodes the above polypeptides. The polypeptides and nucleic acid are useful as pharmaceuticals, for diagnosis of and as antigens for vaccination against TB caused by Mycobacterium tuberculosis, africanum or bovis. The polypeptides are also useful for diagnosing ongoing or previous sensitization in an animal with bacteria belonging to the tuberculosis complex. The invention also describes the use of CFP7A or CFP30A or a T-cell epitope of for the induction of a strong immune response in a mammal; use of CFP7B, CFP19 or MPT59-ESAT6 or a T-cell epitope of for diagnosis of TB in a mammal by performing a DTH type skin test; use of CFP27, CFP30A, RD1-ORF2, RD1-ORF5, MPT59-ESAT6, ESAT6-MPT59, CFP10A, CFP16, CFP19, CFP23, CFP25A, CFP30B, CFP7B or a T-cell epitope of for the preparation of an immunological composition; and for the preparation of a subunit vaccine

XX SQ Sequence 403 AA;
Query Match 100.0%; Score 79; DB 2; Length 403;
Best Local Similarity 100.0%; Pred. No. 9.4e-05; Mismatches 0; Conservative 15; Matches 15; Indels 0; Gaps 0;

QY 1 MTEQOWNFAGIEAAA 15
Db 22 MTEQOWNFAGIEAAA 36

RESULT 36
AAW72942
ID AAW72942 standard; protein; 404 AA.

XX AC AAW72942;
XX DT 21-JAN-1999 (first entry)

XX Mycobacterium tuberculosis antigen MPT59-ESAT6.
 DE
 XX Mycobacterium tuberculosis; antigen; vaccine; immunological, immunogen;
 KW infection.
 XX Mycobacterium tuberculosis.
 OS
 XX WO9844119-A1.
 PN
 XX 08-OCT-1998.
 PD
 XX
 XX 01-APR-1998; 98WO-DK000132.
 PF
 XX 02-APR-1997; 97DK-00000376.
 PR
 XX 18-APR-1997; 97US-0044624P.
 PR
 XX 10-NOV-1997; 97DK-00001277.
 PR
 XX 05-JAN-1998; 98US-0070488P.
 PR
 XX (STAT-) STATENS SERUM INST.
 PA
 XX Andersen P, Nielsen R, Rosenkrands I, Weldingh K, Rasmussen PB;
 PI Oettinger T, Florio W;
 PI
 XX WPI; 1998-542705/46.
 DR
 XX New isolated mycobacteria polypeptides and nucleic acids - used for
 PT developing products for the diagnosis of or vaccination against
 PT mycobacterial infections, particularly tuberculosis.
 PT
 XX Disclosure; Page 232-233; 163pp; English.
 PS
 XX The present sequence represents a Mycobacterium tuberculosis protein.
 CC Products from the present invention, which describes protein fragments
 CC and nucleic acid fragments derived from M.tuberculosis, can be used in
 CC the detection of and prevention of mycobacterial infections. In
 CC particular, the proteins and nucleic acids can be used for the diagnosis
 CC of or vaccination against tuberculosis caused by M. tuberculosis, M.
 CC africanum or M. bovis
 CC
 XX Sequence 404 AA;
 SQ

Query Match 100.0%; Score 79; DB 2; Length 404;
 Best Local Similarity 100.0%; Pred. No. 9.5e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTEQQWNFAGIEAAA 15
 |||||
 DB 310 MTEQQWNFAGIEAAA 324

RESULT 37
 AAY21962
 ID AAY21962 standard; protein; 404 AA.
 XX
 AC AAY21962;
 XX
 DT 06-SEP-1999 (first entry)
 XX
 DE Amino acid sequence of antigen MPT59.
 XX
 KW Immunogenic; Mycobacterium tuberculosis; immune response; infection;
 KW tuberculosis; fusion polypeptide; T-cell epitope; ESAT-6; MPT59; TB;
 KW pharmaceutical; vaccination; M. africanum; M. bovis; CFP7A; CFP30A;
 KW CFP7B; CFP19; CFP27; CFP30A; RD1-ORF; CFP10A; CFP16; CFP19; CFP23;
 KW CFP25A; CFP30B; CFP7B.
 XX
 OS Mycobacterium tuberculosis.
 PN
 XX WO9924577-A1.
 PN
 XX 20-MAY-1999.
 PD
 XX

PF 08-OCT-1998; 98WO-DK000438.
 XX
 PR 10-NOV-1997; 97DK-00001277.
 PR 05-JAN-1998; 98US-0070488P.
 PR 01-APR-1998; 98WO-DK000132.
 XX
 PA (STAT-) STATENS SERUM INST.
 XX
 XX Andersen P, Skjot R;
 PI
 XX WPI; 1999-347282/29.
 DR
 XX New immunogenic fragment of Mycobacterium tuberculosis.
 XX
 XX Example; Page 249-250; 265pp; English.
 PS
 XX The invention describes a substantially pure immunogenic polypeptide
 CC fragment (I) from Mycobacterium tuberculosis that is able to evoke a
 CC protective immune response against infections by mycobacteria belonging
 CC to the tuberculosis complex. The invention provides a (I) fusion
 CC polypeptide comprising at least one polypeptide fragment (I) and at least
 CC one fusion partner; (2) a fusion polypeptide fragment comprising a T-cell
 CC epitope from M. tuberculosis protein ESAT-6, or MPT59 and a second
 CC different amino acid sequence from M. tuberculosis, and/or including a
 CC sequence which protects the first amino acid sequence from in vivo
 CC degradation or post-translational processing; (3) a nucleic acid fragment
 CC that encodes the above polypeptides. The polypeptides and nucleic acid
 CC are useful as pharmaceuticals for diagnosis of and as antigens for
 CC vaccination against TB caused by Mycobacterium tuberculosis, africanum or
 CC bovis. The polypeptides are also useful for diagnosing ongoing or
 CC previous sensitization in an animal with bacteria belonging to the
 CC tuberculosis complex. The invention also describes the use of CFP7A or
 CC CFP30A or a T-cell epitope of for the induction of a strong immune
 CC response in a mammal; use of CFP7B, CFP19 or MPT59-ESAT6 or a T-cell
 CC epitope of for diagnosis of TB in a mammal by performing a DTH type skin
 CC test; use of CFP27, CFP30A, RD1-ORF2, RD1-ORF3, MPT59-ESAT6,
 CC ESAT6-MPT59, CFP10A, CFP16, CFP19, CFP23, CFP25A, CFP30B, CFP7B or a T-
 CC cell epitope of for the preparation of an immunological composition; and
 CC for the preparation of a subunit vaccine
 XX
 XX Sequence 404 AA;
 SQ

Query Match 100.0%; Score 79; DB 2; Length 404;
 Best Local Similarity 100.0%; Pred. No. 9.5e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTEQQWNFAGIEAAA 15
 |||||
 DB 310 MTEQQWNFAGIEAAA 324

RESULT 38
 ADK00561
 ID ADK00561 standard; peptide; 13 AA.
 XX
 AC ADK00561;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Immunogenic lipopeptide of the invention #97.
 XX
 KW T helper cell epitope; B cell epitope; Antibacterial; Antiulcer;
 KW Antiinfertility; Vaccine; antibody.
 XX
 OS Synthetic.
 XX
 PN WO2004014956-A1.
 PN
 PD 19-FEB-2004.
 PD
 XX 12-AUG-2003; 2003WO-AU001018.
 XX
 XX 12-AUG-2002; 2002US-0402838P.
 PR

XX PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
 XX PI Jackson D, Zeng W;
 XX PT WPI; 2004-238735/22.
 XX DR
 XX PT Novel lipopeptide comprising polypeptide having amino acid sequence of T
 PT helper cell epitope and B cell epitope, conjugated to lipid moieties,
 PT useful for eliciting immune response against group A Streptococcus
 PT antigen.
 XX PS Disclosure; SEQ ID NO 97; 194pp; English.
 XX CC The present invention relates to a lipopeptide comprising polypeptide
 CC conjugated to lipid moieties, where polypeptide contains amino acid
 CC sequence of T helper cell epitope and B cell epitope, where amino acid
 CC sequences are different, and internal lysine residues or internal lysine
 CC analog residues for covalent attachment of each of lipid moieties through
 CC seg; amino group or terminal side chain group of lysine or lysine
 CC analog. The peptides are useful in eliciting the production of antibody
 CC against an antigenic B cell epitope in a subject, and are useful for
 CC antibody production, synthetic vaccine production, diagnostic method
 CC employing antibodies and antibody ligands and immunotherapy for
 CC veterinary and human medicine. The method efficiently elicits the
 CC production of antibody against antigenic B cell epitope. The present
 CC sequence represents a novel immunogenic lipopeptide comprising T helper
 CC and B cell epitopes.
 XX SQ Sequence 13 AA;
 Query Match 87.3%; Score 69; DB 8; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00012;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 EQQWNFAGIEAAA 15
 |||||
 Db 1 EQQWNFAGIEAAA 13
 RESULT 39
 AEB44918
 ID AEB44918 standard; peptide; 13 AA.
 AC AEB44918;
 XX 06-OCT-2005 (first entry)
 DT
 DE M. tuberculosis ESAT6 B cell epitope SEQ ID NO 48.
 KW immunogenicity; viral infection; infection; bacterial infection; cancer;
 KW neoplasm; autoimmune disease; immune disorder; inflammation; allergy;
 KW Antibacterial; Virucide; Fungicide; Anti-HIV; Hepatotropic;
 KW Antiparasitic; Cytostatic; Immunosuppressive; Antiarthritic;
 KW antirheumatic; neuroprotective; antidiabetic; gastrointestinal-Gen.;
 KW antiinflammatory; antiulcer; antipsoriatic; dermatological;
 KW antiasthmatic; antiallergic; immunomodulator.
 XX OS Mycobacterium tuberculosis.
 XX OS WO2005070959-A2.
 PN 04-AUG-2005.
 XX 24-JAN-2005; 2005WO-US002251.
 XX 23-JAN-2004; 2004US-0538713P.
 PR 06-OCT-2004; 2004US-0616855P.
 XX (VIEW-) VIEWAX CORP.
 XX Mahairas GG;
 XX

DR XX Immune response altering agent useful for treating autoimmune diseases,
 PT comprises first domain having T/B cell epitopes or Toll-like receptor-
 PT binding proteins, and second domain having heterologous target molecule.
 XX PS Disclosure; SEQ ID NO 48; 130pp; English.
 XX CC The invention relates to an immune response altering agent (I) which
 CC comprises a first domain having one or more components chosen from T cell
 CC epitopes, B cell epitopes, and Toll-like receptor (TLR)-binding proteins
 CC or its TLR-binding domains, and a second domain having heterologous
 CC target molecule against which an immune response is desired. (I) is
 CC useful for altering or inducing an immune response to a target. (I) is
 CC also useful for treating viral infections (e.g., HIV and hepatitis C
 CC virus), bacterial infections (e.g., Staphylococcus and Pseudomonas),
 CC parasites (e.g., Leishmania), fungal infections (e.g., Candida), cancer
 CC (e.g., non-Hodgkin's lymphoma), Hodgkin's disease and leukemia, and
 CC autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,
 CC insulin dependent diabetes, Addison's disease, celiac disease,
 CC inflammatory bowel disease, ulcerative colitis, Crohn's disease, systemic
 CC lupus erythematosus, psoriasis, Sjogren's syndrome, etc. (I) is useful
 CC for treating inflammatory and hyperproliferative skin diseases, and
 CC allergic reactions such as asthma, bronchitis, allergic rhinitis etc. (I)
 CC alters an immune response generated against the heterologous target
 CC molecule. (I) can be applied to wide range of species such as humans, non
 CC -human primates, horses, etc. The present sequence represents the amino
 CC acid sequence of a B-cell epitope used to illustrate the present
 CC invention.
 XX SQ Sequence 13 AA;
 Query Match 87.3%; Score 69; DB 9; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00012;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 EQQWNFAGIEAAA 15
 |||||
 Db 1 EQQWNFAGIEAAA 13
 RESULT 40
 AEB44912
 ID AEB44912 standard; peptide; 13 AA.
 AC AEB44912;
 XX 06-OCT-2005 (first entry)
 DT
 DE Mycobacterium ESAT6 T cell epitope SEQ ID NO 42.
 KW immunogenicity; viral infection; infection; bacterial infection; cancer;
 KW neoplasm; autoimmune disease; immune disorder; inflammation; allergy;
 KW Antibacterial; Virucide; Fungicide; Anti-HIV; Hepatotropic;
 KW Antiparasitic; Cytostatic; Immunosuppressive; Antiarthritic;
 KW antirheumatic; neuroprotective; antidiabetic; gastrointestinal-Gen.;
 KW antiinflammatory; antiulcer; antipsoriatic; dermatological;
 KW antiasthmatic; antiallergic; immunomodulator.
 XX OS Mycobacterium tuberculosis.
 XX OS Mycobacterium bovis.
 PN WO2005070959-A2.
 XX 04-AUG-2005.
 XX 24-JAN-2005; 2005WO-US002251.
 XX 23-JAN-2004; 2004US-0538713P.
 PR 06-OCT-2004; 2004US-0616855P.
 XX (VIEW-) VIEWAX CORP.
 XX

PI Mahairas GG;
 XX WPI; 2005-542270/55.
 XX Immune response altering agent useful for treating autoimmune diseases,
 FT comprises first domain having T/B cell epitopes or Toll-like receptor-
 PT binding proteins, and second domain having heterologous target molecule.
 XX
 XX Disclosure; SEQ ID NO 42; 130pp; English.
 XX
 CC The invention relates to an immune response altering agent (I) which
 CC comprises a first domain having one or more components chosen from T cell
 CC epitopes, B cell epitopes, and Toll-like receptor (TLR)-binding proteins
 CC or its TLR-binding domains, and a second domain having heterologous
 CC target molecule against which an immune response is desired. (I) is
 CC useful for altering or inducing an immune response to a target. (I) is
 CC also useful for treating viral infections (e.g., HIV and hepatitis C
 CC virus), bacterial infections (e.g., Staphylococcus and Pseudomonas),
 CC parasites (e.g., Leishmania), fungal infections (e.g., Candida), and
 CC (e.g., non-Hodgkin's lymphoma, Hodgkin's disease and leukemia), and
 CC autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,
 CC insulin dependent diabetes, Addison's disease, celiac disease,
 CC inflammatory bowel disease, ulcerative colitis, Crohn's disease, systemic
 CC lupus erythematosus, psoriasis, Sjogren's syndrome, etc. (I) is useful
 CC for treating inflammatory and hyperproliferative skin diseases, and
 CC allergic reactions such as asthma, bronchitis, allergic rhinitis etc. (I)
 CC alters an immune response generated against the heterologous target
 CC molecule. (I) can be applied to wide range of species such as humans, non
 CC -human primates, horses, etc. The present sequence represents the amino
 CC acid sequence of a T-cell epitope used to illustrate the present
 CC invention.
 XX
 XX Sequence 13 AA;
 SQ

Query Match 87.3%; Score 69; DB 9; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00012;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EQQWNFAGIEAAA 15
 |||||
 DB 1 EQQWNFAGIEAAA 13

RESULT 41
 AEB45087
 ID AEB45087 standard; peptide; 15 AA.
 XX
 AC AEB45087;
 XX
 DT 06-OCT-2005 (first entry)
 XX
 DE M. tuberculosis ESAT6 peptide fragment SEQ ID NO 217.
 XX
 KW immunogenicity; viral infection; infection; bacterial infection; cancer;
 KW neoplasm; autoimmune disease; immune disorder; inflammation; allergy;
 KW Antibacterial; Virucide; Fungicide; Anti-HIV; Hepatotropic;
 KW Antiparasitic; Cytoprotective; immunosuppressive; antiarthritic;
 KW antirheumatic; neuroprotective; antidiabetic; gastrointestinal-Gen.;
 KW antiinflammatory; antitumor; antipsoriatic; dermatological;
 KW antiasthmatic; anciallergic; Immunomodulator.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN WO2005070959-A2.
 XX
 PD 04-AUG-2005.
 XX
 PF 24-JAN-2005; 2005WO-US002251.
 XX
 PR 23-JAN-2004; 2004US-0538713P.
 XX
 PR 06-OCT-2004; 2004US-0616855P.
 XX
 PA (VIEW-) VIEWAX CORP.

XX Mahairas GG;
 XX WPI; 2005-542270/55.
 XX Immune response altering agent useful for treating autoimmune diseases,
 FT comprises first domain having T/B cell epitopes or Toll-like receptor-
 PT binding proteins, and second domain having heterologous target molecule.
 XX
 XX Claim 65; SEQ ID NO 217; 130pp; English.

CC The invention relates to an immune response altering agent (I) which
 CC comprises a first domain having one or more components chosen from T cell
 CC epitopes, B cell epitopes, and Toll-like receptor (TLR)-binding proteins
 CC or its TLR-binding domains, and a second domain having heterologous
 CC target molecule against which an immune response is desired. (I) is
 CC useful for altering or inducing an immune response to a target. (I) is
 CC also useful for treating viral infections (e.g., HIV and hepatitis C
 CC virus), bacterial infections (e.g., Staphylococcus and Pseudomonas),
 CC parasites (e.g., Leishmania), fungal infections (e.g., Candida), and
 CC (e.g., non-Hodgkin's lymphoma, Hodgkin's disease and leukemia), and
 CC autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,
 CC insulin dependent diabetes, Addison's disease, celiac disease,
 CC inflammatory bowel disease, ulcerative colitis, Crohn's disease, systemic
 CC lupus erythematosus, psoriasis, Sjogren's syndrome, etc. (I) is useful
 CC for treating inflammatory and hyperproliferative skin diseases, and
 CC allergic reactions such as asthma, bronchitis, allergic rhinitis etc. (I)
 CC alters an immune response generated against the heterologous target
 CC molecule. (I) can be applied to wide range of species such as humans, non
 CC -human primates, horses, etc. The present sequence represents the amino
 CC acid sequence of a M. tuberculosis early secretory antigenic target 6,
 CC ESAT6, peptide fragment.

XX Sequence 15 AA;
 SQ

Query Match 74.7%; Score 59; DB 9; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.0068;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QWNFAGIEAAA 15
 |||||
 DB 1 QWNFAGIEAAA 11

RESULT 42
 AAE12275
 ID AAE12275 standard; peptide; 20 AA.
 XX
 AC AAE12275;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Mycobacterium tuberculosis (Mtb) peptide #60.
 XX
 KW Mycobacterium tuberculosis; Mtb peptide; antibacterial; vaccine;
 KW infection; anti-Mtb immune response.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN WO200170774-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 20-MAR-2001; 2001WO-US008906.
 XX
 PR 20-MAR-2000; 2000US-0190834P.
 XX
 PA (UYBR-) UNIV BROWN RES FOUND.
 XX
 XX Degroot AS;
 XX WPI; 2001-616401/71.
 XX

PT New vaccine for immunizing a mammalian subject, preferably humans,
 XX against infection caused by Mycobacterium tuberculosis.

PS Disclosure; Fig 4; 42pp; English.

XX The present invention relates to Mycobacterium tuberculosis (Mtb) vaccine
 CC candidate peptides. The invention also relates to a method for
 CC identifying Mtb vaccine candidate peptides as well as vaccines comprising
 CC these candidate peptides. Vaccines of the invention and Mtb vaccine
 CC candidate peptides are useful for inducing an anti- Mycobacterium
 CC tuberculosis (anti-Mtb) immune response by raising anti-Mtb antibody in a
 CC mammalian subject preferably human. They are used for immunising a
 CC mammalian subject, preferably humans, against infection caused by
 CC Mycobacterium tuberculosis. The present sequence is a Mtb vaccine
 CC candidate peptide

XX Sequence 20 AA;

Query Match 74.7%; Score 59; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.0092;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QWNFAGIEAAA 15
 Db 1 QWNFAGIEAAA 11

RESULT 43

ABE45115
 ID AEB45115 standard; peptide; 10 AA.

XX AC AEB45115;

XX DT 06-OCT-2005 (first entry)

XX DE M. tuberculosis ESAT6 peptide fragment SEQ ID NO 245.

XX immunogenicity; viral infection; infection; bacterial infection; cancer;
 KW neoplasm; autoimmune disease; immune disorder; inflammation; allergy;
 KW Antibacterial; Virucide; Fungicide; Anti-HIV; Hepatotropic;
 KW Antiparasitic; Cytostatic; immunosuppressive; antiarthritic;
 KW antirheumatic; neuroprotective; antidiabetic; gastrointestinal-Gen.;
 KW antiinflammatory; antiulcer; antipsoriatic; dermatological;
 KW antiasthmatic; antiallergic; Immunomodulator.

XX Mycobacterium tuberculosis.

XX WO2005070959-A2.

XX 04-AUG-2005.

XX 24-JAN-2005; 2005WO-US002251.

XX 23-JAN-2004; 2004US-0538713P.

XX 06-OCT-2004; 2004US-0616855P.

XX (VIEW-) VIEWAX CORP.

XX Mahairas GG;

XX WPI; 2005-542270/55.

XX Immune response altering agent useful for treating autoimmune diseases,
 PT comprises first domain having T/B cell epitopes or Toll-like receptor-
 PT binding proteins, and second domain having heterologous target molecule.

XX Claim 65; SEQ ID NO 245; 130pp; English.

XX The invention relates to an immune response altering agent (I) which
 CC comprises a first domain having one or more components chosen from T cell
 CC epitopes, B cell epitopes, and Toll-like receptor (TLR)-binding proteins
 CC or its TLR-binding domains, and a second domain having heterologous
 CC target molecule against which an immune response is desired. (I) is

CC useful for altering or inducing an immune response to a target. (I) is
 CC also useful for treating viral infections (e.g., HIV and hepatitis C
 CC virus), bacterial infections (e.g., Staphylococcus and Pseudomonas),
 CC parasites (e.g., Leishmania), fungal infections (e.g., Candida), cancer
 CC (e.g., non-Hodgkin's lymphoma), Hodgkin's disease and leukemia), and
 CC autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,
 CC insulin dependent diabetes, Addison's disease, celiac disease,
 CC inflammatory bowel disease, ulcerative colitis, Crohn's disease, systemic
 CC lupus erythematosus, psoriasis, Sjogren's syndrome, etc. (I) is useful
 CC for treating inflammatory and hyperproliferative skin diseases, and
 CC allergic reactions such as asthma, bronchitis, allergic rhinitis etc. (I)
 CC alters an immune response generated against the heterologous target
 CC molecule. (I) can be applied to wide range of species such as humans, non
 CC -human primates, horses, etc. The present sequence represents the amino
 CC acid sequence of a M. tuberculosis early secretory antigenic target 6,
 CC ESAT6, peptide fragment.

XX Sequence 10 AA;

Query Match 73.4%; Score 58; DB 9; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0065;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTEQOWNFAG 10

Db 1 MTEQOWNFAG 10

RESULT 44

ABE45116
 ID AEB45116 standard; peptide; 10 AA.

XX AC AEB45116;

XX DT 06-OCT-2005 (first entry)

XX DE M. tuberculosis ESAT6 peptide fragment SEQ ID NO 246.

XX immunogenicity; viral infection; infection; bacterial infection; cancer;
 KW neoplasm; autoimmune disease; immune disorder; inflammation; allergy;
 KW Antibacterial; Virucide; Fungicide; Anti-HIV; Hepatotropic;
 KW Antiparasitic; Cytostatic; immunosuppressive; antiarthritic;
 KW antirheumatic; neuroprotective; antidiabetic; gastrointestinal-Gen.;
 KW antiinflammatory; antiulcer; antipsoriatic; dermatological;
 KW antiasthmatic; antiallergic; Immunomodulator.

XX Mycobacterium tuberculosis.

XX WO2005070959-A2.

XX 04-AUG-2005.

XX 24-JAN-2005; 2005WO-US002251.

XX 23-JAN-2004; 2004US-0538713P.

XX 06-OCT-2004; 2004US-0616855P.

XX (VIEW-) VIEWAX CORP.

XX Mahairas GG;

XX WPI; 2005-542270/55.

XX Immune response altering agent useful for treating autoimmune diseases,
 PT comprises first domain having T/B cell epitopes or Toll-like receptor-
 PT binding proteins, and second domain having heterologous target molecule.

XX Claim 65; SEQ ID NO 246; 130pp; English.

XX The invention relates to an immune response altering agent (I) which
 CC comprises a first domain having one or more components chosen from T cell
 CC epitopes, B cell epitopes, and Toll-like receptor (TLR)-binding proteins
 CC or its TLR-binding domains, and a second domain having heterologous

CC target molecule against which an immune response is desired. (I) is
CC useful for altering or inducing an immune response to a target. (I) is
CC also useful for treating viral infections (e.g., HIV and hepatitis C
CC virus), bacterial infections (e.g., Staphylococcus and Pseudomonas),
CC parasites (e.g., Leishmania), fungal infections (e.g., Candida), cancer
CC (e.g., non-Hodgkin's lymphoma, Hodgkin's disease and leukemia), and
CC autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,
CC inflammatory bowel disease, Addison's disease, celiac disease,
CC insulin dependent diabetes, ulcerative colitis, Crohn's disease, systemic
CC lupus erythematosus, psoriasis, Sjogren's syndrome, etc. (I) is useful
CC for treating inflammatory and hyperproliferative skin diseases, and
CC allergic reactions such as asthma, bronchitis, allergic rhinitis etc. (I)
CC alters an immune response generated against the heterologous target
CC molecule. (I) can be applied to wide range of species such as humans, non
CC human primates, horses, etc. The present sequence represents the amino
CC acid sequence of a M. tuberculosis early secretory antigenic target 6,
CC ESAT6, peptide fragment.
XX
XX
SQ Sequence 10 AA;
Query Match 68.4%; Score 54; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 WNPAGIEAAA 15
DB 1 WNPAGIEAAA 10
RESULT 45
AAY94595
ID AAY94595 standard; peptide; 15 AA.
XX
AC AAY94595;
XX
DT 28-NOV-2000 (first entry)
XX
DE Mycobacterium tuberculosis ESAT-6 peptide ES6.
XX
XM Tuberculosis; infection diagnosis; ESAT-6.
XX
XX Mycobacterium tuberculosis.
XX
FN WO20026248-A2.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-GB003635.
XX
XX
PR 04-NOV-1998; 98GB-00024213.
PR 04-NOV-1998; 98US-0107004P.
XX
XX (ISIS-) ISIS INNOVATION LTD.
XX
XX Lalvani A, Pathan AA;
PI
DR WPI; 2000-365579/31.
XX
XX
XX Novel method of diagnosing infection, or exposure of a host, to a
PT mycobacterium comprising contacting T cells from the host with ESAT-6
PT derived peptides.
XX
XX
PS Claim 1; Page 3; 33pp; English.
XX
XX The present sequence is the peptide ES6 derived from the Mycobacterium
CC tuberculosis ESAT-6 gene. This sequence is one of eleven peptides derived
CC from the ESAT-6 gene (see AAY94590 to AAY94600). The peptides are
CC recognised, to varying degrees, by the T cells of patients with
CC tuberculosis. When the peptides are combined together as a panel they
CC provide a high specificity and sensitivity diagnostic test for
CC M.tuberculosis infection. This test has the advantage that it does not
CC give false positives for patients who have been vaccinated with BCG
XX

SQ Sequence 15 AA;
Query Match 68.4%; Score 54; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 WNPAGIEAAA 15
DB 1 WNPAGIEAAA 10
RESULT 46
ABG30952
ID ABG30952 standard; peptide; 15 AA.
XX
AC ABG30952;
XX
DT 21-OCT-2002 (first entry)
XX
DE Mycobacterium tuberculosis ESAT-6 residues 6-20.
XX
KW ESAT-6; mycobacterial infection; tuberculosis; pulmonary tuberculosis;
KW tuberculosis lymphadenitis; extrapulmonary tuberculosis.
XX
OS Mycobacterium tuberculosis.
XX
FN WO200254072-A2.
XX
PD 11-JUL-2002.
XX
PF 08-JAN-2002; 2002WO-GB000055.
XX
XX
PR 08-JAN-2001; 2001GB-00000432.
PR 08-JAN-2001; 2001US-0259868P.
XX
XX (ISIS-) ISIS INNOVATION LTD.
XX
XX Lalvani A;
PI
DR WPI; 2002-583633/62.
XX
XX Determining the progress of a mycobacterial infection, by direct ex vivo
PT quantitation of ESAT-6-specific T cells.
XX
PS Example 2; Page 40; 53pp; English.
XX
XX The invention describes a method of determining the efficacy of treatment
CC for mycobacterial infection (such as pulmonary tuberculosis, tuberculosis
CC lymphadenitis and extrapulmonary tuberculosis). The method involves
CC determining the level of T cells specific for a mycobacterial antigen
CC that has decreased after the treatment and therefore determining the
CC efficacy of the treatment. The method is useful for determining the
CC efficacy of treatment for mycobacterial infection, the mycobacterial
CC infection is Mycobacterium tuberculosis or M.bovis infection. The
CC invention also describes a method useful for determining the presence of T
CC cells specific for a mycobacterial antigen. Also described in a method
CC for determining the effect of an intervention on a mycobacterial
CC infection in an individual an method for treating an individual
CC infected by a mycobacterium. This sequence represents a peptide of
CC Mycobacterium tuberculosis ESAT-6, the mycobacterial antigen measured in
CC the invention
XX
XX Sequence 15 AA;
Query Match 68.4%; Score 54; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 WNPAGIEAAA 15
DB 1 WNPAGIEAAA 10

```

RESULT 47
AAO17433
ID AAO17433 standard; peptide; 15 AA.
XX
AC AAO17433;
XX
DT 11-JUL-2002 (first entry)
XX
DE Early secreted antigenic target 6 T cell epitope #2.
XX
KW Tuberculosis; TB; vaccination; vaccine; CD4+ T cell immune response;
KW poxvirus vector; HIV; malaria; Helicobacter pylori; influenza; hepatitis;
KW viral infection; leprosy; protozoan parasite; cancer; tuberculostatic;
KW anti-HIV; proteoacide; antibacterial; virucide; hepatotropic;
KW antiinflammatory; antileprotic; cytostatic; epitope.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200224224-A2.
XX
PD 28-MAR-2002.
XX
PF 13-SEP-2001; 2001WO-GB004116.
XX
PR 21-SEP-2000; 2000GB-00023203.
XX
PA (OXO-) OXON PHARMACINES LTD.
XX
PI Hill AVS, Mcshane H, Gilbert S, Reece W, Schneider J;
XX
DR WPI; 2002-394098/42.
XX
PT Inducing CD4+ T-cell response against target antigen by administering a
PT composition comprising a source of CD4+ epitopes which is a non-
PT replicating or replication impaired recombinant poxvirus vector.
XX
PS Example 1; Page 21; 50pp; English.
XX
CC The present invention relates to a method of inducing a CD4+ T-cell
CC response against a target antigen, by administering two different
CC compositions comprising a source of CD4+ T-cell epitope(s) of the target
CC antigen, where the second composition further includes an epitope which
CC is same as the epitope of the first composition, where the source of the
CC epitopes for the compositions is a non-replicating or replication
CC impaired recombinant poxvirus vector. The methods are useful for inducing
CC CD4+ T-cell immune responses against diseases such as tuberculosis, human
CC immunodeficiency virus (HIV) (persistent viral infection), malaria,
CC Helicobacter pylori, influenza, hepatitis (chronic hepatitis B and C),
CC cytomegalovirus (CMV), viral infection, herpes virus-induced disease,
CC leprosy and diseases caused by non-malarial protozoan parasite such as
CC toxoplasma and cancer. The present sequence is an epitope from
CC Mycobacterium tuberculosis useful in the method of the invention
XX
SQ Sequence 15 AA;

Query Match 68.4%; Score 54; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WNFAGIEAAA 15
   |||||
Db 1 WNFAGIEAAA 10

RESULT 48
ADI33342
ID ADI33342 standard; peptide; 15 AA.
XX
AC ADI33342;
XX
DT 22-APR-2004 (first entry)
XX

```

```

DE Mycobacterium tuberculosis ESAT-6 peptide epitope #2.
XX
KW pathogen; vaccine; cellular response; HPV; HIV; SIV; HCV; chlamydia; HBV;
KW BBV; CMV; VZV; HSV; Legionella; Leishmaniasis; influenza;
KW foot and mouth virus; Toxoplasma; Brucella; Cryptococcus; Candida;
KW Aspergillus; Mycobacterium; T cell; ESAT-6; CFP10; virucide; proteoazide;
KW antibacterial; fungicide; epitope.
XX
OS Mycobacterium tuberculosis.
XX
PN WO2004005925-A2.
XX
PD 15-JAN-2004.
XX
PF 07-JUL-2003; 2003WO-GB002936.
XX
PR 05-JUL-2002; 2002GB-00015710.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
PI Lalvani A, Ewer K;
XX
DR WPI; 2004-143006/14.
XX
PT Diagnosing in an individual recent exposure to an agent, useful in
PT treating a disease caused by a pathogen, by determining in vitro or in
PT vivo whether the T cells of recognize a protein having at least 30 amino
PT acids.
XX
PS Claim 16; Page 33; 48pp; English.
XX
CC The invention relates to a novel method for diagnosing in an individual
CC recent exposure to an agent which is a pathogen, vaccine or any other
CC moiety, which induces a cellular response. The pathogen can include: HPV,
CC HIV, SIV, HCV, chlamydia species, HBV, EBV, CMV, VZV, HSV, Legionella, S.
CC typhi, P. falciparum, Leishmaniasis, M. leprae, influenza virus, foot and
CC mouth virus, a Toxoplasma species, a Brucella species, a Cryptococcus
CC species, a Candida species, an Aspergillus species, or Mycobacterium
CC tuberculosis. The invention also provides a vaccine against any of the
CC above pathogens. The method comprises determining in vitro or in vivo
CC whether the T cells of the individual recognize a protein from the agent
CC having a length of at least 30 amino acids. The invention also comprises
CC a protein or epitope peptide which is from ESAT-6 or CFP10. The vaccines
CC of the invention have: virucide, proteoazide, antibacterial, and fungicide
CC activity. The method is useful in diagnosing in an individual recent
CC exposure to an agent which is a pathogen, vaccine or any other moiety
CC which induces a cellular response. The protein described above, the
CC product which prevents or treats a condition caused by a pathogen or the
CC antigen or its analogue is useful in the manufacturing of a medicament
CC for diagnosing and treating an individual recently exposed to a pathogen.
CC This sequence represents a peptide epitope of the invention for
CC recognition by a T cell relating to the invention.
XX
SQ Sequence 15 AA;

Query Match 68.4%; Score 54; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WNFAGIEAAA 15
   |||||
Db 1 WNFAGIEAAA 10

RESULT 49
AAW70180
ID AAW70180 standard; peptide; 10 AA.
XX
AC AAW70180;
XX
DT 07-DEC-1998 (first entry)
XX
DE N-terminal amino acid sequence of CFP, ESAT 6.

```

```

XX Culture filtrate protein; CFP; 2-D PAGE; electrophoretogram; homology;
KW Edman degradation; antigen; antibody; HYB 76-8; HIV;
KW human immunodeficiency virus.
XX
XX Mycobacterium tuberculosis.
XX
XX WO9829132-A1.
XX
XX 09-JUL-1998.
XX
XX 29-DEC-1997; 97WO-US024189.
XX
XX 31-DEC-1996; 96US-0034003P.
XX
XX (UYNV ) UNIV NEW YORK STATE.
XX
XX Laal S, Zolla-Pazner S, Belisle JT;
XX WPI, 1998-387787/33.
XX
XX Early detection of mycobacterial infection - by testing a biological
PT fluid sample from a subject for the presence of antibodies reactive with
PT Mycobacterium tuberculosis antigens.
PT
XX Example 5; Page 91; 170pp; English.
XX
XX Sequences AAW70180-W70207 are N-terminal amino acid sequences of selected
XX culture filtrate proteins (CFPs) of M. tuberculosis. To obtain these
XX sequences, the proteins were resolved by 2-D PAGE, transferred to a
XX membrane by electrophoretogram, stained, destained, and lastly the
XX immobilised proteins were subjected to Edman degradation. This particular
XX sequence is from the 12kDa protein ESAR 6 and has been found to be
XX reactive with the antibody HYB 76-8. These antigens and antibodies that
XX form against them can be used for the early detection of mycobacterial
XX disease, particularly in subjects infected with human immunodeficiency
XX virus (HIV)
XX
XX Sequence 10 AA;
XX
XX Query Match 65.8%; Score 52; DB 2; Length 10;
XX Best Local Similarity 90.0%; Pred. No. 0.066;
XX Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 TEQOWNFAGI 11
XX |||||:||||
XX Db 1 TEQOWDFAGI 10
XX
XX RESULT 50
XX AAE05636
XX ID AAE05636 standard; peptide; 10 AA.
XX
XX AC AAE05636;
XX
XX 24-SEP-2001 (first entry)
XX
XX N-terminal peptide #1 obtained by 2D-PAGE analysis of CFPs.
XX
XX Mycobacterial disease; infection; 88-kDa protein; tuberculosis; TB;
KW culture filtrate protein; CFP; early antigen; serodiagnosis;
KW human immunodeficiency virus; HIV.
XX
XX Mycobacterium tuberculosis.
XX
XX US6245331-B1.
XX
XX 12-JUN-2001.
XX
XX 31-DEC-1997; 97US-00001984.
XX
XX 02-JAN-1997; 97US-0034003P.
XX
XX

```

PA (UYNV-) UNIV NEW YORK MEDICAL CENT.
 PA (COLS) UNIV COLORADO STATE.
 XX
 PI Laal S, Zolla-Pazner S, Belisle JT;
 XX WPI; 2001-424324/45.
 DR
 XX
 XX Detecting a mycobacterial disease (tuberculosis) in individuals comprise
 PT assaying a biological sample for the presence of anti-Mycobacterium
 PT tuberculosis antibodies or M. tuberculosis antigen-antibody complex.
 XX
 XX Claim 18; Col 58; 96pp; English.
 PS
 XX The present invention relates to a method for early detection of active
 CC mycobacterial disease or infection comprising assaying a biological fluid
 CC sample for the presence of early antibodies specific for an 88-kDa
 CC Mycobacterium tuberculosis (Mt) protein or immune complexes consisting of
 CC an 88-kDa M. tuberculosis protein antigen complexed with an antibody
 CC specific for the antigen. The method is useful for the early and rapid
 CC detection of mycobacterial disease, particularly tuberculosis, in
 CC individuals at heightened risk of developing tuberculosis. This
 CC method includes human immunodeficiency virus (HIV)-infected subjects
 CC or other immunocompromised individuals. The method is a rapid and
 CC inexpensive screening procedure for detecting mycobacterial disease. The
 CC present sequence is a N-terminal peptide of the product obtained by
 CC comparative 2D-PAGE analysis of culture filtrate proteins (CFPs) from
 CC three Mt type strains (H37Rv, H37Ra and Erdman), used in the
 CC serodiagnosis of tuberculosis (TB)
 CC
 XX Sequence 10 AA;

Query Match 65.8%; Score 52; DB 4; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.066;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 TEQOWNFAGI 11
 |||||:||||
 Db 1 TEQOWDFAGI 10

Search completed: May 4, 2006, 15:13:04
 Job time : 408.5 secs

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OM protein - protein search, using sw model

Run on: May 4, 2006, 14:59:41 ; Search time 322 Seconds
(without alignments)
20.468 Million cell updates/sec

Title: US-09-830-839-6

Perfect score: 77

Sequence: 1 WNFAGIEAAASAIQ 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : A Geneseq 21.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	77	100.0	15	3	Aay94595 Mycobacte
2	77	100.0	15	5	Abg30952 Mycobacte
3	77	100.0	15	5	Aao17433 Early sec
4	77	100.0	15	8	Adi33342 Mycobacte
5	77	100.0	20	4	Aae12275 Mycobacte
6	77	100.0	20	9	Aeb44911 Mycobacte
7	77	100.0	20	9	Aeb45107 M. tuberc
8	77	100.0	51	2	Aaw32339 Mycobacte
9	77	100.0	51	2	Aaw32466 Mycobacte
10	77	100.0	51	2	Aaw64334 Mycobacte
11	77	100.0	51	2	Aaw81701 M. tuberc
12	77	100.0	51	2	Aay38988 M. tuberc
13	77	100.0	51	2	Aay39131 M. tuberc
14	77	100.0	51	4	Aao1897 Mycobacte
15	77	100.0	51	5	Aae29716 Mycobacte
16	77	100.0	51	5	Aae17580 Mycobacte
17	77	100.0	95	2	Aaw11494 ESAT6. 3/
18	77	100.0	95	2	Aay29788 Mycobacte
19	77	100.0	95	2	Aay29890 Mycobacte
20	77	100.0	95	4	Aab35219 M. tubercu
21	77	100.0	95	5	Abg30968 Mycobacte
22	77	100.0	95	5	Aam50740 Mycobacte
23	77	100.0	95	7	Ade28550 Mycobacte
24	77	100.0	95	8	Adi33376 Mycobacte

25	77	100.0	95	8	ADN36323	Adn16323 Mycobacte
26	77	100.0	95	9	AEb45084	Aeb45084 M. tuberc
27	77	100.0	142	7	ADR28541	Ade28541 Human/Myc
28	77	100.0	145	7	ADR28543	Ade28543 Human/Myc
29	77	100.0	146	7	ADR28545	Ade28545 Human/Myc
30	77	100.0	146	7	ADR28547	Ade28547 Human/Myc
31	77	100.0	196	2	AAW29888	Aay29888 Mycobacte
32	77	100.0	403	2	AAW72943	Aaw72943 Mycobacte
33	77	100.0	403	2	AAW21963	Aay21963 Amino aci
34	77	100.0	404	2	AAW72942	Aaw72942 Mycobacte
35	77	100.0	404	2	AAW21962	Aay21962 Amino aci
36	71	92.2	15	9	AEb45087	Aeb45087 M. tuberc
37	71	92.2	19	2	AAW35548	Aaw35548 ESAT-6 an
38	66	85.7	16	7	ADL34423	Adl34423 MHC/HLA p
39	66	85.7	20	4	AAE12276	Aae12276 Mycobacte
40	62	80.5	17	3	AAE88581	Aae88581 Antigenic
41	60	77.9	13	4	AAE12274	Aae12274 Mycobacte
42	54	70.1	10	9	AEb45116	Aeb45116 M. tuberc
43	54	70.1	13	8	ADK00561	Adk00561 Immunogen
44	54	70.1	13	9	AEb44918	Aeb44918 M. tuberc
45	54	70.1	13	9	AEb44912	Aeb44912 Mycobacte
46	54	70.1	15	3	AAE94590	Aay94590 Mycobacte
47	54	70.1	15	5	ABG30951	Abg30951 Mycobacte
48	54	70.1	15	5	AAO17432	Aao17432 Early sec
49	54	70.1	15	8	ADI33341	Adi33341 Mycobacte
50	54	70.1	15	9	AEb45088	Aeb45088 M. tuberc
51	54	70.1	15	9	AEb45086	Aeb45086 M. tuberc
52	50	64.9	9	9	AEb44913	Aeb44913 Mycobacte
53	47	61.0	714	5	AEb55108	Aeb55108 Lactococc
54	44	57.1	10	9	AEb45117	Aeb45117 M. tuberc
55	44	57.1	15	3	AAE94599	Aay94599 Mycobacte
56	44	57.1	15	5	ABG30953	Abg30953 Mycobacte
57	44	57.1	15	8	ADI33343	Adi33343 Mycobacte
58	44	57.1	20	9	AEb45108	Aeb45108 M. tuberc
59	44	57.1	491	8	ADU07699	Adu07699 Amino aci
60	43	55.8	400	8	ADS43420	Ads43420 Bacterial
61	42.5	55.2	141	8	ADS15005	Ads15005 Pseudomon
62	42.5	55.2	556	7	ABO69047	Abog69047 Pseudomon
63	42	54.5	116	9	ABM94289	Abm94289 M. xanthu
64	42	54.5	158	5	ABP66046	Abp66046 Bifidobac
65	42	54.5	409	2	AAV35136	Aay35136 Chlamydia
66	41	53.2	149	8	ADI67173	Adi67173 Lactobaci
67	41	53.2	282	7	ADE12782	Ade12782 L. rhamno
68	41	53.2	443	8	ADN26405	Adn26405 Bacterial
69	41	53.2	445	6	ABU49075	Abu49075 Protein e
70	41	53.2	528	6	ABU22840	Abu22840 Protein e
71	41	53.2	540	5	ABE54282	Abbe54282 Lactococc
72	41	53.2	893	6	ABU41797	Abu41797 Protein e
73	40	51.9	68	6	ABM66077	Abm66077 Propionib
74	40	51.9	81	4	AAU42989	Aau42989 Propionib
75	40	51.9	81	6	ABM39508	Abm39508 Propionib
76	40	51.9	403	4	AAW40540	Aam40540 Human pol
77	40	51.9	1997	7	ADJ69207	Adj69207 Human hea
78	40	51.9	2293	3	AAV69197	Aay69197 Amino aci
79	39	50.6	9	2	AAW61077	Aaw61077 Amino aci
80	39	50.6	9	6	ABG75869	Abg75869 Mycobacte
81	39	50.6	9	8	ADQ88619	Adq88619 Mycobacte
82	39	50.6	140	3	AAE41828	Aae41828 Human ORF
83	39	50.6	162	4	AAW40271	Aam40271 Human pol
84	39	50.6	162	4	AAW39538	Aay39538 Human pro
85	39	50.6	162	4	AAW72606	Aay72606 Human Ele
86	39	50.6	162	7	ADE59120	Ade59120 Human Pro
87	39	50.6	209	3	AAE36643	Aag36643 Arabidops
88	39	50.6	212	8	ADR66010	Adr66010 Human pro
89	39	50.6	212	8	ADR66908	Adr66908 Human pro
90	39	50.6	221	3	AAV91434	Aay91434 Human sec
91	39	50.6	228	4	AAW42057	Aam42057 Human pol
92	39	50.6	232	3	AAE36642	Aag36642 Arabidops
93	39	50.6	234	4	ADM19867	Adm19867 Protein e
94	39	50.6	239	4	AAU21624	Aau21624 Novel hum
95	39	50.6	239	7	ADC46285	Adc46285 Human neo
96	39	50.6	253	4	AAW23550	Aam23550 Human EST
97	39	50.6	264	4	AAU19423	Aau19423 Human dia

98	39	50.6	270	9	ADW26647	Fructo-o-
99	39	50.6	317	4	ABG03344	Novel hum
100	39	50.6	321	6	ABG03344	Human nuc
101	39	50.6	323	8	ADT60159	Plant pol
102	39	50.6	324	5	ADP69069	Human pol
103	39	50.6	326	8	ADW13610	Human bet
104	39	50.6	329	8	ADY05386	Plant ful
105	39	50.6	335	4	ABG28518	Novel hum
106	39	50.6	413	7	ABO81042	Pseudomon
107	39	50.6	459	4	ADW19860	Protein e
108	39	50.6	514	4	AAB95225	Human pro
109	39	50.6	514	6	ABO07190	Human p53
110	39	50.6	514	8	ADJ75513	Marker ge
111	39	50.6	514	8	ADJ76263	Marker ge
112	39	50.6	514	9	ADY70514	Human bet
113	39	50.6	514	9	AEA23030	Mouse C21
114	39	50.6	514	9	AEA23030	Human C21
115	39	50.6	529	6	ABG39789	Protein e
116	39	50.6	563	4	ABG08370	Novel hum
117	39	50.6	654	3	ABY93662	Human GTP
118	39	50.6	654	4	AAB92621	Human pro
119	39	50.6	654	5	ABE97197	Novel hum
120	39	50.6	654	8	ABM80608	Tumour-hu
121	39	50.6	658	4	ABG47806	Human bet
122	39	50.6	674	6	ABG53104	Human put
123	39	50.6	753	4	ABG53104	Human pro
124	39	50.6	753	4	ABG51039	Human pro
125	39	50.6	753	8	AUS74299	PRO polyp
126	39	50.6	765	5	ADP25599	Streptoco
127	39	50.6	765	8	ADV89830	Streptoco
128	39	50.6	765	8	ADV81083	Streptoco
129	39	50.6	765	8	ADV83221	Streptoco
130	39	50.6	1137	6	ABU32051	Protein e
131	39	50.6	1138	7	ABO67057	Klebsiell
132	39	50.6	1444	8	ADN61347	Painibaci
133	39	50.6	1444	8	ADN21520	Painibaci
134	39	50.6	1487	8	ADP47746	Human inf
135	39	50.6	1866	8	ADP47905	Human inf
136	39	50.6	1866	8	ADP12959	Protein e
137	39	50.6	1866	9	ADV44759	Human nuc
138	39	50.6	1866	9	ADV4759	Human nuc
139	38	49.4	37	4	ADX72837	Plant ful
140	38	49.4	37	4	AMX19317	Peptide #
141	38	49.4	37	4	ABB38641	Peptide #
142	38	49.4	37	4	AMX32100	Peptide #
143	38	49.4	37	4	ABB23728	Protein #
144	38	49.4	37	4	AMW1815	Human bon
145	38	49.4	37	4	ABG53499	Human liv
146	38	49.4	37	4	ABG53499	Human liv
147	38	49.4	95	5	ABU05360	M. tuberc
148	38	49.4	185	7	ABO64819	Klebsiell
149	38	49.4	191	3	ABO64819	Klebsiell
150	38	49.4	297	6	ADN21921	Protein e
151	38	49.4	302	8	ADN24730	Bacterial
152	38	49.4	303	8	ADN21972	Bacterial
153	38	49.4	349	8	ADY10259	Plant ful
154	38	49.4	349	8	ADY10259	Plant ful
155	38	49.4	365	7	ABO81420	Pseudomon
156	38	49.4	366	3	ABY93237	An Escher
157	38	49.4	371	8	ADT60692	Plant pol
158	38	49.4	394	4	ABO04271	Novel hum
159	38	49.4	418	2	AMW44185	Chloramph
160	38	49.4	422	8	ADN73955	Arabidops
161	38	49.4	422	8	ADN73955	Thale cre
162	38	49.4	422	8	ADT56474	Thale cre
163	38	49.4	425	6	ABU45178	Protein e
164	38	49.4	435	7	ABO74474	Pseudomon
165	38	49.4	443	6	ABU47132	Protein e
166	38	49.4	443	6	ABU47132	Protein e
167	38	49.4	444	6	ABU14922	Protein e
168	38	49.4	444	6	ABU13889	Protein e
169	38	49.4	469	8	ADT60691	Plant pol
170	38	49.4	483	4	ABG06770	Novel hum

171	38	49.4	507	4	ABG070101
172	38	49.4	530	6	ADU919782
173	38	49.4	530	6	ADU909316
174	38	49.4	624	7	AD121578
175	38	49.4	702	6	ADA55074
176	38	49.4	764	5	AD808358
177	38	49.4	844	5	AB892005
178	38	49.4	962	6	ADA27163
179	38	49.4	1146	5	ABP53245
180	38	49.4	1549	7	ABM88721
181	38	49.4	1684	4	ABM52738
182	37.5	48.7	403	3	ABG53244
183	37.5	48.7	403	3	ABG34040
184	37.5	48.7	435	3	ABG35243
185	37.5	48.7	435	3	ABG34039
186	37.5	48.7	500	3	ABG34038
187	37.5	48.7	519	8	ADY09033
188	37	48.1	94	4	AAQ00586
189	37	48.1	136	3	AAQ05108
190	37	48.1	136	3	ABG20433
191	37	48.1	140	6	AB000881
192	37	48.1	153	3	ABG34922
193	37	48.1	153	9	AD4217687
194	37	48.1	183	3	AAQ54107
195	37	48.1	183	3	ABG20432
196	37	48.1	183	8	ADY57773
197	37	48.1	209	7	ABD575267
198	37	48.1	223	8	ADX52142
199	37	48.1	256	6	ABW15925
200	37	48.1	295	6	ABW67411
201	37	48.1	320	3	AAV69157
202	37	48.1	360	3	AAV69157
203	37	48.1	360	3	ADY71869
204	37	48.1	377	3	ADY75615
205	37	48.1	382	6	ABU21496
206	37	48.1	398	8	ABG66648
207	37	48.1	404	8	ADX91164
208	37	48.1	472	8	AD5277779
209	37	48.1	472	9	ABW96262
210	37	48.1	475	7	ABD72092
211	37	48.1	479	7	ADG33826
212	37	48.1	490	5	ABB55389
213	37	48.1	496	5	ABB55385
214	37	48.1	542	8	ADN99439
215	37	48.1	550	4	ABG69049
216	37	48.1	551	2	AAW61643
217	37	48.1	553	5	ABG49057
218	37	48.1	567	9	AEA49206
219	37	48.1	770	5	ABF25600
220	37	48.1	898	5	ABM92362
221	37	48.1	947	7	ABD72589
222	37	48.1	981	9	ABM90649
223	37	48.1	1138	7	ABD77206
224	37	48.1	1223	8	ABG44058
225	37	48.1	1321	6	ADA22697
226	37	48.1	1438	8	ADQ03082
227	37	48.1	1648	5	ABB54925
228	37	48.1	1649	8	AD529427
229	37	48.1	1743	4	AAU03368
230	37	48.1	1743	5	ABG92713
231	37	48.1	1774	5	ABG92809
232	36.5	47.4	621	7	ADMO5724
233	36	46.8	98	7	AD49417
234	36	46.8	98	8	AD240557
235	36	46.8	132	6	AAU11638
236	36	46.8	132	6	AAW68491
237	36	46.8	152	6	ABU46315
238	36	46.8	229	4	AAU30165
239	36	46.8	240	8	ADN21821
240	36	46.8	242	8	ADN24580
241	36	46.8	242	8	ADN24580
242	36	46.8	252	7	ADC01171
243	36	46.8	252	8	ADRS1215

Abg07015	Novel human
Abul9782	Protein e
Agd09316	Novel pro
Adi21578	Novel hum
Ada55074	Human pro
Abg98305	Novel pro
Abb92005	Herbicida
Adp27163	ARVCF pro
App53245	Human MDP
Abm87231	Rice abio
Abm52738	Escherich
Agg35244	Zea maye
Agg34040	Zea maye
Agg35243	Zea maye
Agg34039	Zea maye
Agg34038	Zea maye
AdgY09033	Plant full
Aac00586	Human pol
Agd45108	Arabidops
Agd20433	Arabidops
Abo000881	POLYPEPT
Aab43922	Human can
Adi217687	Human h25
Agd45107	Arabidops
Agd20432	Arabidops
Adi25773	Plant pol
AboY75267	Pseudomon
Adi252142	Der fl al
Ahm15925	Mycobacte
Abm67411	Photorhab
Abm65780	Bifidobac
Aay69157	Peptidea
Adi217689	Human h25
Abx75615	Neisseria
Abu21496	Protein e
Adi26648	Plant full
Adx91164	Plant full
Adx827779	Bacterialia
Abm96262	M. xanthu
AboY72092	Pseudomon
Agd33826	Actinomyc
Abb55389	Lactococc
Abb55385	Lactococc
Adi99439	Novel hum
Abm9049	Hordeum v
Aaw61643	Nicotiana
Abb49057	Listeria
Aea49206	L. rhamnu
Abp25600	Streptococ
Abm92362	M. xanthu
AboY72589	Pseudomon
Abm90649	M. xanthu
AboY77206	Pseudomon
Abd44058	Bacterial
Adg22697	A. gossyp
Adg30382	P. aerugi
Abb54925	Lactococc
Adi29427	Bacterial
Abu92318	Cochlioba
Agb92713	Protein e
Abg92809	C. hetero
Adm5724	Human pro
Adi49417	Multi-epi
Adi24095	Spigene c
Adi40597	HCV PC3
Abu11638	Human MDP
Abm11638	Human MDP
Aaw68491	Heavy char
Aau46451	Protein e
Aau30155	Novel hu
Adm21821	Bacterial
Adm44590	Bacterial
Adc01171	Enterococ
Adi51215	Anti-bio

244	36	46.8	254	2	AAW42382	Aaw42382 Thermococ	317	36	46.8	1522	9	ADW07657	Adw07657 Human MPF
245	36	46.8	254	6	AAO27236	Aao27236 Thermococ	318	36	46.8	1522	9	ADY70460	Ady70460 Human bet
246	36	46.8	294	7	ABO64416	Ab064416 Klebsiell	319	36	46.8	1522	9	ADY70718	Ady70718 Human nlc
247	36	46.8	303	5	ABP26130	Abp26130 Streptoco	320	36	46.8	1534	7	ADF04897	Adf04897 Bacterial
248	36	46.8	308	7	ADA49421	Ada49421 Multi-epi	321	36	46.8	1547	6	ABU96680	Abu96680 Human nuc
249	36	46.8	308	7	ADA49423	Ada49423 Multi-epi	322	36	46.8	1562	5	ABP43703	Abp43703 Alpha -NA
250	36	46.8	308	8	ADO24101	Ado24101 Epigene c	323	36	46.8	2154	8	ADN73223	Adn73223 Thale cre
251	36	46.8	308	8	ADO24099	Ado24099 Epigene c	324	36	46.8	2154	8	ADT04691	Adt04691 Thale cre
252	36	46.8	308	9	ADX40834	Adx40834 HCV fusio	325	36	46.8	3413	8	AAW52849	Aaw52849 A. medite
253	36	46.8	308	9	ADZ40603	Adz40603 HCV 4312	326	36	46.8	4464	8	ADN22366	Adn22366 Bacterial
254	36	46.8	308	9	ADZ40601	Adz40601 HCV 2431	327	35.5	46.1	467	7	ABO80983	Ab080983 Pseudomon
255	36	46.8	314	8	ADO80560	Ado80560 Caulobact	328	35.5	46.1	514	8	ADS21826	Ads21826 Bacterial
256	36	46.8	319	3	AG04710	Ag04710 Arabidops	329	35.5	46.1	539	8	ADS27740	Ads27740 Bacterial
257	36	46.8	321	3	AG04709	Ag04709 Arabidops	330	35.5	46.1	679	6	AAU33586	Aau33586 Pseudomon
258	36	46.8	321	3	ABO67390	Ab067390 Klebsiell	331	35.5	46.1	679	6	ABU15576	Abu15576 Protein e
259	36	46.8	328	7	ABO64469	Ab064469 Klebsiell	332	35	45.5	15	9	ABE45089	Aeb45089 M. tuberc
260	36	46.8	340	3	AG04708	Ag04708 Arabidops	333	35	45.5	29	2	AAR36448	Aar36448 DFI-3(21-
261	36	46.8	359	6	ABU44190	Abu44190 Protein e	334	35	45.5	29	2	AAR34688	Aar34688 DFI-3(21-
262	36	46.8	368	7	ABO67236	Ab067236 Klebsiell	335	35	45.5	29	2	AAR51796	Aar51796 Der f I d
263	36	46.8	376	4	ABG60245	Abg60245 Rice form	336	35	45.5	29	2	AAR51733	Aar51733 Der p I d
264	36	46.8	383	6	ABU25869	Abu25869 Protein e	337	35	45.5	29	2	AAW717125	Aaw717125 Dermatoph
265	36	46.8	383	8	ADY76271	Ady76271 Plant ful	338	35	45.5	29	2	AAW71971	Aaw71971 Dermatoph
266	36	46.8	383	8	ADY77941	Ady77941 Plant ful	339	35	45.5	29	2	AAW71914	Aaw71914 Dermatoph
267	36	46.8	384	5	ABB93475	Abb93475 Herbicida	340	35	45.5	29	2	AAW50425	Aaw50425 Dermatoph
268	36	46.8	384	5	AAE37612	Aae37612 Arabidops	341	35	45.5	29	2	AAW50362	Aaw50362 Dermatoph
269	36	46.8	386	8	ADX96587	Adx96587 Plant ful	342	35	45.5	29	4	AAU19028	Aau19028 T-cell ep
270	36	46.8	389	7	ABO62023	Ab062023 Klebsiell	343	35	45.5	29	4	AAU18965	Aau18965 T-cell ep
271	36	46.8	390	4	AAW39625	Aaw39625 Human pol	344	35	45.5	47	5	ABM96244	Abm96244 M. xanthu
272	36	46.8	394	9	ADY61001	Ady61001 Abiotic s	345	35	45.5	55	5	ABP31209	Abp31209 Human hyd
273	36	46.8	396	4	AAW41411	Aaw41411 Human pol	346	35	45.5	58	2	AAW12525	Aaw12525 Human 5'
274	36	46.8	401	8	ADY13351	Ady13351 Plant ful	347	35	45.5	80	3	AAW00067	Aaw00067 Human sec
275	36	46.8	404	4	AAW67128	Aaw67128 Amino aci	348	35	45.5	81	8	ADR87222	Adr87222 Dust mite
276	36	46.8	405	4	ABG22253	Abg22253 Novel hum	349	35	45.5	86	4	AAU55727	Aau55727 Propionib
277	36	46.8	406	8	ADY13656	Ady13656 Plant ful	350	35	45.5	86	6	ABW52246	Abw52246 Propionib
278	36	46.8	420	8	ADX66772	Adx66772 Plant ful	351	35	45.5	90	4	AAU30492	Aau30492 Novel hum
279	36	46.8	429	7	ADH85932	Adh85932 Enterococ	352	35	45.5	90	5	ABU60995	Abu60995 Lung spec
280	36	46.8	434	4	AAW93837	Aaw93837 Human pro	353	35	45.5	94	3	AAW00065	Aaw00065 Human sec
281	36	46.8	458	6	AAW51504	Aaw51504 Propionib	354	35	45.5	94	3	AAW00054	Aaw00054 Human sec
282	36	46.8	458	6	ABW51623	Abw51623 Propionib	355	35	45.5	97	3	AAW00068	Aaw00068 Human sec
283	36	46.8	455	7	ADE50886	Ade50886 V. parado	356	35	45.5	99	3	AAW00055	Aaw00055 Human sec
284	36	46.8	466	7	ADG33812	Adg33812 Actinomyc	357	35	45.5	99	3	AAW00046	Aaw00046 Human sec
285	36	46.8	470	6	ABU38985	Abu38985 Protein e	358	35	45.5	99	3	AAW00066	Aaw00066 Human sec
286	36	46.8	476	7	ADG33824	Adg33824 Actinomyc	359	35	45.5	100	4	ABG23455	Abg23455 Novel hum
287	36	46.8	477	7	ADG33830	Adg33830 Actinomyc	360	35	45.5	102	3	AAW00071	Aaw00071 Human sec
288	36	46.8	482	7	ADG33828	Adg33828 Actinomyc	361	35	45.5	102	3	AAW00047	Aaw00047 Human sec
289	36	46.8	483	7	ABO66501	Ab066501 Klebsiell	362	35	45.5	103	3	AAW00061	Aaw00061 Human sec
290	36	46.8	523	4	ABB76814	Abb76814 Brassica	363	35	45.5	104	7	ABM89099	Abm89099 Rice abio
291	36	46.8	552	4	ABB71495	Abb71495 Drosophil	364	35	45.5	104	7	ABM89099	Abm89099 Rice abio
292	36	46.8	552	4	ABB71493	Abb71493 Drosophil	365	35	45.5	106	3	AAW03722	Aaw03722 Human sec
293	36	46.8	582	3	AAW07557	Aaw07557 Protein e	366	35	45.5	107	3	AAW03723	Aaw03723 Human sec
294	36	46.8	612	9	ABE18186	Aeb18186 Gibberell	367	35	45.5	107	3	AAW03724	Aaw03724 Human sec
295	36	46.8	689	3	AAW91312	Aaw91312 Group B S	368	35	45.5	115	3	AAW00051	Aaw00051 Human sec
296	36	46.8	700	4	ABW60376	Abw60376 Drosophil	369	35	45.5	116	3	AAW00050	Aaw00050 Human sec
297	36	46.8	721	6	ABU01671	Abu01671 S. pneumo	370	35	45.5	117	2	AAW22358	Aaw22358 Protein e
298	36	46.8	721	6	ABP81401	Abp81401 Streptoco	371	35	45.5	117	2	AAW38623	Aaw38623 Human hea
299	36	46.8	721	6	ADT50119	Adt50119 S.pneumon	372	35	45.5	117	2	AAW03950	Aaw03950 DNA fragm
300	36	46.8	724	5	ABP26011	Abp26011 Streptoco	373	35	45.5	117	2	AAW41113	Aaw41113 Human VHI
301	36	46.8	724	5	ABP26011	Abp26011 Streptoco	374	35	45.5	117	2	AAW24777	Aaw24777 Human VHI
302	36	46.8	727	5	ABP27424	Abp27424 Streptoco	375	35	45.5	117	2	AAW40381	Aaw40381 Amino aci
303	36	46.8	727	8	ADU69633	Adu69633 S.agalact	376	35	45.5	118	4	AAW78637	Aaw78637 Human pro
304	36	46.8	727	8	ADV89552	Adv89552 Streptoco	377	35	45.5	121	3	AAW00049	Aaw00049 Human sec
305	36	46.8	727	8	ADV82963	Adv82963 Streptoco	378	35	45.5	121	3	AAW00063	Aaw00063 Human sec
306	36	46.8	727	8	ADV80805	Adv80805 Streptoco	379	35	45.5	121	3	AAW00059	Aaw00059 Human sec
307	36	46.8	730	8	ADN17946	Adn17946 Bacterial	380	35	45.5	126	3	AAW00057	Aaw00057 Human sec
308	36	46.8	746	9	ABE27185	Aeb27185 Pinus rad	381	35	45.5	126	3	AAW00069	Aaw00069 Human sec
309	36	46.8	759	9	ABM96962	Abm96962 M. xanthu	382	35	45.5	126	3	AAW00053	Aaw00053 Human sec
310	36	46.8	788	7	ABM85648	Abm85648 Mouse pro	383	35	45.5	129	3	AAW00058	Aaw00058 Human sec
311	36	46.8	912	8	ABW52560	Abw52560 Escherich	384	35	45.5	129	3	AAW00052	Aaw00052 Human sec
312	36	46.8	943	8	ADJ48752	Adj48752 Oil-assoc	385	35	45.5	129	3	AAW00070	Aaw00070 Human sec
313	36	46.8	943	8	ADJ50227	Adj50227 Oil-assoc	386	35	45.5	133	3	AAW64724	Aaw64724 Human 5'
314	36	46.8	994	7	ABM87489	Abm87489 Rice abio	387	35	45.5	133	8	ADU72288	Adu72288 Signal pe
315	36	46.8	1120	6	ABU15091	Abu15091 Protein e	388	35	45.5	133	9	ADZ73279	Adz73279 Human inc
316	36	46.8	1444	4	ABB59604	Abb59604 Drosophil	389	35	45.5	138	6	ABU9684	Abu9684 Alpha-2 a

390	35	45.5	140	6	ABU89683	Abu89683 Alpha-2 a	463	35	45.5	245	2	AAy50356	AAy50356 Dermatoph
391	35	45.5	141	6	ABU25648	Abu25648 Protein e	464	35	45.5	245	4	AAU18959	AAU18959 House dus
392	35	45.5	142	3	AAy64711	Human 5'	465	35	45.5	248	5	ABG17812	ABG17812 European
393	35	45.5	143	3	AAyG00664	Human sec	466	35	45.5	258	4	ABG17521	ABG17521 Novel hum
394	35	45.5	142	3	AAyG00060	Human sec	467	35	45.5	261	8	ADY13514	ADY13514 Plant ful
395	35	45.5	142	3	ADU72275	Signal pe	468	35	45.5	263	3	AAg36620	AAg36620 Arabidops
396	35	45.5	142	3	ADZ73866	Human inc	469	35	45.5	268	3	ADT59875	ADT59875 Plant pol
397	35	45.5	143	3	AAyG00048	Human sec	470	35	45.5	271	3	AAg36619	AAg36619 Arabidops
398	35	45.5	150	9	ADY34110	Monoclonal	471	35	45.5	276	3	AAy98466	AAy98466 Partial s
399	35	45.5	153	6	ABR41572	Human Dir	472	35	45.5	279	3	AAy98980	AAy98980 Streptoco
400	35	45.5	153	8	ADR87233	Chimeric	473	35	45.5	279	8	ADV80233	ADV80233 Streptoco
401	35	45.5	158	5	ABP28339	Streptoco	474	35	45.5	282	2	AAr78162	AAr78162 Recombina
402	35	45.5	159	4	ABP28332	O. sativa	475	35	45.5	282	2	AAr78163	AAr78163 Recombina
403	35	45.5	159	7	AAAB47472	Rice sorb	476	35	45.5	282	8	ADL27398	ADL27398 PolyPepti
404	35	45.5	159	9	AAE33528	Rice sorb	477	35	45.5	284	2	AAy27229	AAy27229 Amino aci
405	35	45.5	159	9	ADY33668	Rice sorb	478	35	45.5	288	8	ADR97743	ADR97743 European
406	35	45.5	160	5	ABP28968	Streptoco	479	35	45.5	288	8	ABR91643	ABR91643 Microbial
407	35	45.5	165	3	AAAB53325	Human col	480	35	45.5	292	5	ABP30086	ABP30086 Streptoco
408	35	45.5	185	4	ADX78142	Plant ful	481	35	45.5	292	8	ADV82357	ADV82357 Streptoco
409	35	45.5	188	4	AAU14524	Human nov	482	35	45.5	296	6	ABJ25437	ABJ25437 Aspergill
410	35	45.5	188	4	AAU14523	Human nov	483	35	45.5	296	6	ABJ26037	ABJ26037 Aspergill
411	35	45.5	188	8	ADH80842	Human pol	484	35	45.5	296	8	ADQ30830	ADQ30830 E cunicul
412	35	45.5	190	8	ADH80841	Human pol	485	35	45.5	296	8	ADR86486	ADR86486 Aspergill
413	35	45.5	193	3	AAg33912	Arabidops	486	35	45.5	296	9	ADY78295	ADY78295 D. pteron
414	35	45.5	196	3	AAg33911	Arabidops	487	35	45.5	297	9	ADY78307	ADY78307 D. pteron
415	35	45.5	211	2	AAy25678	Euroglyph	488	35	45.5	298	9	ADY78280	ADY78280 D. pteron
416	35	45.5	211	7	ADY25679	Euroglyph	489	35	45.5	299	9	ADY78304	ADY78304 D. pteron
417	35	45.5	212	7	ADY25678	Euroglyph	490	35	45.5	299	9	ADY78301	ADY78301 D. pteron
418	35	45.5	212	7	ADY25679	Euroglyph	491	35	45.5	302	4	AAE98348	AAE98348 D. pteron
419	35	45.5	212	8	ADY05206	Plant ful	492	35	45.5	302	4	AAE98330	AAE98330 D. pteron
420	35	45.5	216	8	ADY07502	Plant ful	493	35	45.5	302	4	AAE98346	AAE98346 D. pteron
421	35	45.5	218	9	ADY78283	D. pteron	494	35	45.5	302	5	AAE50623	AAE50623 Recombina
422	35	45.5	220	8	ADN26819	Bacterial	495	35	45.5	302	6	AAE36748	AAE36748 Dermatoph
423	35	45.5	222	2	AAAS2742	Protein a	496	35	45.5	302	6	AAE36753	AAE36753 Dermatoph
424	35	45.5	222	4	AAU07746	House dus	497	35	45.5	302	6	AAE36747	AAE36747 Dermatoph
425	35	45.5	222	4	AAU07748	House dus	498	35	45.5	302	6	AAE36752	AAE36752 Dermatoph
426	35	45.5	222	4	AAU07747	House dus	499	35	45.5	302	6	AAE36750	AAE36750 Dermatoph
427	35	45.5	222	5	AAAB98347	D. pteron	500	35	45.5	302	6	AAE36751	AAE36751 Dermatoph
428	35	45.5	222	5	ABG67025	House dus	501	35	45.5	302	8	ADR97695	ADR97695 European
429	35	45.5	222	5	ABG67032	House dus	502	35	45.5	302	8	ADR97703	ADR97703 European
430	35	45.5	222	5	ABG67027	House dus	503	35	45.5	302	8	ADR97692	ADR97692 European
431	35	45.5	222	5	ABG67033	House dus	504	35	45.5	302	8	ADR97701	ADR97701 European
432	35	45.5	222	5	ABG67026	House dus	505	35	45.5	302	8	ADR97699	ADR97699 European
433	35	45.5	222	5	ABG67029	House dus	506	35	45.5	302	8	ADR97737	ADR97737 European
434	35	45.5	222	5	ABG67028	House dus	507	35	45.5	302	8	ADR97737	ADR97737 European
435	35	45.5	222	5	ABG67024	House dus	508	35	45.5	302	8	ADR97697	ADR97697 European
436	35	45.5	222	5	ABG67031	House dus	509	35	45.5	302	8	ADR97697	ADR97697 European
437	35	45.5	222	5	ABG67023	House dus	510	35	45.5	302	9	ADY78286	ADY78286 D. pteron
438	35	45.5	222	5	ABG67034	House dus	511	35	45.5	302	9	ADY78292	ADY78292 D. pteron
439	35	45.5	222	5	AAO20568	Cysteine	512	35	45.5	302	9	ADY78289	ADY78289 D. pteron
440	35	45.5	222	5	ABB98533	Cysteine	513	35	45.5	303	2	AAr78161	AAr78161 Recombina
441	35	45.5	222	5	ADK52140	Diet plal	514	35	45.5	303	2	AAr78160	AAr78160 Recombina
442	35	45.5	222	8	ADR87225	Diet mice	515	35	45.5	303	4	AAE98338	AAE98338 D. farina
443	35	45.5	222	8	ADU49578	D. pteron	516	35	45.5	303	4	AAE98327	AAE98327 D. farina
444	35	45.5	223	2	AAr78159	Recombina	517	35	45.5	303	4	AAE98335	AAE98335 D. farina
445	35	45.5	223	4	AAAB98328	D. farina	518	35	45.5	303	4	AAE98344	AAE98344 D. farina
446	35	45.5	223	4	AAAB98336	D. farina	519	35	45.5	303	4	AAE98337	AAE98337 D. farina
447	35	45.5	223	4	AAAB98345	D. pteron	520	35	45.5	303	4	AAE98349	AAE98349 D. farina
448	35	45.5	223	4	AAAB98331	D. pteron	521	35	45.5	303	9	ADY78316	ADY78316 D. pteron
449	35	45.5	223	4	AAAB98339	D. farina	522	35	45.5	303	9	ADY78319	ADY78319 D. pteron
450	35	45.5	223	4	AAAB98340	D. farina	523	35	45.5	303	9	ADY78310	ADY78310 D. pteron
451	35	45.5	224	8	ADS28574	Bacterial	524	35	45.5	303	9	ADY78298	ADY78298 D. pteron
452	35	45.5	225	3	AAAG06543	Arabidops	525	35	45.5	304	3	AAO6541	AAO6541 Tick alle
453	35	45.5	225	3	AAAG06542	Arabidops	526	35	45.5	307	3	AAO6541	AAO6541 Arabidops
454	35	45.5	229	3	AAAG06542	Arabidops	527	35	45.5	309	3	AAO6541	AAO6541 Arabidops
455	35	45.5	242	7	AAAP86881	Rice abio	528	35	45.5	315	2	AAy08594	AAy08594 D. pteron
456	35	45.5	245	1	AAAP94864	Pre pro D	529	35	45.5	319	2	AAy25588	AAy25588 D. farina
457	35	45.5	245	2	AAAT22433	Der p I a	530	35	45.5	319	6	ABB80127	ABB80127 Derf fl.
458	35	45.5	245	2	AAAR39359	Dermatoph	531	35	45.5	319	7	ADC34838	ADC34838 House dus
459	35	45.5	245	2	AAAR51727	Der p I	532	35	45.5	319	9	ABM95355	ABM95355 M. xanthu
460	35	45.5	245	2	AAAR47063	Protein a	533	35	45.5	320	2	AAr49920	AAr49920 Protein a
461	35	45.5	245	2	AAAR66545	Der p I a	534	35	45.5	320	2	AAy25580	AAy25580 D. pteron
462	35	45.5	245	2	AAW71908	Dermatoph	535	35	45.5	320	2	AAy25580	AAy25580 D. pteron

536	35	45.5	320	2	AAY08592	D. pteron	609	35	45.5	476	6	ABU08022	Monoclonal
537	35	45.5	320	2	AAY08593	D. pteron	610	35	45.5	476	7	ADF65788	Human ant
538	35	45.5	320	2	AAY08595	D. pteron	611	35	45.5	476	7	ADM05603	Human pro
539	35	45.5	320	4	AAB98329	D. pteron	612	35	45.5	476	8	ADJ92523	Human SO5
540	35	45.5	320	6	ABU11147	House dus	613	35	45.5	476	8	ADV99723	Human rab
541	35	45.5	320	6	ABB80128	Der pl. 6	614	35	45.5	477	7	ADM05604	Human pro
542	35	45.5	320	6	ABP98482	Amino aci	615	35	45.5	477	8	ADQ65990	Novel hum
543	35	45.5	320	7	ADC34830	House dus	616	35	45.5	477	8	ADR10091	Human pro
544	35	45.5	320	7	ADE38098	European	617	35	45.5	477	8	ADU07675	Pseudomon
545	35	45.5	320	8	ADK52158	Full leng	618	35	45.5	481	7	ABO82916	Pseudomon
546	35	45.5	320	8	ADM57314	Modular a	619	35	45.5	482	7	ADG10730	Human STA
547	35	45.5	320	8	ADQ14389	European	620	35	45.5	486	7	ADG10842	Human STA
548	35	45.5	320	8	ADS2096	Major mit	621	35	45.5	489	5	AAU93047	Arabidops
549	35	45.5	320	8	ADS14367	Dust mite	622	35	45.5	489	7	ADBE37227	Plant yie
550	35	45.5	320	8	ADU49570	D. pteron	623	35	45.5	489	8	ADI41757	Plant tra
551	35	45.5	320	9	ADY63827	Dermatoph	624	35	45.5	489	9	ADW78303	Xenopus l
552	35	45.5	321	2	AAR22431	Der f i a	625	35	45.5	490	3	AYG68725	Putative
553	35	45.5	321	2	AAR39361	Dermatoph	626	35	45.5	495	4	AGG89956	C. glutami
554	35	45.5	321	2	AAR51729	Der f i.	627	35	45.5	495	7	ADL65675	C. glutami
555	35	45.5	321	2	AAR47065	Protein a	628	35	45.5	495	7	ABO72763	Pseudomon
556	35	45.5	321	2	AAR78165	Recombina	629	35	45.5	504	4	ABB66372	Drosophil
557	35	45.5	321	2	AAR78164	Recombina	630	35	45.5	506	9	ADW70231	Thale cre
558	35	45.5	321	2	AAW71910	Dermatoph	631	35	45.5	506	9	AEBS1410	Phosphome
559	35	45.5	321	4	AAY50358	Dermatoph	632	35	45.5	519	8	ADQ66844	Novel hum
560	35	45.5	321	4	AAU18961	House dus	633	35	45.5	522	3	AYG68677	Amino aci
561	35	45.5	321	5	ABG71810	American	634	35	45.5	524	9	AEA44228	Anti-TPO
562	35	45.5	321	5	ABG90146	C glutami	635	35	45.5	524	9	AEA44189	Anti-TPO
563	35	45.5	321	8	ADQ14390	American	636	35	45.5	524	9	AEA43937	Anti-TPO
564	35	45.5	321	8	ADS2097	Major mit	637	35	45.5	524	9	AEA44195	Anti-TPO
565	35	45.5	321	8	ADS14368	Dust mite	638	35	45.5	524	9	AEA44195	Anti-TPO
566	35	45.5	321	8	ADU49572	D. farina	639	35	45.5	525	5	ABB91103	Herbicida
567	35	45.5	321	8	AAR76479	Recombina	640	35	45.5	525	6	ADB08798	Alloicoc
568	35	45.5	321	5	ABG90146	C glutami	641	35	45.5	529	7	ADL22688	Human dis
569	35	45.5	321	2	AAY08596	D. pteron	642	35	45.5	531	8	ADX76565	Plant ful
570	35	45.5	321	2	AAY08597	D. pteron	643	35	45.5	533	8	ADX73490	Plant ful
571	35	45.5	321	2	ADS21047	Bacterial	644	35	45.5	533	8	ADQ30799	Drosophil
572	35	45.5	321	7	ABO68926	Pseudomon	645	35	45.5	553	8	ADQ30799	E. cunicul
573	35	45.5	321	8	ADQ18002	Human sof	646	35	45.5	601	8	ADN18270	Bacterial
574	35	45.5	321	8	ADS26285	Bacterial	647	35	45.5	627	7	ADBE97370	Human imm
575	35	45.5	321	8	ADS26285	Bacterial	648	35	45.5	627	9	ADY16877	PRO polyp
576	35	45.5	321	8	ADS27044	Bacterial	649	35	45.5	627	9	ADY05578	Plant ful
577	35	45.5	321	8	ADY23310	Plant ful	650	35	45.5	697	8	ADN61375	Pseudomon
578	35	45.5	321	7	ABM87702	Rice abio	651	35	45.5	744	7	ABO82199	Pseudomon
579	35	45.5	321	5	AAU93107	Arabidops	652	35	45.5	749	7	ABO68131	Pseudomon
580	35	45.5	321	7	ADD30102	Plant yie	653	35	45.5	786	6	ADBE9272	Phototrab
581	35	45.5	321	8	ADI41985	Plant tra	654	35	45.5	831	8	ADS21941	Bacterial
582	35	45.5	381	8	ADI42928	Plant tra	655	35	45.5	847	7	ADC94547	E. faeciu
583	35	45.5	384	7	ADP06059	Bacterial	656	35	45.5	860	7	ADC38519	MHC A pro
584	35	45.5	394	7	ADP070928	Pseudomon	657	35	45.5	873	6	ABU09779	Maidennal
585	35	45.5	399	8	ADN17990	Bacterial	658	35	45.5	873	8	ADM98978	Diterpene
586	35	45.5	405	8	ADK67297	Plant ful	659	35	45.5	903	2	AAW37389	Human add
587	35	45.5	406	8	ADK67297	Plant ful	660	35	45.5	903	2	AAW37391	Human add
588	35	45.5	409	8	ADK78317	Aminotran	661	35	45.5	979	6	ABU19448	Protein e
589	35	45.5	423	5	ABP40691	Staphyloc	662	35	45.5	993	6	ABM69310	Phototrab
590	35	45.5	423	6	ABU15234	Protein e	663	35	45.5	1056	6	AAU24308	Cycloceit
591	35	45.5	423	6	ADSO7970	Staphyloc	664	35	45.5	1066	6	ABU45347	Protein e
592	35	45.5	426	8	ADS28853	Bacterial	665	35	45.5	1116	6	ABM69308	Phototrab
593	35	45.5	428	4	ABG17824	Novel hum	666	35	45.5	1116	6	ABU21548	Protein e
594	35	45.5	437	8	ADT57458	Plant pol	667	35	45.5	1120	6	ABU47563	Protein e
595	35	45.5	449	3	AAU96476	Soybean 4	668	35	45.5	1120	6	ABU46980	Protein e
596	35	45.5	454	7	ABO81267	Pseudomon	669	35	45.5	1127	6	ABM69131	Phototrab
597	35	45.5	455	2	AAW41076	P. furios	670	35	45.5	1131	6	ABM67711	Phototrab
598	35	45.5	459	4	ABB62646	Drosophil	671	35	45.5	1265	2	AAW68594	Human met
599	35	45.5	459	7	ADJ37943	D melanog	672	35	45.5	1265	7	ADI39110	Homo eapi
600	35	45.5	467	2	AAW41077	T. litora	673	35	45.5	1285	7	ADJ68745	Human hea
601	35	45.5	469	8	ADS44861	Bacterial	674	35	45.5	1267	2	AAU4232	Rickettsi
602	35	45.5	473	4	AAU64475	Human typ	675	35	45.5	1422	3	AAU82069	Hepatitis
603	35	45.5	473	4	AAU64471	Human typ	676	35	45.5	1422	3	AAU82069	Hepatitis
604	35	45.5	473	4	AAU64469	Human typ	677	35	45.5	1532	2	AAU27231	Amino aci
605	35	45.5	473	4	AAU64473	Human typ	678	35	45.5	1566	2	AAU79643	Immunodom
606	35	45.5	473	7	ADJ53182	Rebeccamy	679	35	45.5	1572	5	ABP65360	Bifidobac
607	35	45.5	473	7	ADM05599	Human pro	680	35	45.5	1669	4	ABM64003	Drosophil
608	35	45.5	476	2	AAR31023	Antibody	681	35	45.5	1858	9	ABM93444	M. xanthu

682	35	45.5	1859	8	ADS30492	AdS30492 Bacterial
683	35	45.5	1978	2	AAV27230	Aav27230 Amino aci
684	35	45.5	1981	2	AAW42634	Aaw42634 Protein e
685	35	45.5	2004	6	ABP79896	Abp79896 N. gonorr
686	35	45.5	2004	6	ABP76777	Abp76777 N. gonorr
687	35	45.5	2015	5	ABH78067	Abh78067 Amino aci
688	35	45.5	2015	5	ABU37848	Abu37848 Protein e
689	35	45.5	2015	9	ABH91664	Abh91664 Microbial
690	35	45.5	2079	2	AAW59926	Aaw59926 GAP prote
691	35	45.5	2079	8	ADN19371	Adn19371 Bacterial
692	35	45.5	4067	8	ADS73542	Ads73542 Glycopept
693	34.5	44.8	53	4	AAW58337	Aaw58337 Human bra
694	34.5	44.8	53	4	AAW6208	Aaw6208 Peptide #
695	34.5	44.8	99	2	AAV13208	Aav13208 Human sec
696	34.5	44.8	161	7	ABO73930	AbO73930 Pseudomon
697	34.5	44.8	212	3	AAAB43182	AaB43182 Human ORF
698	34.5	44.8	212	4	AAAB55882	AaB55882 Human ORF
699	34.5	44.8	212	4	AAAB36585	AaB36585 Human FLE
700	34.5	44.8	294	3	AAAG14555	Aag14555 Arabidops
701	34.5	44.8	294	3	AAAG27442	Aag27442 Arabidops
702	34.5	44.8	294	3	AAAG27735	Aag27735 Arabidops
703	34.5	44.8	324	3	AAAG27734	Aag27734 Arabidops
704	34.5	44.8	324	3	AAAG27441	Aag27441 Arabidops
705	34.5	44.8	324	3	AAAG14554	Aag14554 Arabidops
706	34.5	44.8	324	9	AEBS95619	Aeb95619 Thale cre
707	34.5	44.8	385	9	ADV70586	Adv70586 Brevibac
708	34.5	44.8	385	9	ADW15128	Adw15128 B. lactof
709	34.5	44.8	390	3	AAAG27733	Aag27733 Arabidops
710	34.5	44.8	394	8	ADNA8140	Adn8140 Thermoco
711	34.5	44.8	598	8	ADN21486	Adn21486 Bacterial
712	34.5	44.8	637	8	ADS26569	Ads26569 Bacterial
713	34.5	44.8	641	8	ADS42579	Ads42579 Bacterial
714	34.5	44.8	650	7	ADB65482	Adb65482 Human pro
715	34.5	44.8	707	3	AAAB53401	AaB53401 Human col
716	34.5	44.8	713	4	AAAB95876	Aab95876 Human pro
717	34.5	44.8	713	8	ADQ88458	Adq88458 Human GAD
718	34.5	44.8	713	9	ADY70445	Ady70445 Human bet
719	34.5	44.8	713	9	ADY70706	Ady70706 Human nic
720	34.5	44.8	757	6	ABU39604	Abu39604 Protein e
721	34	44.2	14	2	AAU97228	Aau97228 Brucella
722	34	44.2	34	4	AAAM34289	Aam34289 Peptide #
723	34	44.2	34	4	AAAM74149	Aam74149 Human bio
724	34	44.2	34	4	ABG55929	Abg55929 Human liv
725	34	44.2	34	5	ABG44073	Abg44073 Human pep
726	34	44.2	54	6	ABO14019	AbO14019 Novel hum
727	34	44.2	54	8	ADN60716	Adn60716 Human sec
728	34	44.2	55	2	AAV27614	Aav27614 Human sec
729	34	44.2	55	8	ADG78425	Adg78425 Human sec
730	34	44.2	58	3	AAAG00662	Aag00662 Human imm
731	34	44.2	60	4	AAAB9615	Aab9615 Human imm
732	34	44.2	61	4	AAU56045	Aau56045 Propionib
733	34	44.2	61	6	ABMS2564	Abms2564 Propionib
734	34	44.2	67	7	ADFS9711	Adf59711 Human pol
735	34	44.2	68	8	ADG22497	Adg22497 Cyanophag
736	34	44.2	73	5	ABP02467	Abp02467 Human ORF
737	34	44.2	77	6	ABR40599	AbR40599 Catalpa s
738	34	44.2	77	7	ADG23497	Adg23497 Polypepti
739	34	44.2	80	4	ABBI15791	Abbi15791 Human ner
740	34	44.2	82	5	ABP08654	Abp08654 Human ORF
741	34	44.2	84	9	ADY65102	Ady65102 S. mansoni
742	34	44.2	89	8	ADK48055	Adk48055 Streptoco
743	34	44.2	92	4	AAU40100	Aau40100 Propionib
744	34	44.2	92	4	AAU66244	Aau66244 Propionib
745	34	44.2	92	6	ABM62763	Abm62763 Propionib
746	34	44.2	92	6	ABM36619	Abm36619 Propionib
747	34	44.2	92	7	ABO61087	AbO61087 Streptoco
748	34	44.2	96	5	ABP29140	Abp29140 Streptoco
749	34	44.2	97	5	ABP03772	Abp03772 Human ORF
750	34	44.2	99	3	ABAB1264	AbaB1264 Human ORF
751	34	44.2	99	5	ABP08949	Abp08949 Human ORF
752	34	44.2	100	5	ADK34425	Adk34425 Novel hum
753	34	44.2	113	5	ABBA49293	Abba49293 Listeria
754	34	44.2	115	5	ABP33134	Abp33134 Human iso

755	34	44.2	121	7	ABO73261	AbO73261 Pseudomon
756	34	44.2	133	7	ADC88286	Adc88286 Ribosomal
757	34	44.2	137	6	ARM65915	Arm65915 Propionib
758	34	44.2	141	6	ABU46498	Abu46498 Protein e
759	34	44.2	141	6	ABU23733	Abu23733 Protein e
760	34	44.2	148	2	AAW32352	Aaw32352 Mycobacte
761	34	44.2	148	2	AAW32420	Aaw32420 Mycobacte
762	34	44.2	148	2	AAW64292	Aaw64292 Mycobacte
763	34	44.2	148	2	AAW81655	Aaw81655 M. tuberc
764	34	44.2	148	2	AAV38957	Aav38957 M. tuberc
765	34	44.2	148	2	AAV39094	Aav39094 M. tuberc
766	34	44.2	148	2	AAV38829	Aav38829 Novel hum
767	34	44.2	155	5	ADK35829	Adk35829 Secreted
768	34	44.2	155	2	AAW72886	Aaw72886 Mycobacte
769	34	44.2	161	4	AAU23604	Aau23604 Novel hum
770	34	44.2	161	6	AAU21268	Aau21268 Protein e
771	34	44.2	162	2	AAU21903	Aau21903 Amino aci
772	34	44.2	162	5	AAW50735	Aaw50735 Mycobacte
773	34	44.2	163	5	ABP64047	Abp64047 Human ORF
774	34	44.2	165	5	ABP25438	Abp25438 Streptoco
775	34	44.2	169	3	AAAG10430	Aag10430 Arabidops
776	34	44.2	170	2	AAW06939	Aaw06939 Cagi locu
777	34	44.2	176	9	AEA20212	Aea20212 Novel hum
778	34	44.2	178	4	AAU03697	Aau03697 Group B S
779	34	44.2	188	9	ABM92421	Abm92421 M. xanthu
780	34	44.2	202	8	ADR94730	Adr94730 Novel S.
781	34	44.2	202	9	AEA58600	Aea58600 Streptoco
782	34	44.2	209	8	AAO19614	Aao19614 Human nuc
783	34	44.2	209	8	ADR09622	Adr09622 Human pro
784	34	44.2	212	3	AAAG10429	Aag10429 Arabidops
785	34	44.2	214	9	AEA25867	Aea25867 C. elegan
786	34	44.2	214	9	AEA25892	Aea25892 C. elegan
787	34	44.2	221	4	ABG04153	Abg04153 Novel hum
788	34	44.2	222	6	ABU32306	Abu32306 Protein e
789	34	44.2	224	8	ADP04509	Adp04509 Sea squir
790	34	44.2	225	7	ADP07460	Adp07460 Klebsiell
791	34	44.2	230	8	ADK68163	Adk68163 Plant ful
792	34	44.2	237	5	ABG68915	Abg68915 Lawsonia
793	34	44.2	239	4	ABE79522	Abe79522 Corynebac
794	34	44.2	240	4	ADM20087	Adm20087 Protein e
795	34	44.2	247	6	AAAG81386	Aag81386 Human APP
796	34	44.2	247	6	ADA55320	Ada55320 Human pro
797	34	44.2	258	4	AAE79521	Aae79521 Corynebac
798	34	44.2	258	4	AAE18896	Aae18896 A maize c
799	34	44.2	262	9	ABE42082	AbE42082 L. pneumo
800	34	44.2	269	6	ABU01670	Abu01670 S. pneumo
801	34	44.2	269	6	ABP81400	Abp81400 Streptoco
802	34	44.2	269	6	ABU36398	Abu36398 Protein e
803	34	44.2	275	9	ABE38912	Abe38912 L. pneumo
804	34	44.2	284	4	AAU23006	Aau23006 Novel hum
805	34	44.2	296	8	ADX72011	Adx72011 Plant ful
806	34	44.2	297	7	ABO68337	AbO68337 Pseudomon
807	34	44.2	297	8	ADR91360	Adr91360 Tomato Le
808	34	44.2	303	2	AAW06516	Aaw06516 Flavobact
809	34	44.2	303	2	AAW69531	Aaw69531 Flavobact
810	34	44.2	303	6	ADA36927	Ada36927 Acinetoba
811	34	44.2	310	4	ABG21536	Abg21536 Novel hum
812	34	44.2	314	7	ABO78871	AbO78871 Pseudomon
813	34	44.2	317	2	AAK26061	Aak26061 Growth Fa
814	34	44.2	320	3	AAAG10428	Aag10428 Arabidops
815	34	44.2	320	9	ABM95081	Abm95081 M. xanthu
816	34	44.2	322	3	AAO7103	Aao7103 Arabidops
817	34	44.2	324	7	ABO71765	AbO71765 Pseudomon
818	34	44.2	325	5	AAU51715	Aau51715 Helicobac
819	34	44.2	326	2	AAU20119	Aau20119 B. burgdo
820	34	44.2	326	3	AAO71102	Aao71102 Arabidops
821	34	44.2	329	3	AAAB51794	AaB51794 Gene 21 h
822	34	44.2	329	9	ADM17330	Adm17330 Eucalyptu
823	34	44.2	330	8	ADY09473	Ady09473 Plant ful
824	34	44.2	330	8	ADX94684	Adx94684 Plant ful
825	34	44.2	331	7	ABO63122	AbO63122 Klebsiell
826	34	44.2	334	6	ABU39211	Abu39211 Protein e
827	34	44.2	337	7	ABO79509	AbO79509 Pseudomon

828	34	44.2	338	3	AAG10548	Aag10548 Arabidops	901	34	44.2	505	6	ABR75067	AbR75067 Human sec
829	34	44.2	339	7	ABU35795	Abu35795 Protein e	902	34	44.2	505	6	ABR94829	AbR94829 Human sec
830	34	44.2	340	6	ABM89156	Abm89156 Rice abio	903	34	44.2	505	6	ABO25162	ABO25162 Novel hum
831	34	44.2	341	8	ABJ18769	Abj18769 Pseudomon	904	34	44.2	505	6	ABU85802	Abu85802 Human PRO
832	34	44.2	341	8	ADSI15017	Adsi15017 Pseudomon	905	34	44.2	505	6	ABU98962	Abu98962 Novel hum
833	34	44.2	342	3	AGI10547	AgI10547 Arabidops	906	34	44.2	505	6	ABU98177	Abu98177 Novel hum
834	34	44.2	349	4	AAM16425	Aam16425 Peptide #	907	34	44.2	505	6	ABU91883	Abu91883 Novel hum
835	34	44.2	349	4	ABB35416	Abb35416 Peptide #	908	34	44.2	505	6	ABU9576	Abu9576 Human PRO
836	34	44.2	349	4	AAM28924	Aam28924 Peptide #	909	34	44.2	505	6	ABU86417	Abu86417 Human sec
837	34	44.2	349	4	ABB30250	Abb30250 Peptide #	910	34	44.2	505	6	ABU67630	Abu67630 Human sec
838	34	44.2	349	4	ABB20853	Abb20853 Protein #	911	34	44.2	505	6	ABU80658	Abu80658 Human PRO
839	34	44.2	349	4	AAM68618	Aam68618 Human bon	912	34	44.2	505	6	ABR99576	AbR99576 Human sec
840	34	44.2	349	4	AAM56240	Aam56240 Human bra	913	34	44.2	505	6	ABR98966	AbR98966 Human sec
841	34	44.2	349	4	ABG50278	Abg50278 Human liv	914	34	44.2	505	6	ABO16489	ABO16489 Human sec
842	34	44.2	349	4	AAM04159	Aam04159 Peptide #	915	34	44.2	505	6	ABR92389	AbR92389 Human sec
843	34	44.2	349	5	ABG38196	Abg38196 Human pep	916	34	44.2	505	6	ABO19030	ABO19030 Human sec
844	34	44.2	349	2	RAY20118	Ray20118 B. burgdo	917	34	44.2	505	6	ABR78451	AbR78451 Human sec
845	34	44.2	365	4	ABG15914	Abg15914 Novel hum	918	34	44.2	505	6	ABU85187	Abu85187 Novel hum
846	34	44.2	385	8	ADS29074	AdS29074 Bacterial	919	34	44.2	505	6	ABO00326	ABO00326 Novel hum
847	34	44.2	385	9	ABM97263	Abm97263 M. xanthu	920	34	44.2	505	6	ABO11658	ABO11658 Human sec
848	34	44.2	386	8	ADS24445	AdS24445 Bacterial	921	34	44.2	505	6	ABO02303	ABO02303 Human sec
849	34	44.2	388	2	RAY42435	Ray42435 Cuticle-d	922	34	44.2	505	6	ABU88877	Abu88877 Novel hum
850	34	44.2	388	2	AAW98515	Aaw98515 H. pylori	923	34	44.2	505	6	ABU67280	Abu67280 Novel hum
851	34	44.2	398	2	AAW71547	Aaw71547 Helicobac	924	34	44.2	505	6	ABU83572	Abu83572 Human sec
852	34	44.2	398	4	AAB46335	Aab46335 H. pylori	925	34	44.2	505	6	ABO06373	ABO06373 Novel hum
853	34	44.2	404	3	AAG10546	Aag10546 Arabidops	926	34	44.2	505	6	ABR59409	AbR59409 Human sec
854	34	44.2	404	8	ADP29292	Adp29292 Human sec	927	34	44.2	505	6	ABO09471	ABO09471 Human sec
855	34	44.2	412	2	RAY11085	Ray11085 H. pylori	928	34	44.2	505	6	ABO19335	ABO19335 Novel hum
856	34	44.2	417	7	ADB64328	AdB64328 Human pro	929	34	44.2	505	6	ABO11353	ABO11353 Human sec
857	34	44.2	417	9	AEA19975	Aea19975 Novel hum	930	34	44.2	505	6	ABR66971	AbR66971 Human sec
858	34	44.2	422	6	ABM67299	Abm67299 Phototrab	931	34	44.2	505	6	ABO16184	ABO16184 Human sec
859	34	44.2	437	6	ABU38661	Abu38661 Protein e	932	34	44.2	505	6	ABO13890	ABO13890 Human sec
860	34	44.2	437	7	ABM90284	Abm90284 Rice abio	933	34	44.2	505	6	ABU65793	Abu65793 Human sec
861	34	44.2	444	6	ABJ25545	Abj25545 Aspergill	934	34	44.2	505	6	ABO07641	ABO07641 Human PRO
862	34	44.2	461	2	AAR75365	Aar75365 Phytase.	935	34	44.2	505	6	ABO03828	ABO03828 Human sec
863	34	44.2	461	2	AAU23849	Aau23849 Amino aci	936	34	44.2	505	6	ABR67276	AbR67276 Human sec
864	34	44.2	461	5	ABP53627	Abp53627 Phytase a	937	34	44.2	505	6	ABO15879	ABO15879 Human sec
865	34	44.2	461	8	AEA21436	Aea21436 Schwannio	938	34	44.2	505	6	ABU56160	Abu56160 Human sec
866	34	44.2	466	9	ADS27504	AdS27504 Bacterial	939	34	44.2	505	6	ABU65488	Abu65488 Human PRO
867	34	44.2	466	9	ABM94981	Abm94981 M. xanthu	940	34	44.2	505	6	ABU95433	Abu95433 Novel hum
868	34	44.2	468	4	AAB66707	Aab66707 C. glutami	941	34	44.2	505	6	ABU71336	Abu71336 Human PRO
869	34	44.2	468	5	ABG80325	Abg80325 C. glutam	942	34	44.2	505	6	ABO07946	ABO07946 Human PRO
870	34	44.2	474	6	ABU30004	Abu30004 Protein e	943	34	44.2	505	6	ABR70187	AbR70187 Human sec
871	34	44.2	475	6	ABU29756	Abu29756 Protein e	944	34	44.2	505	6	ABR69520	AbR69520 Human sec
872	34	44.2	478	7	ADC97241	Adc97241 E. faeciu	945	34	44.2	505	6	ABO01661	ABO01661 Human PRO
873	34	44.2	485	8	ADS28987	AdS28987 Bacterial	946	34	44.2	505	6	ABU81463	Abu81463 Human PRO
874	34	44.2	487	7	ABO76701	AbO76701 Pseudomon	947	34	44.2	505	6	ABR60260	AbR60260 Human sec
875	34	44.2	487	8	ADN21635	Adn21635 Bacterial	948	34	44.2	505	6	ABR67995	AbR67995 Human sec
876	34	44.2	491	7	ABO69233	ABO69233 Pseudomon	949	34	44.2	505	6	ABR65383	AbR65383 Human sec
877	34	44.2	492	4	ABG08723	Abg08723 Novel hum	950	34	44.2	505	6	ABR68605	AbR68605 Human sec
878	34	44.2	492	7	ADC97318	Adc97318 E. faeciu	951	34	44.2	505	6	ABR72017	AbR72017 Human sec
879	34	44.2	495	8	ADN46229	Adn46229 Thermoco	952	34	44.2	505	6	ABU85497	Abu85497 Human PRO
880	34	44.2	498	8	ADU07681	Adu07681 Amino aci	953	34	44.2	505	6	ABU89187	Abu89187 Human sec
881	34	44.2	502	7	ADJ11510	Adj11510 Rice prot	954	34	44.2	505	6	ABU83267	Abu83267 Human sec
882	34	44.2	502	8	ADN24391	Adn24391 Bacterial	955	34	44.2	505	6	ABU95123	Abu95123 Novel hum
883	34	44.2	504	8	ADJ49082	Adj49082 Oil-assoc	956	34	44.2	505	6	ABU90671	Abu90671 Novel hum
884	34	44.2	505	2	AAW69249	Aaw69249 Human p56	957	34	44.2	505	6	ABU84182	Abu84182 Human sec
885	34	44.2	505	3	RAY78947	Ray78947 Human p56	958	34	44.2	505	6	ABU93833	Abu93833 Novel hum
886	34	44.2	505	4	AAB31191	Aab31191 Amino aci	959	34	44.2	505	6	ABR65078	AbR65078 Human sec
887	34	44.2	505	4	AAU29248	Aau29248 Human PRO	960	34	44.2	505	6	ABR68910	AbR68910 Human sec
888	34	44.2	505	6	ABU58624	Abu58624 Human PRO	961	34	44.2	505	6	ABO06726	ABO06726 Human sec
889	34	44.2	505	6	ABU88172	Abu88172 Novel hum	962	34	44.2	505	6	ABR99271	AbR99271 Human sec
890	34	44.2	505	6	ABU84487	Abu84487 Human sec	963	34	44.2	505	6	ABU57155	Abu57155 Human PRO
891	34	44.2	505	6	ABR66361	AbR66361 Human sec	964	34	44.2	505	6	ABU72048	Abu72048 Novel hum
892	34	44.2	505	6	ABR65751	AbR65751 Human sec	965	34	44.2	505	6	ABU86107	Abu86107 Novel hum
893	34	44.2	505	6	ABU99691	Abu99691 Human sec	966	34	44.2	505	6	ABU82394	Abu82394 Novel hum
894	34	44.2	505	6	ABU82930	Abu82930 Human PRO	967	34	44.2	505	6	ABU87405	Abu87405 Human PRO
895	34	44.2	505	6	ABU90051	Abu90051 Novel hum	968	34	44.2	505	6	ABU67149	Abu67149 Novel hum
896	34	44.2	505	6	ABR68300	AbR68300 Human sec	969	34	44.2	505	6	ABU83877	Abu83877 Human PRO
897	34	44.2	505	6	ABU96353	Abu96353 Novel hum	970	34	44.2	505	6	ABO08251	ABO08251 Human PRO
898	34	44.2	505	6	ABU92784	Abu92784 Human sec	971	34	44.2	505	6	ABU81962	Abu81962 Novel hum
899	34	44.2	505	6	ABO08861	ABO08861 Human sec	972	34	44.2	505	6	ABU66126	Abu66126 Novel hum
900	34	44.2	505	6	ABO02913	ABO02913 Human sec	973	34	44.2	505	6	ABR59955	AbR59955 Human sec

974 34 44.2 505 6 ABU94143 Novel hum
975 34 44.2 505 6 ABO00016 Novel hum
976 34 44.2 505 6 ABR66666 Human sec
977 34 44.2 505 6 ABR91084 Human sec
978 34 44.2 505 6 ABU94511 Human PRO
979 34 44.2 505 6 ABU79393 Human PRO
980 34 44.2 505 6 ABU86722 Human sec
981 34 44.2 505 6 ABU87027 Human hum
982 34 44.2 505 6 ABU94816 Human PRO
983 34 44.2 505 6 ABO04743 Human PRO
984 34 44.2 505 6 ABR70492 Human sec
985 34 44.2 505 6 ABU98657 Human PRO
986 34 44.2 505 6 ABR66056 Human sec
987 34 44.2 505 6 ABR64773 Human sec
988 34 44.2 505 6 ABU79698 Human PRO
989 34 44.2 505 6 ABU93089 Human sec
990 34 44.2 505 6 ABU96048 Human PRO
991 34 44.2 505 6 ABU91268 Human hum
992 34 44.2 505 6 ABU90361 Novel hum
993 34 44.2 505 6 ABO09776 Human sec
994 34 44.2 505 6 ABO11048 Human sec
995 34 44.2 505 6 ABR71102 Human PRO
996 34 44.2 505 6 ABU87710 Human PRO
997 34 44.2 505 6 ABU91578 Human PRO
998 34 44.2 505 6 ABU84792 Human sec
999 34 44.2 505 6 ABR69882 Human sec
1000 34 44.2 505 6 ABU80259 Human PRO

ALIGNMENTS

RESULT 1
AAY94595
ID AAY94595 standard; peptide; 15 AA.
AC AAY94595;
XX
XX
DT 28-NOV-2000 (first entry)
XX
XX
DE Mycobacterium tuberculosis ESAT-6 peptide ES6.
XX
XX
KW Tuberculosis; infection diagnosis; ESAT-6.
XX
XX
OS Mycobacterium tuberculosis.
XX
XX
FN WO200026248-A2.
XX
XX
PD 11-MAY-2000.
XX
XX
PF 03-NOV-1999; 99WO-GB003635.
XX
XX
PR 04-NOV-1998; 98GB-00024213.
PR 04-NOV-1998; 98US-0107004P.
XX
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
XX
PI Lalvani A, Pathan AA;
XX
XX
DR WPI; 2000-365579/31.
XX
XX
PT Novel method of diagnosing infection, or exposure of a host, to a
PT mycobacterium comprising contacting T cells from the host with ESAT-6
PT derived peptides.
XX
XX
PS Claim 1; Page 3; 33pp; English.
XX
XX
CC The present sequence is the peptide ES6 derived from the Mycobacterium
CC tuberculosis ESAT-6 gene. This sequence is one of eleven peptides derived
CC from the ESAT-6 gene (see AAY94595 to AAY94600). The peptides are
CC recognised, to varying degrees, by the T cells of patients with
CC tuberculosis. When the peptides are combined together as a panel they
CC provide a high specificity and sensitivity diagnostic test for

CC M.tuberculosis infection. This test has the advantage that it does not
CC give false positives for patients who have been vaccinated with BCG
XX
XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 77; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WNFAGIEAASAIQ 15
DB 1 WNFAGIEAASAIQ 15
RESULT 2
ABG30952
ID ABG30952 standard; peptide; 15 AA.
XX
XX
AC ABG30952;
XX
XX
DT 21-OCT-2002 (first entry)
XX
XX
DE Mycobacterium tuberculosis ESAT-6 residues 6-20.
XX
XX
KW ESAT-6; mycobacterial infection; tuberculosis; pulmonary tuberculosis;
KW tuberculosis lymphadenitis; extrapulmonary tuberculosis.
XX
XX
OS Mycobacterium tuberculosis.
XX
XX
FN WO200254072-A2.
XX
XX
PD 11-JUL-2002.
XX
XX
PF 08-JAN-2002; 2002WO-GB0000055.
XX
XX
PR 08-JAN-2001; 2001GB-00000432.
PR 08-JAN-2001; 2001US-0259868P.
XX
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
XX
PI Lalvani A;
XX
XX
DR WPI; 2002-583633/62.
XX
XX
PT Determining the progress of a mycobacterial infection, by direct ex vivo
PT quantitation of ESAT-6-specific T cells.
XX
XX
PS Example 2; Page 40; 53pp; English.
XX
XX
CC The invention describes a method of determining the efficacy of treatment
CC for mycobacterial infection (such as pulmonary tuberculosis, tuberculosis
CC lymphadenitis and extrapulmonary tuberculosis). The method involves
CC determining the level of T cells specific for a mycobacterial antigen
CC that has decreased after the treatment and therefore determining the
CC efficacy of the treatment. The method is useful for determining the
CC efficacy of treatment for mycobacterial infection, the mycobacterial
CC infection is Mycobacterium tuberculosis or M.bovis infection. The
CC invention also describes a method useful for determining the presence of T
CC cells specific for a mycobacterial antigen. Also described in a method
CC for determining the effect of an intervention on a mycobacterial
CC infection in an individual an method for treating an individual
CC infected by a mycobacterium. This sequence represents a peptide of
CC Mycobacterium tuberculosis ESAT-6, the mycobacterial antigen measured in
CC the invention
XX
XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 77; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WNFAGIEAASAIQ 15

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Db      1  WNFAGIEAAASAIQ 15
|||||
RESULT 3
AAO17433
ID  AAO17433 standard; peptide; 15 AA.
XX
AC  AAO17433;
XX
DT  11-JUL-2002 (first entry)
XX
DE  Early secreted antigenic target 6. T cell epitope #2.
XX
KW  Tuberculosis; TB; vaccination; vaccine; CD4+ T cell immune response;
KW  poxvirus vector; HIV; malaria; Helicobacter pylori; influenza; hepatitis;
KW  viral infection; leprosy; protozoan parasite; cancer; tuberculostatic;
KW  anti-HIV; protozoicide; antibacterial; virucide; hepatotropic;
KW  antiinflammatory; antileptotic; cytostatic; epitope.
XX
OS  Mycobacterium tuberculosis.
XX
PN  WO200224224-A2.
XX
PD  28-MAR-2002.
XX
PF  13-SEP-2001; 2001WO-GB004116.
XX
PR  21-SEP-2000; 2000GB-00023203.
XX
PA  (OXO-) OXON PHARMACINES LTD.
XX
PI  Hill AVS, Mcshane H, Gilbert S, Reece W, Schneider J;
XX
WPI; 2002-394098/42.
XX
PT  Inducing CD4+ T-cell response against target antigen by administering a
PT  composition comprising a source of CD4+ epitopes which is a non-
PT  replicating or replication impaired recombinant poxvirus vector.
XX
PS  Example 1; Page 21; 50pp; English.
XX
CC  The present invention relates to a method of inducing a CD4+ T-cell
CC  response against a target antigen, by administering two different
CC  compositions comprising a source of CD4+ T-cell epitope(s) of the target
CC  antigen, where the second composition further includes an epitope which
CC  is same as the epitope of the first composition, where the source of the
CC  epitopes for the compositions is a non-replicating or replication
CC  impaired recombinant poxvirus vector. The methods are useful for inducing
CC  CD4+ T-cell immune responses against diseases such as tuberculosis, human
CC  immunodeficiency virus (HIV) (persistent viral infection), malaria,
CC  Helicobacter pylori, influenza, hepatitis (chronic hepatitis B and C),
CC  cytomegalovirus (CMV), viral infection, herpes virus-induced disease,
CC  leprosy and diseases caused by non-malarial protozoan parasite such as
CC  toxoplasma and cancer. The present sequence is an epitope from
CC  Mycobacterium tuberculosis useful in the method of the invention
XX
SQ  Sequence 15 AA;

Query Match      100.0%; Score 77; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1  WNFAGIEAAASAIQ 15
    |||||
DB  1  WNFAGIEAAASAIQ 15
    |||||

RESULT 4
ADI33342
ID  ADI33342 standard; peptide; 15 AA.
XX
AC  ADI33342;
XX

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XX  22-APR-2004 (first entry)
XX  Mycobacterium tuberculosis ESAT-6 peptide epitope #2.
XX
XX  pathogen; vaccine; cellular response; HPV; HIV; SIV; HCV; chlamydia; HBV;
XX  EBV; CMV; VZV; HSV; Legionella; Leishmaniasis; influenza;
XX  foot and mouth virus; Toxoplasma; Brucella; Cryptococcus; Candida;
XX  Aspergillus; Mycobacterium; T cell; ESAT-6; CFP10; virucide; protozoicide;
XX  antibacterial; fungicide; epitope.
XX
XX  Mycobacterium tuberculosis.
XX
XX  WO2004005925-A2.
XX
XX  15-JAN-2004.
XX
XX  07-JUL-2003; 2003WO-GB002936.
XX
XX  05-JUL-2002; 2002GB-00015710.
XX
XX  (ISIS-) ISIS INNOVATION LTD.
XX
XX  Lalvani A, Ewer K;
XX
XX  WPI; 2004-143006/14.
XX
XX  Diagnosing in an individual recent exposure to an agent, useful in
XX  treating a disease caused by a pathogen, by determining in vitro or in
XX  vivo whether the T cells of recognize a protein having at least 30 amino
XX  acids.
XX
XX  Claim 16; Page 33; 48pp; English.
XX
XX  The invention relates to a novel method for diagnosing in an individual
XX  recent exposure to an agent which is a pathogen, vaccine or any other
XX  moiety, which induces a cellular response. The pathogen can include: HPV,
XX  HIV, SIV, HCV, chlamydia species, HBV, EBV, CMV, VZV, HSV, Legionella, S.
XX  typhi, P. falciparum, Leishmaniasis, M. leprae, influenza virus, foot and
XX  mouth virus, a Toxoplasma species, a Brucella species, a Cryptococcus
XX  species, a Candida species, an Aspergillus species, or Mycobacterium
XX  tuberculosis. The invention also provides a vaccine against any of the
XX  above pathogens. The method comprises determining in vitro or in vivo
XX  whether the T cells of the individual recognize a protein from the agent
XX  having a length of at least 30 amino acids. The invention also comprises
XX  a protein or epitope peptide which is from ESAT-6 or CFP10. The vaccines
XX  of the invention have: virucide, protozoicide, antibacterial, and fungicide
XX  exposure to an agent which is a pathogen, vaccine or any other moiety
XX  which induces a cellular response. The protein described above, the
XX  product which prevents or treats a condition caused by a pathogen or the
XX  antigen or its analogue is useful in the manufacturing of a medicament
XX  for diagnosing and treating an individual recently exposed to a pathogen.
XX  This sequence represents a peptide epitope of the invention for
XX  recognition by a T cell relating to the invention.
XX
XX  Sequence 15 AA;

Query Match      100.0%; Score 77; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1  WNFAGIEAAASAIQ 15
    |||||
DB  1  WNFAGIEAAASAIQ 15
    |||||

RESULT 5
AAE12275
ID  AAE12275 standard; peptide; 20 AA.
XX
XX  AAE12275;
XX

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XX PD 04-AUG-2005.
XX PF 24-JAN-2005; 2005WO-US002251.
XX PR 23-JAN-2004; 2004US-0538713P.
XX PR 06-OCT-2004; 2004US-0616855P.
XX PA (VIEW-) VIEVAX CORP.
XX PI Mahairas GG;
XX PR WPI; 2005-542270/55.
XX PT Immune response altering agent useful for treating autoimmune diseases,
XX PT comprises first domain having T/B cell epitopes or Toll-like receptor-
XX PT binding proteins, and second domain having heterologous target molecule.
XX PS Claim 65; SEQ ID NO 237; 130pp; English.
XX CC The invention relates to an immune response altering agent (I) which
XX CC comprises a first domain having one or more components chosen from T cell
XX CC epitopes, B cell epitopes, and Toll-like receptor (TLR)-binding proteins
XX CC or its TLR-binding domains, and a second domain having heterologous
XX CC target molecule against which an immune response is desired. (I) is
XX CC useful for altering or inducing an immune response to a target. (I) is
XX CC also useful for treating viral infections (e.g., HIV and hepatitis C
XX CC virus), bacterial infections (e.g., Staphylococcus and Pseudomonas),
XX CC parasites (e.g., Leishmania), fungal infections (e.g., Candida), cancer
XX CC (e.g., non-Hodgkin's lymphoma, Hodgkin's disease and leukemia), and
XX CC autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,
XX CC insulin dependent diabetes, Addison's disease, celiac disease,
XX CC inflammatory bowel disease, ulcerative colitis, Crohn's disease, systemic
XX CC lupus erythematosus, psoriasis, Sjogren's syndrome, etc. (I) is useful
XX CC for treating inflammatory and hyperproliferative skin diseases, and
XX CC allergic reactions such as asthma, bronchitis, allergic rhinitis etc. (I)
XX CC alters an immune response generated against the heterologous target
XX CC molecule. (I) can be applied to wide range of species such as humans, non
XX CC -human primates, horses, etc. The present sequence represents the amino
XX CC acid sequence of a M. tuberculosis early secretory antigenic target 6,
XX CC ESAT6, peptide fragment.
XX SQ Sequence 20 AA;

Query Match 100.0%; Score 77; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAIQG 15
DB 6 WNFAGIEAAASAIQG 20

RESULT 8
AAW32339
ID AAW32339 standard; protein; 51 AA.
XX AC AAW32339;
XX DT 13-JAN-1998 (first entry)
XX DE Mycobacterium tuberculosis antigen ESAT-6.
XX KW Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant;
XX KW skin testing; M.tuberculosis.
XX OS Mycobacterium tuberculosis.
XX PN W09709429-A2.
XX PR 13-MAR-1997.
XX PF 30-AUG-1996; 96WO-US014675.

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XX PR 01-SEP-1995; 95US-00523435.
XX PR 22-SEP-1995; 95US-00532136.
XX PR 22-MAR-1996; 96US-00620280.
XX PR 05-JUN-1996; 96US-00658800.
XX PR 12-JUL-1996; 96US-00680573.
XX PA (CORI-) CORIXA CORP.
XX PI Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton R;
XX PR Vedvick TH, Twardzik DR;
XX PR WPI; 1997-192904/17.
XX PR N-PSDB; AAT91463.
XX PT New immunogenic polypeptide(s) from soluble M. tuberculosis antigens -
XX PT useful for diagnosis of M. tuberculosis infection.
XX PS Claim 43; Page 147; 190pp; English.
XX CC A new immunogenic polypeptide has been developed comprising an
XX CC immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its
XX CC variant differing only in conservative substitutions and/or
XX CC modifications). The present sequence represents a specifically claimed
XX CC sequence of the ESAT-6 M.tuberculosis antigen. The immunogenic
XX CC polypeptide can be used to diagnose M.tuberculosis infection by forming
XX CC complexes with specific antibodies in the sample. Fragments of DNA
XX CC encoding the immunogenic polypeptide can be used as diagnostic primers or
XX CC probes and agents that bind to the antigen, especially monoclonal
XX CC antibodies or equivalent polyclonal antibodies, are also used for
XX CC diagnosis
XX SQ Sequence 51 AA;

Query Match 100.0%; Score 77; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAIQG 15
DB 6 WNFAGIEAAASAIQG 20

RESULT 9
AAW32466
ID AAW32466 standard; protein; 51 AA.
XX AC AAW32466;
XX DT 09-JAN-1998 (first entry)
XX DE Mycobacterium tuberculosis antigen ESAT-6.
XX KW Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant;
XX KW skin testing; M.tuberculosis.
XX OS Mycobacterium tuberculosis.
XX PN W09709428-A2.
XX PR 13-MAR-1997.
XX PF 30-AUG-1996; 96WO-US014674.
XX PR 01-SEP-1995; 95US-00523436.
XX PR 22-SEP-1995; 95US-00533634.
XX PR 22-MAR-1996; 96US-00620874.
XX PR 05-JUN-1996; 96US-00659683.
XX PR 12-JUL-1996; 96US-00680574.
XX PA (CORI-) CORIXA CORP.
XX PI Reed SG, Skeiky YA, Dillon DC, Campos-Neto A, Houghton R;

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RESULT 12
AAV38988
ID AAY38988 standard; protein; 51 AA.
XX
AC AAY38988;
XX
DT 05-NOV-1999 (first entry)
XX
DE M. tuberculosis recombinant antigen protein ESAT-6.
XX
KW Antigen; diagnosis; detection; infection; antibody; immunisation;
XX vaccine; immunity.
XX
OS Mycobacterium tuberculosis.
XX
PN WO9942118-A2.
XX
PD 26-AUG-1999.
XX
PF 17-FEB-1999; 99WO-US003265.
XX
PR 18-FEB-1998; 98US-00024753.
XX 05-MAY-1998; 98US-00072596.
XX (CORI-) CORIXA CORP.
XX
PI Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton R;
PI Vedvick TS, Twardzik DR, Lodes MJ, Hendrickson RC;
XX
DR WPI; 1999-527416/44.
XX N-PSDB; AAZ19091.
XX
PT New polypeptide comprising antigenic portions of M. tuberculosis.
XX
PS Claim 51; Page 165; 323pp; English.
XX
CC This invention describes novel recombinant antigens and their encoding
CC nucleic acids derived from Mycobacterium tuberculosis. The novel
CC polypeptides are useful for detecting M. tuberculosis infection in a
CC biological sample by detecting antibodies which bind with the
CC polypeptides, and are useful as vaccines for immunizing against M.
CC tuberculosis infection. The new detection methods are needed as current
CC vaccination strategies do not provide 100% immunity
XX
SQ Sequence 51 AA;

Query Match 100.0%; Score 77; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAIQG 15
DB 6 WNFAGIEAAASAIQG 20

RESULT 13
AAV39131
ID AAY39131 standard; protein; 51 AA.
XX
AC AAY39131;
XX
DT 05-NOV-1999 (first entry)
XX
DE M. tuberculosis ESAT-6 amino acid sequence.
XX
KW Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen;
KW immunotherapy; diagnosis; immunisation; vaccine; infection;
XX immune response; skin test.
XX
OS Mycobacterium tuberculosis.
XX
PN WO9942076-A2.
XX

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PD 26-AUG-1999.
XX
PF 17-FEB-1999; 99WO-US003268.
XX
PR 18-FEB-1998; 98US-00025197.
XX 05-MAY-1998; 98US-00072967.
XX (CORI-) CORIXA CORP.
XX
PI Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton R;
PI Vedvick TS, Twardzik DR, Lodes MJ, Hendrickson RC;
XX
DR WPI; 1999-527409/44.
XX N-PSDB; AAZ19303.
XX
PT New antigens from Mycobacterium tuberculosis useful in diagnostic skin
XX tests and protective or therapeutic vaccines or compositions.
XX
PS Disclosure; Page 120; 299pp; English.
XX
CC The present invention describes polypeptides comprising an immunogenic
CC part of a Mycobacterium tuberculosis antigen (Ag). Also described are
CC vaccines and fusion protein containing M. tuberculosis Ag's. M.
CC tuberculosis Ag's, DNAs encoding them, derived fusion proteins and other
CC polypeptides fragments, can be used in pharmaceutical compositions or
CC vaccines to generate a protective or therapeutic immune response to M.
CC tuberculosis and as reagents in skin tests for diagnosis of tuberculosis.
CC Ag can induce proliferation of, or cytokine secretion by, T, B or natural
CC killer cells and/or macrophages in tuberculosis-immune subjects. AAZ19249
CC to AAZ19460 and AAY39083 to AAY39225 are used in the exemplification of
XX the present invention
XX
SQ Sequence 51 AA;

Query Match 100.0%; Score 77; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAIQG 15
DB 6 WNFAGIEAAASAIQG 20

RESULT 14
AAU01897
ID AAU01897 standard; protein; 51 AA.
XX
AC AAU01897;
XX
DT 29-AUG-2001 (first entry)
XX
DE Mycobacterium tuberculosis partial antigen ESAT-6.
XX
KW ESAT-6; antigen; vaccine; tuberculosis; AIDS;
XX acquired immunodeficiency disease.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200124820-A1.
XX
PD 12-APR-2001.
XX
PF 10-OCT-2000; 2000WO-US028095.
XX
PR 07-OCT-1999; 99US-0158338P.
XX 07-OCT-1999; 99US-0158425P.
XX (CORI-) CORIXA CORP.
XX
PI Skeiky Y, Reed S, Houghton RL, McNeill PD, Dillon DC, Lodes ML;
XX WPI; 2001-290576/30.
XX N-PSDB; AAS03787.
XX

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XX Vaccinating against Mycobacteria infections in mammals using fusion
PT proteins comprising combinations of heterologous antigens.
XX
XX Disclosure; Page 164; 168pp; English.
XX
XX The sequence represents Mycobacterium tuberculosis ESAT-6 antigen.
CC Compositions comprising at least 2 heterologous antigens, as a fusion
CC protein, and vectors expressing the fusion proteins are used as vaccines
CC to prophylactically immunise mammals (especially humans) against
CC infection by Mycobacteria. The compositions contain at least 2
CC heterologous antigens that increase the serological sensitivity of
CC individuals infected with tuberculosis, a disease frequently affecting
CC patients with acquired immunodeficiency disease, AIDS
XX
XX Sequence 51 AA;
SQ

Query Match 100.0%; Score 77; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
QY 1 WNFAGIERAASAIQG 15
DB 6 WNFAGIERAASAIQG 20

RESULT 15
AAE29716
ID AAE29716 standard; protein; 51 AA.
XX
XX AAE29716;
XX
XX 27-JAN-2003 (first entry)
XX
XX Mycobacterium tuberculosis ESAT-6 antigenic protein.
XX Vaccine; immunity; diagnostic agent; gene therapy; ESAT-6 antigen.
XX
XX Mycobacterium tuberculosis.
XX WO200272792-A2.
XX
XX 19-SEP-2002.
XX
XX 13-MAR-2002; 2002WO-US008223.
XX
XX 13-MAR-2001; 2001US-0275837P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Skeiky Y, Brannon M, Guderian J;
XX
XX WPI; 2002-759844/82.
XX N-PSDB; AAD29716.
XX
XX New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF,
PT M15 or 6H polynucleotide, useful as vaccine to elicit protective immunity
PT against pathogenic microorganisms e.g. Leishmania and Mycobacterium
PT tuberculosis.
XX
XX Disclosure; Page 106; 155pp; English.
XX
XX The invention relates to a recombinant nucleic acid molecule encoding a
CC fusion polypeptide. The recombinant nucleic acid comprises a heterologous
CC polynucleotide sequence encoding an antigen or an antigenic fragment from
CC Mycobacterium sp. and a Leishmania polynucleotide sequence encoding a
CC polypeptide or its fragment. The Leishmania polynucleotide is selected
CC from TSA, LeIF, M15, and 6H polynucleotides. Sequences of the invention
CC are used in methods for eliciting immune response in mammals. They are
CC useful as vaccines to elicit protective immunity against pathogenic
CC microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion
CC polypeptides are used for enhancing the expression of polynucleotides, as
CC in vivo diagnostic agents and for raising antibodies in a non-human

CC animal. The invention is used in gene therapy. The present sequence is M.
CC tuberculosis ESAT-6 antigenic protein
XX
XX Sequence 51 AA;
SQ

Query Match 100.0%; Score 77; DB 5; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
QY 1 WNFAGIERAASAIQG 15
DB 6 WNFAGIERAASAIQG 20

RESULT 16
AAE17580
ID AAE17580 standard; protein; 51 AA.
XX
XX AAE17580;
XX
XX 22-APR-2002 (first entry)
XX
XX Mycobacterium species ESAT-6 protein.
XX Fusion protein; antigen; serological sensitivity; immune response;
XX tuberculosis; infection; vaccine; ESAT-6 protein.
XX
XX Mycobacterium sp.
XX WO200198460-A2.
XX
XX 27-DEC-2001.
XX
XX 20-JUN-2001; 2001WO-US019959.
XX
XX 20-JUN-2000; 2000US-00597796.
XX 01-FEB-2001; 2001US-0265737P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Skeiky Y, Reed S, Alderson M;
XX
XX WPI; 2002-147798/19.
XX N-PSDB; AAD28351.
XX
XX Composition comprising MTB39 antigen and MTB32A antigen from
PT Mycobacterium species, useful for eliciting immune response in a subject.
XX
XX Claim 9; Page 122; 136pp; English.
XX
XX The present invention relates to fusion proteins containing at least two
CC Mycobacterium species antigens, nucleotides encoding them and
CC compositions comprising such fusion proteins. The present invention
CC particularly relates to nucleic acids encoding fusion proteins that
CC include two or more individual M. tuberculosis antigens which increase
CC the serological sensitivity of sera from individuals infected with
CC tuberculosis and methods for their use in diagnosis, prevention and
CC treatment of tuberculosis infection. Sequences of the invention are
CC useful for eliciting an immune response in a mammal, e.g., human,
CC immunised with BCG. They are useful in the diagnosis, treatment and
CC prevention of Mycobacterium infection. The fusion proteins and the
CC polynucleotides are useful as diagnostic tools in patients infected with
CC Mycobacterium, in vitro and in vivo assays for detecting humoral
CC antibodies or cell-mediated immunity against M. tuberculosis, for the
CC diagnosis of an infection or monitoring of disease progression, as
CC immunogens to generate or elicit a protective immune response in a
CC patient and for raising anti-M. tuberculosis antibodies in a non-human
CC animal. Sequences of the invention are also used as vaccines. MTB32A
CC fusion proteins of the invention are useful as in vivo diagnostic agents
CC for intradermal skin test. The present sequence is Mycobacterium species
CC ESAT-6 protein
XX
XX Sequence 51 AA;
SQ

Query Match 100.0%; Score 77; DB 5; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAIQG 15
| | | | | | | | | | | | | | |
DB 6 WNFAGIEAAASAIQG 20

RESULT 17

AAW11494
ID AAW11494 standard; protein; 95 AA.

XX AC AAW11494;

XX DT 27-MAR-1997 (first entry)

XX DE ESAT6.

XX KW ESAT6; Mycobacterium tuberculosis; 6kDa antigen; tuberculosis complex;

XX KW HYB76-8 reactive antigen; interferon-gamma; memory T-lymphocyte; vaccine;

XX KW M. africanum; M. bovis; delayed-type hypersensitivity reaction; therapy.

XX OS Mycobacterium tuberculosis.

XX PN WO9501441-A1.

XX PD 12-JAN-1995.

XX PF 01-JUL-1994; 94WO-DK000273.

XX PR 02-JUL-1993; 93DK-00000798.

XX PA (STAT-) STATENS SERUMINSTITUT.

XX PI Andersen P, Andersen AB, Haslov K, Sorensen A;

XX DR WPI; 1995-061005/08.

XX DR N-PSDB; AAT51422.

XX PT Vaccine for tuberculosis induces interferon-gamma release from T-

XX PT lymphocytes - comprises an antigen released from mycobacteria, for

XX PT immunisation of humans.

XX PS Claim 5; Page 61-63; 101pp; English.

XX CC This sequence represents the Mycobacterium tuberculosis ESAT6. ESAT6 is

XX CC also known as the 6kDa antigen, or the HYB76-8 reactive antigen. ESAT6 is

XX CC released from metabolising bacteria, and can be isolated from short term

XX CC filtrates grown as shaken cultures for 7 days. ESAT6 also induces a

XX CC release of interferon-gamma from reactivated memory T-lymphocytes. This

XX CC protein sequence is included in the vaccine of the invention. The vaccine

XX CC is for immunising an animal (including humans) against tuberculosis

XX CC caused by a Mycobacterium belonging to the tuberculosis complex. The

XX CC Mycobacterium of the tuberculosis complex are, M. tuberculosis, M.

XX CC africanum, and M. bovis. The vaccine can evoke a protective immune

XX CC response against tuberculosis or a delayed-type hypersensitivity

XX CC reaction. The protein can also be included in a composition for

XX CC diagnosing tuberculosis. The composition is injected intradermally, and a

XX CC skin reaction is an indicator of tuberculosis

XX SQ Sequence 95 AA;

Query Match 100.0%; Score 77; DB 2; Length 95;

Best Local Similarity 100.0%; Pred. No. 2.6e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAIQG 15

| | | | | | | | | | | | | | |

DB 6 WNFAGIEAAASAIQG 20

RESULT 18

AAZ29788

ID AAZ29788 standard; protein; 95 AA.

XX AC AAZ29788;

XX DT 08-NOV-1999 (first entry)

XX DE Mycobacterial tuberculosis ESAT-6 protein.

XX KW Mycobacterial; ESAT-6; 6 kDa antigen; tuberculosis; infection;

XX KW immunological response; diagnosis; vaccine.

XX OS Mycobacterium tuberculosis.

XX PN US955077-A.

XX PD 21-SEP-1999.

XX PF 05-JUN-1995; 95US-00465640.

XX PR 20-SEP-1993; 93US-00123182.

XX PR 01-JUL-1994; 94WO-DK000273.

XX PA (STAT-) STATENS SERUMINSTITUT.

XX PI Andersen P, Haslov K, Sorensen AL, Andersen AB;

XX DR WPI; 1999-539545/45.

XX DR N-PSDB; AAZ08877.

XX PT Polypeptide secreted from Mycobacterium is useful as a vaccine against

XX PT tuberculosis.

XX PS Claim 24; Fig 10C; 39pp; English.

XX CC The present invention describes a purified or non-naturally occurring

XX CC polypeptide (I) released from a metabolising mycobacteria comprising an

XX CC ESAT6, also called the 6 kDa antigen. The present sequence represents

XX CC Mycobacterium tuberculosis ESAT-6 protein. Also described is a purified

XX CC or non-naturally occurring polypeptide (II) with the ability to elicit a

XX CC delayed type hypersensitivity reaction which comprises a T cell epitope

XX CC of (I). (II) can be used with a carrier or vehicle in a composition for

XX CC diagnosing tuberculosis caused by mycobacteria belonging to the

XX CC tuberculosis complex, i.e. Mycobacterium tuberculosis, M. bovis and M.

XX CC africanum. The composition can be used to detect microbial antibodies or

XX CC components of mycobacteria in samples or in animals through the use of

XX CC immunoassays. (II) can be used as a vaccine for immunising an animal,

XX CC including humans against tuberculosis caused by mycobacteria of the

XX CC tuberculosis-complex. (II) induce a release of IFN-gamma from reactivated

XX CC T-lymphocytes evoking a protective immune response. Vaccine containing

XX CC (II) has the same protective potency as the live BCG vaccine against

XX SQ Sequence 95 AA;

Query Match 100.0%; Score 77; DB 2; Length 95;

Best Local Similarity 100.0%; Pred. No. 2.6e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAIQG 15

| | | | | | | | | | | | | | |

DB 6 WNFAGIEAAASAIQG 20

RESULT 19

AAZ29890

ID AAZ29890 standard; protein; 95 AA.

XX AC AAZ29890;

XX DT 18-NOV-1999 (first entry)

XX XX

DE	Mycobacterium tuberculosis ESAT-6 protein sequence.
KX	
XX	Mycobacterial; lactic acid bacterium; diagnosis; skin test; vaccine;
KW	delayed type hypersensitivity; DTH; ESAT-6 homodimer; tuberculosis;
KW	interferon-gamma release.
OS	
XX	Mycobacterium tuberculosis.
PN	WO9945119-A2.
PD	10-SEP-1999.
PF	05-MAR-1999; 99WO-DK000109.
PR	06-MAR-1998; 98DK-00000306.
PR	06-MAR-1998; 98US-C077105P.
PA	(STAT-) STATENS SERUM INST.
PJ	Jensen CL, Folkersen J;
DR	WPI, 1999-551043/46.
DR	N-PSDB; AA221132.
PT	New mycobacterial polypeptide produced in lactic acid bacteria, useful in
PT	tuberculosis diagnosis and vaccines.
PS	Disclosure; Page 75-76; 76pp; English.
CC	The present invention describes a bioactive polypeptide (or immunologically equivalent analogue) produced in lactic acid bacteria which reacts with lymphoid cells primed with Mycobacterium tuberculosis complex mycobacteria (M. tuberculosis, M. africanum or M. bovis). The polypeptide and ESAT-6 polypeptides are useful in compositions for diagnosis of and vaccination against tuberculosis caused by M. tuberculosis complex mycobacteria. The ESAT-6 polypeptide can be used to diagnose ongoing/previous sensitisation with these bacteria by detecting cytokine release when contacting blood samples with the polypeptide. The bioactive polypeptide may be used in diagnostic compositions and vaccines for mycobacteria other than of the M. tuberculosis complex, e.g. M. avium which infects poultry and occasionally humans, M. leprae; they are especially useful when they do not react with lymphoid cells previously primed with M. tuberculosis complex mycobacteria, and so do not give rise to a diagnostic reaction in individuals infected with these bacteria. The polypeptides may also be used in vitro diagnostic tests e.g. stimulation of interferon-gamma release from lymphocytes. The polypeptide has similar or higher bioactivity as currently used tuberculin reagent in the standard delayed type hypersensitivity (DTH) skin test for tuberculosis, but may have greater specificity, being better able to discriminate between lymphoid cells primed from tuberculosis and from previous vaccination. The present sequence represents M. tuberculosis ESAT-6 used in the exemplification of the present invention
XX	Sequence 95 AA;
SQ	
Query Match	100.0%; Score 77; DB 2; Length 95;
Best local similarity	100.0%; Pred. NO. 2.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
OY	1 WNPAGIEAASAIQG 15
DB	6 WNPAGIEAASAIQG 20
RESULT 20	
AAB35219	
ID	AAB35219 standard; protein; 95 AA.
AC	AAB35219;
XX	
DT	24-APR-2001 (first entry)
XX	

CC composition may be utilised in gene therapy and vaccine development. The
CC current sequence is that of the Mycobacterium tuberculosis ESAT-6 protein
CC of the invention.

XX SQ Sequence 95 AA;

Query Match 100.0%; Score 77; DB 7; Length 95;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNPAGIEAAASAIQG 15
|||||
Db 6 WNPAGIEAAASAIQG 20

RESULT 24

ADI33376
ID ADI33376 standard; peptide; 95 AA.

XX AC ADI33376;

XX DT 22-APR-2004 (first entry)

XX DE Mycobacterium tuberculosis ESAT-6 protein.

XX KW pathogen; vaccine; cellular response; HPV; HIV; SIV; HCV; chlamydia; HBV;
XX EBV; CMV; VZV; HSV; Legionella; Leishmaniasis; Influenza;
XX foot and mouth virus; Toxoplasma; Brucella; Cryptococcus; Candida;
XX Aspergillus; Mycobacterium; T cell; ESAT-6; CFP10; virucide; protozoide;
XX antibacterial; fungicide; epitope.

XX OS Mycobacterium tuberculosis.

XX PN WO2004005925-A2.

XX PD 15-JAN-2004.

XX PF 07-JUL-2003; 2003WO-GB002936.

XX PR 05-JUL-2002; 2002GB-00015710.

XX PA (ISIS-) ISIS INNOVATION LTD.

XX PI Lalvani A, Ewer K;

XX PT WPI; 2004-143006/14.

XX DR Diagnosing in an individual recent exposure to an agent, useful in
XX treating a disease caused by a pathogen, by determining in vitro or in
XX vivo whether the T cells of recognize a protein having at least 30 amino
XX acids.

XX PS Disclosure; Page 21-22; 48pp; English.

XX CC The invention relates to a novel method for diagnosing in an individual
XX recent exposure to an agent which is a pathogen, vaccine or any other
XX moiety, which induces a cellular response. The pathogen can include: HPV,
XX HIV, SIV, HCV, chlamydia species, HBV, EBV, CMV, VZV, HSV, Legionella, S.
XX typhi, P. falciparum, Leishmaniasis, M. leprae, influenza virus, foot and
XX mouth virus, a Toxoplasma species, a Brucella species, a Cryptococcus
XX species, a Candida species, an Aspergillus species, or Mycobacterium
XX tuberculosis. The invention also provides a vaccine against any of the
XX above pathogens. The method comprises determining in vitro or in vivo
XX whether the T cells of the individual recognize a protein from the agent
XX having a length of at least 30 amino acids. The invention also comprises
XX a protein or epitope peptide which is from ESAT-6 or CFP10. The vaccines
XX of the invention have: virucide, protozoide, antibacterial, and fungicide
XX activity. The method is useful in diagnosing in an individual recent
XX exposure to an agent which is a pathogen, vaccine or any other moiety
XX which induces a cellular response. The protein described above, the
XX product which prevents or treats a condition caused by a pathogen or the
XX antigen or its analogue is useful in the manufacturing of a medicament
XX for diagnosing and treating an individual recently exposed to a pathogen.

CC This sequence represents the Mycobacterium tuberculosis ESAT-6 protein
CC used in the invention.

XX SQ Sequence 95 AA;

Query Match 100.0%; Score 77; DB 8; Length 95;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNPAGIEAAASAIQG 15
|||||
Db 6 WNPAGIEAAASAIQG 20

RESULT 25

ADN36323
ID ADN36323 standard; protein; 95 AA.

XX AC ADN36323;

XX DT 15-JUL-2004 (first entry)

XX DE Mycobacterium tuberculosis antigen ESAT-6.

XX KW antibacterial; antiparasitic; virucide; immunosuppressive; cytostatic;
XX Gene therapy; vaccine; single-chain variable region fragment; scFv;
XX antigen-presenting cell; dendritic cell; infectious disease;
XX autoimmune disease; cancer; CD11c.

XX OS Mycobacterium tuberculosis.

XX PN WO2004035619-A1.

XX PD 29-APR-2004.

XX PF 20-OCT-2003; 2003WO-AU001392.

XX PR 18-OCT-2002; 2002US-0420232P.

XX PA (CENT-) CENTENARY INST CANCER MEDICINE & CELL BI.

XX PI Britton W, Demangel C;

XX DR WPI; 2004-365152/34.

XX N-PSDB; ADN36322.

XX PT New antibody single-chain variable region fragments capable of targeting
XX antigen-presenting cells, useful for preventing or treating diseases,
XX e.g. infectious diseases, autoimmune diseases or cancer.

XX PS Claim 20; SEQ ID NO 18; 82pp; English.

XX CC The invention relates to a single-chain variable region fragment (scFv)
XX comprising a heavy chain variable region (VH) operably linked to a light
XX chain variable region (VL), where the scFv is capable of specifically
XX binding to a molecule on the surface of an antigen-presenting cell (APC).
XX The composition and methods are useful for targeting antigens to antigen-
XX presenting cells, such as dendritic cells. These may be used for
XX preventing and/or treating diseases, such as infectious diseases,
XX autoimmune diseases or cancer. This sequence corresponds to the
XX Mycobacterium tuberculosis antigen ESAT-6. This sequence can be fused to
XX a scFv protein sequence to form a fusion protein.

XX SQ Sequence 95 AA;

Query Match 100.0%; Score 77; DB 8; Length 95;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNPAGIEAAASAIQG 15
|||||
Db 6 WNPAGIEAAASAIQG 20

RESULT 26

AEB45084
ID AEB45084 standard; protein; 95 AA.

XX AC AEB45084;
XX DT

XX 06-OCT-2005 (first entry)

XX M. tuberculosis early secretory antigenic target 6, ESAT6.

XX immunogenicity; viral infection; infection; bacterial infection; cancer;
KW neoplasm; autoimmune disease; immune disorder; inflammation; allergy;
KW Antibacterial; Virucide; Fungicide; Anti-HIV; Hepatotropic;
KW Antiparasitic; Cytostatic; immunosuppressive; antiarthritic;
KW antirheumatic; neuroprotective; antidiabetic; gastrointestinal-Gen.;
KW antiinflammatory; antitumor; antiparasitic; dermatological;
KW antiasthmatic; antiallergic; immunomodulator.

XX Mycobacterium tuberculosis.

XX OS

XX PN WO2005070959-A2.

XX PD 04-AUG-2005.

XX 24-JAN-2005; 2005WO-US002251.

XX 23-JAN-2004; 2004US-0538713P.

XX 06-OCT-2004; 2004US-0616855P.

XX (VIEW-) VIEWAX CORP.

XX PA Mahairas GG;

XX PI WPI; 2005-542270/55.

XX Immune response altering agent useful for treating autoimmune diseases,
PT comprises first domain having T/B cell epitopes or Toll-like receptor-
PT binding proteins, and second domain having heterologous target molecule.

XX Claim 59; SEQ ID NO 214; 130pp; English.

XX The invention relates to an immune response altering agent (I) which
CC comprises a first domain having one or more components chosen from T cell
CC epitopes, B cell epitopes, and Toll-like receptor (TLR)-binding proteins
CC or its TLR-binding domain, and a second domain having heterologous
CC target molecule against which an immune response is desired. (I) is
CC useful for altering or inducing an immune response to a target. (I) is
CC also useful for treating viral infections (e.g., HIV and hepatitis C
CC virus), bacterial infections (e.g., Staphylococcus and Pseudomonas),
CC parasites (e.g., Leishmania), fungal infections (e.g., Candida), cancer
CC (e.g., non-Hodgkin's lymphoma, Hodgkin's disease and leukemia), and
CC autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,
CC insulin dependent diabetes, Addison's disease, celiac disease,
CC inflammatory bowel disease, ulcerative colitis, Crohn's disease, systemic
CC lupus erythematosus, psoriasis, Sjogren's syndrome, etc. (I) is useful
CC for treating inflammatory and hyperproliferative skin diseases, and
CC allergic reactions such as asthma, bronchitis, allergic rhinitis etc. (I)
CC alters an immune response generated against the heterologous target
CC molecule. (I) can be applied to wide range of species such as humans, non
CC -human primates, horses, etc. The present sequence represents the amino
CC acid sequence of the M. tuberculosis early secretory antigenic target 6,
CC ESAT6.

XX SQ Sequence 95 AA;

Query Match 100.0%; Score 77; DB 9; Length 95;

Best Local Similarity 100.0%; Pred. No. 2.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WNFAGIEAASAIQG 15

Db 6 WNFAGIEAASAIQG 20

RESULT 27

ADE28541

ID ADE28541 standard; protein; 142 AA.

XX AC ADE28541;

XX 29-JAN-2004 (first entry)

XX Human/Mycobacterium tuberculosis ESAT-6/CD1a fusion construct protein.

XX CD1 fusion protein; endosomal targeting; antibacterial; virucide;
KW cytostatic; antidiabetic; antiinflammatory; dermatological;
KW immunosuppressive; neuroprotective; immune response; microbial;
KW viral infection; autoimmune disorder; diabetes; lupus;
KW multiple sclerosis; cancer; gene therapy; vaccine; human; ESAT-6/CD1a;
KW chimeric.

XX OS Chimeric.

XX OS Synthetic.

XX OS Homo sapiens.

XX OS Mycobacterium tuberculosis.

XX PN WO2003066820-A2.

XX 14-AUG-2003.

XX 05-FEB-2003; 2003WO-US003550.

XX 05-FEB-2002; 2002US-0355432P.

XX (REGC) UNIV CALIFORNIA.

XX Modlin RL;

XX WPI; 2003-748121/70.

XX N-PSDB; ADE28540.

XX New chimeric nucleic acid molecule encoding a CD1 fusion protein, useful
PT for inducing an immune response against antigens associated with, e.g.
PT microbial or viral infections, autoimmune disorders or cancer.

XX Claim 26; Fig 9A; 114pp; English.

XX The invention relates to a novel chimeric nucleic acid molecule
CC consisting of a nucleotide sequence encoding a CD1 fusion protein
CC comprising a CD1 endosomal targeting sequence or its fragment and an
CC antigen of interest. The polynucleotide of the invention demonstrates
CC antibacterial, virucide, cytostatic, antidiabetic, antiinflammatory,
CC dermatological, immunosuppressive and neuroprotective activities whilst
CC the composition and methods may be useful for inducing an immune response
CC against antigens of interest which are associated with microbial or viral
CC infections, autoimmune disorders including diabetes, lupus and multiple
CC sclerosis and antigens associated with cancers. Furthermore, the
CC composition may be utilised in gene therapy and vaccine development. The
CC current sequence is that of the human/Mycobacterium tuberculosis ESAT-
CC 6/CD1a fusion construct protein of the invention.

XX SQ Sequence 142 AA;

Query Match 100.0%; Score 77; DB 7; Length 142;

Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WNFAGIEAASAIQG 15

Db 25 WNFAGIEAASAIQG 39

RESULT 28

ADE28543

ID ADE28543 standard; protein; 145 AA.

```

XX AC ADE28543;
XX AC 29-JAN-2004 (first entry)
XX DE Human/Mycobacterium tuberculosis ESAT-6/CD1b fusion construct protein.
XX KW CD1 fusion protein; endosomal targeting; antibacterial; virucide;
XX KW cytostatic; antidiabetic; antiinflammatory; dermatological;
XX KW immunosuppressive; neuroprotective; immune response; microbial;
XX KW viral infection; autoimmune disorder; diabetes; lupus;
XX KW multiple sclerosis; cancer; gene therapy; vaccine; human; ESAT-6/CD1b;
XX KW chimeric.
XX OS Chimeric.
XX OS Synthetic.
XX OS Homo sapiens.
XX OS Mycobacterium tuberculosis.
XX PN WO2003066820-A2.
XX PD 14-AUG-2003.
XX PP 05-FEB-2003; 2003WO-US003550.
XX PR 05-FEB-2002; 2002US-0355432P.
XX PR (REGC ) UNIV CALIFORNIA.
XX PA Modlin RL;
XX PI WPI; 2003-748121/70.
XX DR N-PSDB; ADE28542.
XX PT New chimeric nucleic acid molecule encoding a CD1 fusion protein, useful
XX PT for inducing an immune response against antigens associated with, e.g.
XX PT microbial or viral infections, autoimmune disorders or cancer.
XX PS Example 1, Fig 9B; 114pp; English.
XX CC The invention relates to a novel chimeric nucleic acid molecule
XX CC consisting of a nucleotide sequence encoding a CD1 fusion protein
XX CC comprising a CD1 endosomal targeting sequence or its fragment and an
XX CC antigen of interest. The polynucleotide of the invention demonstrates
XX CC antibacterial, virucide, cytostatic, antidiabetic, antiinflammatory,
XX CC dermatological, immunosuppressive and neuroprotective activities whilst
XX CC against antigens of interest which are associated with an immune response
XX CC the composition and methods may be useful for inducing an immune response
XX CC against antigens of interest which are associated with microbial or viral
XX CC infections, autoimmune disorders including diabetes, lupus and multiple
XX CC sclerosis and antigens associated with cancers. Furthermore, the
XX CC composition may be utilised in gene therapy and vaccine development. The
XX CC current sequence is that of the human/Mycobacterium tuberculosis ESAT-
XX CC 6/CD1b fusion construct protein of the invention.
XX SQ Sequence 145 AA;
XX Query Match 100.0%; Score 77; DB 7; Length 145;
XX Best Local Similarity 100.0%; Pred. No. 4.1e-05;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 WNPAGTAAASAIQ 15
XX DB 25 WNPAGTAAASAIQ 39
XX RESULT 29
XX ID ADE28545 standard; protein; 146 AA.
XX AC ADE28545;
XX XX 29-JAN-2004 (first entry)
XX DT
XX XX

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DE XX Human/Mycobacterium tuberculosis ESAT-6/CD1c fusion construct protein.
XX KW CD1 fusion protein; endosomal targeting; antibacterial; virucide;
XX KW cytostatic; antidiabetic; antiinflammatory; dermatological;
XX KW immunosuppressive; neuroprotective; immune response; microbial;
XX KW viral infection; autoimmune disorder; diabetes; lupus;
XX KW multiple sclerosis; cancer; gene therapy; vaccine; human; ESAT-6/CD1c;
XX KW chimeric.
XX OS Chimeric.
XX OS Synthetic.
XX OS Homo sapiens.
XX OS Mycobacterium tuberculosis.
XX PN WO2003066820-A2.
XX PD 14-AUG-2003.
XX PP 05-FEB-2003; 2003WO-US003550.
XX PR 05-FEB-2002; 2002US-0355432P.
XX PR (REGC ) UNIV CALIFORNIA.
XX PA Modlin RL;
XX PI WPI; 2003-748121/70.
XX DR N-PSDB; ADE28544.
XX PT New chimeric nucleic acid molecule encoding a CD1 fusion protein, useful
XX PT for inducing an immune response against antigens associated with, e.g.
XX PT microbial or viral infections, autoimmune disorders or cancer.
XX PS Example 1; Fig 9C; 114pp; English.
XX CC The invention relates to a novel chimeric nucleic acid molecule
XX CC consisting of a nucleotide sequence encoding a CD1 fusion protein
XX CC comprising a CD1 endosomal targeting sequence or its fragment and an
XX CC antigen of interest. The polynucleotide of the invention demonstrates
XX CC antibacterial, virucide, cytostatic, antidiabetic, antiinflammatory,
XX CC dermatological, immunosuppressive and neuroprotective activities whilst
XX CC against antigens of interest which are associated with microbial or viral
XX CC infections, autoimmune disorders including diabetes, lupus and multiple
XX CC sclerosis and antigens associated with cancers. Furthermore, the
XX CC composition may be utilised in gene therapy and vaccine development. The
XX CC current sequence is that of the human/Mycobacterium tuberculosis ESAT-
XX CC 6/CD1c fusion construct protein of the invention.
XX SQ Sequence 146 AA;
XX Query Match 100.0%; Score 77; DB 7; Length 146;
XX Best Local Similarity 100.0%; Pred. No. 4.1e-05;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 WNPAGTAAASAIQ 15
XX DB 25 WNPAGTAAASAIQ 39
XX RESULT 30
XX ID ADE28547 standard; protein; 146 AA.
XX AC ADE28547;
XX XX 29-JAN-2004 (first entry)
XX DT
XX XX Human/Mycobacterium tuberculosis ESAT-6/CD1d fusion construct protein.
XX KW CD1 fusion protein; endosomal targeting; antibacterial; virucide;
XX KW cytostatic; antidiabetic; antiinflammatory; dermatological;
XX KW immunosuppressive; neuroprotective; immune response; microbial;

```

KW viral infection; autoimmune disorder; diabetes; lupus;
 KW multiple sclerosis; cancer; gene therapy; vaccine; human; ESAT-6/CDId;
 KW chimeric.
 XX
 OS Chimeric.
 OS Synthetic.
 OS Homo sapiens.
 OS Mycobacterium tuberculosis.
 XX
 XX WO2003066820-A2.
 XX
 XX 14-AUG-2003.
 PD
 XX
 XX 05-FEB-2003; 2003WO-US003550.
 PF
 XX
 XX 05-FEB-2002; 2002US-0355432P.
 PR
 XX
 XX (REGC) UNIV CALIFORNIA.
 PA
 XX
 XX Modlin RL;
 PI
 XX
 XX WPI; 2003-748121/70.
 DR
 XX N-PSDB; ADE28546.
 DR
 XX
 XX New chimeric nucleic acid molecule encoding a CD1 fusion protein, useful
 PT for inducing an immune response against antigens associated with, e.g.
 PT microbial or viral infections, autoimmune disorders or cancer.
 PT
 XX
 XX Example 1; Fig 9D; 114pp; English.
 PS
 XX
 XX The invention relates to a novel chimeric nucleic acid molecule
 CC consisting of a nucleotide sequence encoding a CD1 fusion protein
 CC comprising a CD1 endosomal targeting sequence or its fragment and an
 CC antigen of interest. The polynucleotide of the invention demonstrates
 CC antibacterial, virucidal, cytostatic, antidiabetic, antiinflammatory,
 CC dermatological, immunosuppressive and neuroprotective activities whilst
 CC the composition and methods may be useful for inducing an immune response
 CC against antigens of interest which are associated with microbial or viral
 CC infections, autoimmune disorders including diabetes, lupus and multiple
 CC sclerosis and antigens associated with cancers. Furthermore, the
 CC composition may be utilised in gene therapy and vaccine development. The
 CC current sequence is that of the human/Mycobacterium tuberculosis ESAT-
 CC 6/CDId fusion construct protein of the invention.
 XX
 XX Sequence 146 AA;
 SQ
 Query Match 100.0%; Score 77; DB 7; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WNFAGIEAAASAIQG 15
 DB 25 WNFAGIEAAASAIQG 39
 |||||
 RESULT 31
 AAY29888
 ID AAY29888 standard; protein; 196 AA.
 XX
 AC AAY29888;
 XX
 XX 18-NOV-1999 (first entry)
 DT
 XX
 XX Mycobacterium tuberculosis ESAT-6 protein sequence.
 DE
 XX
 XX Mycobacterial; lactic acid bacterium; diagnosis; skin test; vaccine;
 KW delayed type hypersensitivity; DTH; ESAT-6 homodimer; tuberculosis;
 KW interferon-gamma release.
 XX
 XX Mycobacterium tuberculosis.
 OS
 XX
 XX WO9945119-A2.
 PN
 XX
 XX

PD 10-SEP-1999.
 XX
 PF 05-MAR-1999; 99WO-DK000109.
 XX
 PR 06-MAR-1998; 98DK-00000306.
 PR 06-MAR-1998; 98US-0077105P.
 XX
 XX (STAT-) STATENS SERUM INST.
 PA
 XX
 XX Jensen CL, Folkersen J;
 PI
 XX WPI; 1999-551043/46.
 DR N-PSDB; AAZ21131.
 DR
 XX
 XX New mycobacterial polypeptide produced in lactic acid bacteria, useful in
 PT tuberculosis diagnosis and vaccines.
 PT
 XX
 XX Disclosure; Page 74; 76pp; English.
 PS
 XX
 XX The present invention describes a bioactive polypeptide (or
 CC immunologically equivalent analogue) produced in lactic acid bacteria
 CC which reacts with lymphoid cells primed with Mycobacterium tuberculosis
 CC complex mycobacteria (M. tuberculosis, M. africanum or M. bovis). The
 CC polypeptide and ESAT-6 polypeptides are useful in compositions for
 CC diagnosis of and vaccination against tuberculosis caused by M.
 CC tuberculosis complex mycobacteria. The ESAT-6 polypeptide can be used to
 CC diagnose ongoing/previous sensitisation with these bacteria by detecting
 CC cytokine release when contacting blood samples with the polypeptide. The
 CC bioactive polypeptide may be used in diagnostic compositions and
 CC vaccines for mycobacteria other than of the M. tuberculosis complex, e.g.
 CC M. avium which infects poultry and occasionally humans, M. leprae; they
 CC are especially useful when they do not react with lymphoid cells
 CC previously primed with M. tuberculosis complex mycobacteria, and so do
 CC not give rise to a diagnostic reaction in individuals infected with these
 CC bacteria. The polypeptides may also be used in in vitro diagnostic tests
 CC e.g. stimulation of interferon-gamma release from lymphocytes. The
 CC polypeptide has similar or higher bioactivity as currently used
 CC tuberculin reagent in the standard delayed type hypersensitivity (DTH)
 CC skin test for tuberculosis, but may have greater specificity, being
 CC better able to discriminate between lymphoid cells primed from
 CC tuberculosis and from previous vaccination. The present sequence
 CC represents M. tuberculosis ESAT-6 used in the exemplification of the
 XX present invention
 XX
 XX Sequence 196 AA;
 SQ
 Query Match 100.0%; Score 77; DB 2; Length 196;
 Best Local Similarity 100.0%; Pred. No. 5.6e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WNFAGIEAAASAIQG 15
 DB 10 WNFAGIEAAASAIQG 24
 |||||
 RESULT 32
 AAW72943
 ID AAW72943 standard; protein; 403 AA.
 XX
 AC AAW72943;
 XX
 XX 21-JAN-1999 (first entry)
 DT
 XX
 XX Mycobacterium tuberculosis antigen ESAT6-MPT59.
 DE
 XX
 XX Mycobacterium tuberculosis; antigen; vaccine; immunological; immunogen;
 KW infection.
 KW
 XX
 XX Mycobacterium tuberculosis.
 OS
 XX
 XX WO9844119-A1.
 PN
 XX
 XX 08-OCT-1998.
 PD

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XX 01-APR-1998; 98WO-DK000132.
XX
XX 02-APR-1997; 97DK-00000376.
PR 18-APR-1997; 97US-0044624P.
PR 10-NOV-1997; 97DK-00001277.
PR 05-JAN-1998; 98US-0070488P.
XX
XX (STAT-) STATENS SERUM INST.
XX
XX Andersen P, Nielsen R, Rosenkrands I, Weldingh K, Rasmussen PB;
PI Oettinger T, Florio W;
XX
XX WPI; 1998-542705/46.
XX
XX New isolated mycobacteria polypeptides and nucleic acids - used for
PT developing products for the diagnosis of or vaccination against
PT mycobacterial infections, particularly tuberculosis.
XX
XX Disclosure; Page 233-234; 163pp; English.
XX
XX The present sequence represents a Mycobacterium tuberculosis protein.
CC Products from the present invention, which describes protein fragments
CC and nucleic acid fragments derived from M.tuberculosis, can be used in
CC the detection of and prevention of mycobacterial infections. In
CC particular, the proteins and nucleic acids can be used for the diagnosis
CC of or vaccination against tuberculosis caused by M. tuberculosis, M.
CC africanum or M. bovis
XX
XX Sequence 403 AA;
SQ
Query Match 100.0%; Score 77; DB 2; Length 403;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAIQG 15
Db | | | | | | | | | | | | | | |
27 WNFAGIEAAASAIQG 41

RESULT 33
AAV21963
ID AAV21963 standard; protein; 403 AA.
XX
XX AAV21963;
XX
XX 06-SEP-1999 (first entry)
XX
XX Amino acid sequence of antigen ESAT-6.
XX
XX Immunogenic; Mycobacterium tuberculosis; immune response; infection;
KW tuberculosis; fusion polypeptide; T-cell epitope; ESAT-6; MPT59; TB;
KW pharmaceutical; vaccination; M. africanum; M. bovis; CFP7A; CFP30A;
KW CFP7B; CFP19; CFP27; CFP30A; RD1-ORF; CFP16; CFP19; CFP23;
KW CFP25A; CFP30B; CFP7B.
XX
XX Mycobacterium tuberculosis.
OS
XX WO9924577-A1.
XX
XX 20-MAY-1999.
XX
XX 08-OCT-1998; 98WO-DK000438.
XX
XX 10-NOV-1997; 97DK-00001277.
PR 05-JAN-1998; 98US-0070488P.
PR 01-APR-1998; 98WO-DK000132.
XX
XX (STAT-) STATENS SERUM INST.
XX
XX Andersen P, Skjot R;
PI
XX WPI; 1999-347282/29.
DR

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XX New immunogenic fragment of Mycobacterium tuberculosis.
XX
XX Example; Page 250-251; 265pp; English.
XX
XX The invention describes a substantially pure immunogenic polypeptide
CC fragment (1) from Mycobacterium tuberculosis that is able to evoke a
CC protective immune response against infections by mycobacteria belonging
CC to the tuberculosis complex. The invention provides a (1) fusion of at
CC least one polypeptide fragment comprising a (1) fusion of at least
CC one fusion partner; (2) a fusion polypeptide fragment comprising a T-cell
CC epitope from M. tuberculosis protein ESAT-6, or MPT59 and a second
CC different amino acid sequence from M. tuberculosis, and/or including a
CC sequence which protects the first amino acid sequence from in vivo
CC degradation or post-translational processing; (3) a nucleic acid fragment
CC that encodes the above polypeptides. The polypeptides and nucleic acid
CC are useful as pharmaceuticals, for diagnosis of and as antigens for
CC vaccination against TB caused by Mycobacterium tuberculosis, africanum or
CC bovis. The polypeptides are also useful for diagnosing ongoing or
CC previous sensitization in an animal with bacteria belonging to the
CC tuberculosis complex. The invention also describes the use of CFP7A or
CC CFP30A or a T-cell epitope of for the induction of a strong immune
CC response in a mammal; use of CFP7B, CFP19 or MPT59-ESAT6 or a T-cell
CC epitope of for diagnosis of TB in a mammal by performing a DTH type skin
CC test; use of CFP27, CFP30A, RD1-ORF2, RD1-ORF3, MPT59-ESAT6,
CC ESAT6-MPT59, CFP10A, CFP16, CFP19, CFP23, CFP25A, CFP30B, CFP7B or a T-
CC cell epitope of for the preparation of an immunological composition; and
CC for the preparation of a subunit vaccine
XX
XX Sequence 403 AA;
SQ
Query Match 100.0%; Score 77; DB 2; Length 403;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAIQG 15
Db | | | | | | | | | | | | | | |
27 WNFAGIEAAASAIQG 41

RESULT 34
AAW72942
ID AAW72942 standard; protein; 404 AA.
XX
XX AAW72942;
XX
XX 21-JAN-1999 (first entry)
XX
XX Mycobacterium tuberculosis antigen MPT59-ESAT6.
XX
XX Mycobacterium tuberculosis; antigen; vaccine; immunological; immunogen;
KW infection.
XX
XX Mycobacterium tuberculosis.
OS
XX WO9844119-A1.
XX
XX 08-OCT-1998.
XX
XX 01-APR-1998; 98WO-DK000132.
XX
XX 02-APR-1997; 97DK-00000376.
PR 18-APR-1997; 97US-0044624P.
PR 10-NOV-1997; 97DK-00001277.
PR 05-JAN-1998; 98US-0070488P.
XX
XX (STAT-) STATENS SERUM INST.
XX
XX Andersen P, Nielsen R, Rosenkrands I, Weldingh K, Rasmussen PB;
PI Oettinger T, Florio W;
XX
XX WPI; 1998-542705/46.
DR
XX

```

PT New isolated mycobacteria polypeptides and nucleic acids - used for
 PT developing products for the diagnosis of or vaccination against
 PT mycobacterial infections, particularly tuberculosis.

PS Disclosure; Page 232-233; 163pp; English.

XX The present sequence represents a Mycobacterium tuberculosis protein.
 CC Products from the present invention, which describes protein fragments
 CC and nucleic acid fragments derived from M.tuberculosis, can be used in
 CC the detection of and prevention of mycobacterial infections. In
 CC particular, the proteins and nucleic acids can be used for the diagnosis
 CC of or vaccination against tuberculosis caused by M. tuberculosis, M.
 CC africanum or M. bovis

XX Sequence 404 AA;

Query Match 100.0%; Score 77; DB 2; Length 404;
 Best Local Similarity 100.0%; Pred. No. 0.00012;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAASAIQ 15
 |||||
 Db 315 WNFAGIEAASAIQ 329

RESULT 35

AA21962
 ID AAY21962 standard; protein; 404 AA.

XX AC AAY21962;

XX DT 06-SEP-1999 (first entry)

XX DE Amino acid sequence of antigen MPT59.

XX Immunogenic; Mycobacterium tuberculosis; immune response; infection;
 KW tuberculosis; fusion polypeptide; T-cell epitope; ESAT-6; MPT59; TB;
 KW pharmaceutical; vaccination; M. africanum; M. bovis; CFP7A; CFP30A;
 KW CFP7B; CFP19; CFP23; CFP30A; RD1-ORF; CFP10A; CFP16; CFP19; CFP23;
 KW CFP25A; CFP30B; CFP7B.

XX Mycobacterium tuberculosis.

XX WO9924577-A1.

XX 20-MAY-1999.

XX 08-OCT-1998; 98WO-DK000438.

XX 10-NOV-1997; 97DK-00001277.

XX 05-JAN-1998; 98US-0070488P.

XX 01-APR-1998; 98WO-DK000132.

XX (STAT-) STATENS SERUM INST.

XX Andersen P, Skjot R;

XX WPI; 1999-347282/29.

XX New immunogenic fragment of Mycobacterium tuberculosis.

XX Example; Page 249-250; 265pp; English.

XX The invention describes a substantially pure immunogenic polypeptide
 CC fragment (I) from Mycobacterium tuberculosis that is able to evoke a
 CC protective immune response against infections by mycobacteria belonging
 CC to the tuberculosis complex. The invention provides a (1) fusion
 CC polypeptide comprising at least one polypeptide fragment (I) and at least
 CC one fusion partner; (2) a fusion polypeptide fragment comprising a T-cell
 CC epitope from M. tuberculosis protein ESAT-6, or MPT59 and a second
 CC different amino acid sequence from M. tuberculosis, and/or including a
 CC sequence which protects the first amino acid sequence from in vivo
 CC degradation or post-translational processing; (3) a nucleic acid fragment

CC that encodes the above polypeptides. The polypeptides and nucleic acid
 CC are useful as pharmaceuticals, for diagnosis of and as antigens for
 CC vaccination against TB caused by Mycobacterium tuberculosis, africanum or
 CC bovis. The polypeptides are also useful for diagnosing ongoing or
 CC previous sensitization in an animal with bacteria belonging to the
 CC tuberculosis complex. The invention also describes the use of CFP7A or
 CC CFP30A or a T-cell epitope of for the induction of a strong immune
 CC response in a mammal; use of CFP7B, CFP19 or MPT59-ESAT6 or a T-cell
 CC epitope of for diagnosis of TB in a mammal by performing a DTH type skin
 CC test; use of CFP27, CFP30A, RD1-ORF2, RD1-ORF3, RD1-ORF5, MPT59-ESAT6,
 CC ESAT6-MPT59, CFP10A, CFP16, CFP19, CFP23, CFP25A, CFP30B, CFP7B or a T-
 CC cell epitope of for the preparation of an immunological composition; and
 CC for the preparation of a subunit vaccine

XX Sequence 404 AA;

Query Match 100.0%; Score 77; DB 2; Length 404;
 Best Local Similarity 100.0%; Pred. No. 0.00012;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAASAIQ 15
 |||||
 Db 315 WNFAGIEAASAIQ 329

RESULT 36

AEB45087

ID AEB45087 standard; peptide; 15 AA.

XX AC AEB45087;

XX DT 06-OCT-2005 (first entry)

XX DE M. tuberculosis ESAT6 peptide fragment SEQ ID NO 217.

XX immunogenicity; viral infection; infection; bacterial infection; cancer;
 KW neoplasm; autoimmune disease; immune disorder; inflammation; allergy;
 KW Antibacterial; Virucide; Fungicide; Anti-HIV; Hepatotropic;
 KW Antiparasitic; Cytostatic; Immunosuppressive; Antiarthritic;
 KW antirheumatic; neuroprotective; antidiabetic; gastrointestinal-Gen.;
 KW antiinflammatory; antiulcer; antipsoriatic; dermatological;
 KW antiasthmatic; anti-allergic; Immunomodulator.

XX Mycobacterium tuberculosis.

XX WO2005070959-A2.

XX 04-AUG-2005.

XX 24-JAN-2005; 2005WO-US002251.

XX 23-JAN-2004; 2004US-0538713P.

XX 06-OCT-2004; 2004US-0616855P.

XX (VIEW-) VIEWAX CORP.

XX Mahairas GG;

XX WPI; 2005-542270/55.

XX Immune response altering agent useful for treating autoimmune diseases,
 PT comprises first domain having T/B cell epitopes or Toll-like receptor-
 PT binding proteins, and second domain having heterologous target molecule.

XX Claim 65; SEQ ID NO 217; 130pp; English.

XX The invention relates to an immune response altering agent (I) which
 CC comprises a first domain having one or more components chosen from T cell
 CC epitopes, B cell epitopes, and Toll-like receptor (TLR)-binding proteins
 CC or its TLR-binding domains, and a second domain having heterologous
 CC target molecule against which an immune response is desired. (I) is
 CC useful for altering or inducing an immune response to a target. (I) is
 CC also useful for treating viral infections (e.g., HIV and hepatitis C

CC virus), bacterial infections (e.g., Staphylococcus and Pseudomonas).
 CC parasites (e.g., Leishmania), fungal infections (e.g., Candida), cancer
 CC (e.g., non-Hodgkin's lymphoma, Hodgkin's disease and leukemia), and
 CC autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,
 CC insulin dependent diabetes, Addison's disease, celiac disease,
 CC inflammatory bowel disease, ulcerative colitis, Crohn's disease, systemic
 CC lupus erythematosus, psoriasis, Sjogren's syndrome, etc. (I) is useful
 CC for treating inflammatory and hyperproliferative skin diseases, and
 CC allergic reactions such as asthma, bronchitis, allergic rhinitis etc. (I)
 CC alters an immune response generated against the heterologous target
 CC molecule. (I) can be applied to wide range of species such as humans, non
 CC -human primates, horses, etc. The present sequence represents the amino
 CC acid sequence of a M. tuberculosis early secretory antigenic target 6,
 CC ESAT6, peptide fragment.

XX Sequence 15 AA;

Query Match 92.2%; Score 71; DB 9; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAASAIQ 14
 |||||
 Db 2 WNFAGIEAASAIQ 15

RESULT 37

AAW35548

ID AAW35548 standard; peptide; 19 AA.

XX AAW35548;

XX 25-MAR-2003 (revised)

DT 22-APR-1998 (first entry)

XX ESAT-6 antigen SEQ ID NO:120 from WO9738011.

XX T-cell stimulatory peptide; immunogen; non-dendritic; carrier; tumour;

XX scaffold; inhibition; metastasis; wound healing; solid phase.

XX Synthetic.

XX WO9738011-A1.

PD 16-OCT-1997.

XX 03-APR-1997; 97WO-DK000146.

XX 03-APR-1996; 96DK-00000398.

XX (PEPR-) PEPRESEARCH AS.

XX Heegaard PMH, Jakobsen PH;

XX WPI; 1997-512645/47.

PT Non-dendritic peptide carrier linked to a solid phase - useful as a
 PT diagnostic agent and as a scaffold for production of chemical
 PT derivatives.

XX Example 32; Page 156; 262pp; English.

XX A non-dendritic peptide carrier (A) has been developed which is coupled
 CC through a linker to a solid phase, forming a complex of (A)-solid phase.
 CC where (A) comprises 10-50 amino acids capable of forming a secondary
 CC structure in a benign buffer after liberation from the solid phase, and
 CC further the (A)-solid phase complex comprises an immunogenic substance
 CC and/or an immune mediator coupled on (A). The present sequence represents
 CC a peptide used in an example from the present invention. An (A)-solid
 CC phase complex can be used as a scaffold for the production of chemical
 CC attachment points. Alternatively (A) is used as a scaffold-peptide for
 CC the incorporation into an Immunostimulating Complex (iscom) resulting an

CC (A)-Iscom complex which is used for the chemical coupling of antigenic
 CC substances in an aqueous solution by conjugation. (A) derivatised with
 CC one or more peptides having fibronectin-, laminin- or vitronectin-like
 CC binding activities can be used for the promotion of cell-attachment to
 CC plastic surfaces, in particular to inhibit tumour growth and metastasis,
 CC and for promotion of wound healing. Also a derivatised (A) can be used
 CC for the selection of specifically-binding aptamers or as a diagnostic
 CC agent. Such diagnostic- (A) molecules could be used to detect molecules
 CC derived from or indicative of pregnancy or of a disease, such as an
 CC infectious, autoimmune or cancerous disease. (Updated on 25-MAR-2003 to
 CC correct PF field.)

XX Sequence 19 AA;

Query Match 92.2%; Score 71; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 5.1e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAASAIQ 14
 |||||
 Db 6 WNFAGIEAASAIQ 19

RESULT 38

ADL34423

ID ADL34423 standard; peptide; 16 AA.

XX AC ADL34423;

XX 20-MAY-2004 (first entry)

XX MHC/HLA peptide #568 for cytomegalovirus vaccine.

XX virucide; vaccine; ligand; Major Histocompatibility Complex; MHC;
 KW Human Leukocyte Antigen; HLA; epitope; cytomegalovirus.

XX Synthetic.

XX WO2003073097-A2.

XX 04-SEP-2003.

XX 27-FEB-2003; 2003WO-EP002005.

XX 28-FEB-2002; 2002AT-00000316.

PR 13-SEP-2002; 2002AT-00001376.

XX (INTE-) INTERCELL AG.

XX Klade C, Schalich J, Vytvytska O, Zauner W, Birmstiel M,
 PI Aichinger G, Otava A, Mattner F;

XX WPI; 2003-731627/69.

XX Isolating ligands which have a binding capacity to Major
 PT Histocompatibility Complex (MHC)/ Human Leukocyte Antigens (HLA)
 PT molecules, by detecting and separating the complex from the ligands which
 PT do not bind to the MHC/HLA molecule.

XX Example I; Page 40; 85pp; English.

XX The invention relates to a method of isolating ligands which have a
 CC binding capacity to a Major Histocompatibility Complex (MHC)/ Human
 CC Leukocyte Antigens (HLA) molecules or a complex comprising the ligand and
 CC the MHC/HLA molecule. The method is useful for isolating ligands which
 CC have a binding capacity to a MHC/HLA molecule or a complex comprising the
 CC ligand and the MHC/HLA molecule. The epitope or peptide is useful for
 CC preparing a vaccine for treating or preventing cytomegalovirus
 CC infections. This sequence corresponds to a peptide of the invention.

XX Sequence 16 AA;

Query Match 85.7%; Score 66; DB 7; Length 16;

Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NFAGIEAAASAIQ 15
|||||
Db 1 NFAGIEAAASAIQ 14

RESULT 39
AAE12276
ID AAE12276 standard; peptide; 20 AA.
XX
AC AAE12276;
XX
DT 18-DEC-2001 (first entry)
XX
DE Mycobacterium tuberculosis (Mtb) peptide #61.
XX
KW Mycobacterium tuberculosis; Mtb peptide; antibacterial; vaccine;
KW infection; anti-Mtb immune response.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200170774-A2.
XX
PD 27-SEP-2001.
XX
PF 20-MAR-2001; 2001WO-US008906.
XX
PR 20-MAR-2000; 2000US-0190834P.
XX
PA (UYBR-) UNIV BROWN RES FOUND.
XX
XX Degroot AS;
PI
XX WPI; 2001-616401/71.
XX
XX New vaccine for immunizing a mammalian subject, preferably humans,
PT against infection caused by Mycobacterium tuberculosis.
XX
PS Disclosure; Fig 4; 42pp; English.
XX
XX The present invention relates to Mycobacterium tuberculosis (Mtb) vaccine
CC candidate peptides. The invention also relates to a method for
CC identifying Mtb vaccine candidate peptides as well as vaccines comprising
CC these candidate peptides. Vaccines of the invention and Mtb vaccine
CC candidate peptides are useful for inducing an anti-Mycobacterium
CC tuberculosis (anti-Mtb) immune response by raising anti-Mtb antibody in a
CC mammalian subject preferably human. They are used for immunising a
CC mammalian subject, preferably humans, against infection caused by
CC Mycobacterium tuberculosis. The present sequence is a Mtb vaccine
CC candidate peptide
XX
SQ Sequence 20 AA;
Query Match 85.7%; Score 66; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NFAGIEAAASAIQ 15
|||||
Db 1 NFAGIEAAASAIQ 14

RESULT 40
AAE88581
ID AAE88581 standard; peptide; 17 AA.
XX
AC AAE88581;
XX
DT 11-AUG-2000 (first entry)
XX
XX Antigenic N-terminal sequence of ESAT-6.
DE

XX Ligand presenting assembly; early secreted antigen target 6; ESAT-6;
KW bacteria; detect; diagnosis; allergen; cancer; vaccine; immune response;
KW neurotropic factor; autoimmune-system related compound; LPA; fungi;
KW parasite; cell-adhesion molecule.
XX
OS Mycobacterium tuberculosis.
XX
XX Key Location/Qualifiers
FT Cross-links 17
FT /note= "ala at position 17 is linked via a linker to Ala
FT at position 17 of an identical peptide, where the linker
FT is COCH2-CH(NH-Lys)-CH2CO, and the Lys residue contained
FT in the linker is also linked to another peptide (see
FT AAY88579)"
XX
PN WO200018791-A1.
XX
XX 06-APR-2000.
PD
XX 29-SEP-1999; 99WO-DK000510.
XX
XX 29-SEP-1998; 98DK-00001233.
PR (STAT-) STATENS SERUM INST.
XX (HOLM/) HOLM A.
PA
XX Holm A, Jorgensen RM, Ostergaard S, Theisen M;
PI
XX WPI; 2000-303438/26.
DR
XX New ligand presenting assemblies useful for diagnosis, treatment and
PT prevention of diseases caused by e.g. viruses, bacteria, toxins,
PT allergens, autoimmune system-related compounds, cancer-related compounds,
PT cell adhesion molecules.
XX
XX Claim 34; Page 81; 100pp; English.
XX
XX This sequence represents an antigenic N-terminal sequence from the
CC Mycobacterium tuberculosis early secreted antigenic target 6 (ESAT-6)
CC protein. The peptide is presented on the new ligand presenting assembly
CC of the invention. The invention relates to method for preparing ligand
CC presenting assemblies (LPAs) comprising: (a) providing by solid phase
CC synthesis, or fragment coupling, ligands comprising desired sequences
CC (e.g. the present sequence), the ligands being attached to a solid phase;
CC (b) if necessary, deprotecting any N-terminal amino groups while the
CC ligands are still attached to the solid phase; (c) reacting the ligands
CC having unprotected N-terminal amino groups with an achiral di-, tri- or
CC tetracarboxylic acid, to provide a construct having a ring structure; and
CC (d) cleaving the construct from the solid phase, to provide an LPA
CC comprising ligands having free C-terminal groups. The LPAs can be used
CC for raising an immune response in an animal. They can also be used in
CC vaccines and for generating antibodies in an animal. Alternatively they
CC can be used for the treatment, alleviation, detection, diagnosis, or
CC prophylaxis of diseases caused by viruses, bacteria, toxins, allergens,
CC autoimmune system-related compounds, cancer related compounds, cell
CC adhesion molecules, neurotropic factors, fungi or parasites. Use of the
CC method enables the preparation of very long ring systems interconnected
CC by reaction with the achiral di-, tri- or tetracarboxylic acid. The ring
CC structure formed between desired sequences further enables additional
CC presentation of desired sequences and chemical moieties. The LPAs provide
CC very flexible systems for polyfunctional constructs, and furthermore,
CC products of high purity are obtained
XX
SQ Sequence 17 AA;
Query Match 80.5%; Score 62; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASA 12
|||||
Db 6 WNFAGIEAAASA 17

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RESULT 41
AAE12274
ID AAE12274 standard; peptide; 13 AA.
XX
AC AAE12274;
XX
DT 18-DEC-2001 (first entry)
XX
DE Mycobacterium tuberculosis (Mtb) peptide #59.
XX
KW Mycobacterium tuberculosis; Mtb peptide; antibacterial; vaccine;
XX infection; anti-Mtb immune response.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200170774-A2.
XX
PD 27-SEP-2001.
XX
PF 20-MAR-2001; 2001WO-US008906.
XX
PR 20-MAR-2000; 2000US-0190834P.
XX
PA (UYER-) UNIV BROWN RES FOUND.
XX
PI Degroot AS;
XX
DR WPI; 2001-616401/71.
XX
PT New vaccine for immunizing a mammalian subject, preferably humans,
PT against infection caused by Mycobacterium tuberculosis.
XX
PS Disclosure; Fig 4; 42pp; English.
XX
CC The present invention relates to Mycobacterium tuberculosis (Mtb) vaccine
CC candidate peptides. The invention also relates to a method for
CC identifying Mtb vaccine candidate peptides as well as vaccines comprising
CC these candidate peptides. Vaccines of the invention and Mtb vaccine
CC candidate peptides are useful for inducing an anti- Mycobacterium
CC tuberculosis (anti-Mtb) immune response by raising anti-Mtb antibody in a
CC mammalian subject preferably human. They are used for immunising a
CC mammalian subject, preferably humans, against infection caused by
CC Mycobacterium tuberculosis. The present sequence is a Mtb vaccine
CC candidate peptide
XX
SQ Sequence 13 AA;

Query Match 77.9%; Score 60; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NFAGIEAASAIQ 14
DB 1 NFAGIEAASAIQ 13
|||||
1 NFAGIEAASAIQ 14

RESULT 42
AEB45116
ID AEB45116 standard; peptide; 10 AA.
XX
AC AEB45116;
XX
DT 06-OCT-2005 (first entry)
XX
DE M. tuberculosis ESAT6 peptide fragment SEQ ID NO 246.
XX
KW immunogenicity; viral infection; infection; bacterial infection; cancer;
KW neoplasm; autoimmune disease; immune disorder; inflammation; allergy;
KW Antibacterial; virucide; fungicide; Anti-HIV; Hepatotropic;
KW Antiparasitic; Cytostatic; immunosuppressive; antiarthritic;
KW antirheumatic; neuroprotective; antidiabetic; gastrointestinal-Gen.;

Query Match 70.1%; Score 54; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAAA 10
DB 1 WNFAGIEAAA 10
|||||
1 WNFAGIEAAA 10

RESULT 43
ADK00561
ID ADK00561 standard; peptide; 13 AA.
XX
AC ADK00561;
XX
DT 06-MAY-2004 (first entry)
XX
DE Immunogenic lipopeptide of the invention #97.
XX
KW T helper cell epitope; B cell epitope; Antibacterial; Antiulcer;
KW Antinfertility; Vaccine; antibody.
XX
OS Synthetic.

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KW antiinflammatory; antiulcer; antipsoriatic; dermatological;
KW antiasthmatic; antiallergic; immunomodulator.
XX
OS Mycobacterium tuberculosis.
XX
PN WO2005070959-A2.
XX
PD 04-AUG-2005.
XX
PF 24-JAN-2005; 2005WO-US002251.
XX
PR 23-JAN-2004; 2004US-0538713P.
PR 06-OCT-2004; 2004US-0616855P.
XX
PA (VIEV-) VIEVAX CORP.
XX
PI Mahairas GG;
XX
DR WPI; 2005-542270/55.
XX
PT Immune response altering agent useful for treating autoimmune diseases,
PT comprises first domain having T/B cell epitopes or Toll-like receptor-
PT binding proteins, and second domain having heterologous target molecule.
XX
PS Claim 65; SEQ ID NO 246; 130pp; English.
XX
CC The invention relates to an immune response altering agent (I) which
CC comprises a first domain having one or more components chosen from T cell
CC epitopes, B cell epitopes, and Toll-like receptor (TLR)-binding proteins
CC or its TLR-binding domains, and a second domain having heterologous
CC target molecule against which an immune response is desired. (I) is
CC useful for altering or inducing an immune response to a target. (I) is
CC also useful for treating viral infections (e.g., HIV and hepatitis C
CC virus), bacterial infections (e.g., Staphylococcus and Pseudomonas),
CC parasites (e.g., Leishmania), fungal infections (e.g., Candida), and
CC (e.g., non-Hodgkin's lymphoma, Hodgkin's disease and leukemia), cancer
CC autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,
CC insulin dependent diabetes, Addison's disease, celiac disease,
CC inflammatory bowel disease, ulcerative colitis, Crohn's disease, systemic
CC lupus erythematosus, psoriasis, Sjogren's syndrome, etc. (I) is useful
CC for treating inflammatory and hyperproliferative skin diseases, and
CC allergic reactions such as asthma, bronchitis, allergic rhinitis etc. (I)
CC alters an immune response generated against the heterologous target
CC molecule. (II) can be applied to wide range of species such as humans, non
CC -human primates, horses, etc. The present sequence represents the amino
CC acid sequence of a M. tuberculosis early secretory antigenic target 6,
CC ESAT6, peptide fragment.
XX
SQ Sequence 10 AA;

Query Match 70.1%; Score 54; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAAA 10
DB 1 WNFAGIEAAA 10
|||||
1 WNFAGIEAAA 10

RESULT 43
ADK00561
ID ADK00561 standard; peptide; 13 AA.
XX
AC ADK00561;
XX
DT 06-MAY-2004 (first entry)
XX
DE Immunogenic lipopeptide of the invention #97.
XX
KW T helper cell epitope; B cell epitope; Antibacterial; Antiulcer;
KW Antinfertility; Vaccine; antibody.
XX
OS Synthetic.

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XX WO2004014956-A1.
 XX 19-FEB-2004.
 XX 12-AUG-2003; 2003WO-AU001018.
 XX 12-AUG-2002; 2002US-0402838P.
 XX (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
 XX Jackson D, Zeng W;
 XX WPI; 2004-238735/22.
 XX Novel lipopeptide comprising polypeptide having amino acid sequence of T
 PT helper cell epitope and B cell epitope, conjugated to lipid moieties,
 PT useful for eliciting immune response against group A Streptococcus
 PT antigen.
 XX Disclosure; SEQ ID NO 97; 194pp; English.
 XX The present invention relates to a lipopeptide comprising polypeptide
 CC conjugated to lipid moieties, where polypeptide contains amino acid
 CC sequence of T helper cell epitope and B cell epitope, where amino acid
 CC sequences are different, and internal lysine residues or internal lysine
 CC analog residues for covalent attachment of each of lipid moieties through
 CC kegr; amino group or terminal side chain group of lysine or lysine
 CC analog. The peptides are useful in eliciting the production of antibody
 CC against an antigenic B cell epitope in a subject, and are useful for
 CC antibody production, synthetic vaccine production, diagnostic method
 CC employing antibodies and antibody ligands and immunotherapy for
 CC veterinary and human medicine. The method efficiently elicits the
 CC production of antibody against antigenic B cell epitope. The present
 CC sequence represents a novel immunogenic lipopeptide comprising T helper
 CC and B cell epitopes.
 XX Sequence 13 AA;
 SQ

Query Match 70.1%; Score 54; DB 8; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.028;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAAA 10
 Db |||||
 4 WNFAGIEAAA 13

RESULT 44
 AEB44918
 ID AEB44918 standard; peptide; 13 AA.
 XX AC AEB44918;
 XX 06-OCT-2005 (first entry)
 XX M. tuberculosis ESAT6 B cell epitope SEQ ID NO 48.
 XX immunogenicity; viral infection; infection; bacterial infection; cancer;
 KW neoplasm; autoimmune disease; immune disorder; inflammation; allergy;
 KW Antibacterial; Virucide; Fungicide; Anti-HIV; Hepatotropic;
 KW Antiparasitic; Cytostatic; immunosuppressive; antiarthritic;
 KW antineumatic; neuroprotective; antidiabetic; gastrointestinal-Gen.;
 KW antiinflammatory; antitumor; antipsoriatic; dermatological;
 KW antiasthmatic; antiallergic; Immunomodulator.
 XX Mycobacterium tuberculosis.
 XX OS Mycobacterium tuberculosis.
 XX WO2005070959-A2.
 XX 04-AUG-2005.
 XX 24-JAN-2005; 2005WO-US002251.
 PF

XX 23-JAN-2004; 2004US-0538713P.
 PR 06-OCT-2004; 2004US-0616855P.
 XX (VIEW-) VIEVAX CORP.
 XX Mahairas GG;
 XX WPI; 2005-542270/55.
 XX Immune response altering agent useful for treating autoimmune diseases,
 PT comprises first domain having T/B cell epitopes or Toll-like receptor-
 PT binding proteins, and second domain having heterologous target molecule.
 XX Disclosure; SEQ ID NO 48; 130pp; English.
 XX The invention relates to an immune response altering agent (I) which
 CC comprises a first domain having one or more components chosen from T cell
 CC epitopes, B cell epitopes, and Toll-like receptor (TLR)-binding proteins
 CC or its TLR-binding domains, and a second domain having heterologous
 CC target molecule against which an immune response is desired. (I) is
 CC useful for altering or inducing an immune response to a target. (I) is
 CC also useful for treating viral infections (e.g., HIV and hepatitis C
 CC virus), bacterial infections (e.g., Staphylococcus and Pseudomonas),
 CC parasites (e.g., Leishmania), fungal infections (e.g., Candida), cancer
 CC (e.g., non-Hodgkin's lymphoma, Hodgkin's disease and leukemia), and
 CC autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,
 CC insulin dependent diabetes, Addison's disease, celiac disease,
 CC inflammatory bowel disease, ulcerative colitis, Crohn's disease, systemic
 CC lupus erythematosus, psoriasis, Sjogren's syndrome, etc. (I) is useful
 CC for treating inflammatory and hyperproliferative skin diseases, and
 CC allergic reactions such as asthma, bronchitis, allergic rhinitis etc. (I)
 CC alters an immune response generated against the heterologous target
 CC molecule. (I) can be applied to wide range of species such as humans, non
 CC human primates, horses, etc. The present sequence represents the amino
 CC acid sequence of a B-cell epitope used to illustrate the present
 CC invention.
 XX Sequence 13 AA;
 SQ

Query Match 70.1%; Score 54; DB 9; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.028;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAAA 10
 Db |||||
 4 WNFAGIEAAA 13

RESULT 45
 AEB44912
 ID AEB44912 standard; peptide; 13 AA.
 XX AC AEB44912;
 XX 06-OCT-2005 (first entry)
 XX Mycobacterium ESAT6 T cell epitope SEQ ID NO 42.
 XX immunogenicity; viral infection; infection; bacterial infection; cancer;
 KW neoplasm; autoimmune disease; immune disorder; inflammation; allergy;
 KW Antibacterial; Virucide; Fungicide; Anti-HIV; Hepatotropic;
 KW Antiparasitic; Cytostatic; immunosuppressive; antiarthritic;
 KW antineumatic; neuroprotective; antidiabetic; gastrointestinal-Gen.;
 KW antiinflammatory; antitumor; antipsoriatic; dermatological;
 KW antiasthmatic; antiallergic; Immunomodulator.
 XX Mycobacterium tuberculosis.
 XX OS Mycobacterium bovis.
 XX WO2005070959-A2.
 XX 04-AUG-2005.
 PD

XX 24-JAN-2005; 2005WO-US002251.
PF
XX
XX 23-JAN-2004; 2004US-0538713P.
PR
XX 06-OCT-2004; 2004US-0616855P.
PR
XX (VIEV-) VIEVAX CORP.
PA
XX
XX Mahairas GG;
PI
XX
XX WPI; 2005-542270/55.
DR
XX
XX Immune response altering agent useful for treating autoimmune diseases,
PT comprises first domain having T/B cell epitopes or Toll-like receptor-
PT binding proteins, and second domain having heterologous target molecule.
PT
XX
XX Disclosure; SEQ ID NO 42; 130pp; English.
PS
XX
XX The invention relates to an immune response altering agent (I) which
CC comprises a first domain having one or more components chosen from T cell
CC epitopes, B cell epitopes, and Toll-like receptor (TLR)-binding proteins
CC or its TLR-binding domains, and a second domain having heterologous
CC target molecule against which an immune response is desired. (I) is
CC useful for altering or inducing an immune response to a target. (I) is
CC also useful for treating viral infections (e.g., HIV and hepatitis C
CC virus), bacterial infections (e.g., Staphylococcus and Pseudomonas)
CC parasites (e.g., Leishmania), fungal infections (e.g., Candida), cancer
CC (e.g., non-Hodgkin's lymphoma, Hodgkin's disease and leukemia), and
CC autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,
CC insulin dependent diabetes, Addison's disease, celiac disease,
CC inflammatory bowel disease, ulcerative colitis, Crohn's disease, systemic
CC lupus erythematosus, psoriasis, Sjogren's syndrome, etc. (I) is useful
CC for treating inflammatory and hyperproliferative skin diseases, and
CC allergic reactions such as asthma, bronchitis, allergic rhinitis etc. (I)
CC alters an immune response generated against the heterologous target
CC molecule. (I) can be applied to wide range of species such as humans, non
CC -human primates, horses, etc. The present sequence represents the amino
CC acid sequence of a T-cell epitope used to illustrate the present
CC invention.
XX
XX
XX Sequence 13 AA;
SQ

Query Match 70.1%; Score 54; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WNFAGIERAA 10
Db 4 WNFAGIERAA 13

RESULT 46
AA94590
ID AA94590 standard; peptide; 15 AA.
XX
XX AA94590;
AC
XX
XX 28-NOV-2000 (first entry)
DT
XX
XX Mycobacterium tuberculosis ESAT-6 peptide ES1.
DE
XX
XX Tuberculosis; infection diagnosis; ESAT-6.
KW
XX
XX Mycobacterium tuberculosis.
OS
XX
XX WO200026248-A2.
PN
XX
XX 11-MAY-2000.
PD
XX
XX 03-NOV-1999; 99WO-GB003635.
PF
XX
XX 04-NOV-1998; 98GB-00024213.
PR
XX 04-NOV-1998; 98US-0107004P.
PR

XX (ISIS-) ISIS INNOVATION LTD.
PA
XX
XX Lalvani A, Pathan AA;
PI
XX
XX WPI; 2000-365579/31.
DR
XX
XX Novel method of diagnosing infection, or exposure of a host, to a
PT mycobacterium comprising contacting T cells from the host with ESAT-6
PT derived peptides.
PT
XX
XX Claim 1; Page 3; 33pp; English.
PS
XX
XX The present sequence is the peptide ES1 derived from the Mycobacterium
CC tuberculosis ESAT-6 gene. This sequence is one of eleven peptides derived
CC from the ESAT-6 gene (see AAY94590 to AAY94600). The peptides with
CC recognised, to varying degrees, by the T cells of patients with
CC tuberculosis. When the peptides are combined together as a panel they
CC provide a high specificity and sensitivity diagnostic test for
CC M.tuberculosis infection. This test has the advantage that it does not
CC give false positives for patients who have been vaccinated with BCG
XX
XX Sequence 15 AA;
SQ

Query Match 70.1%; Score 54; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WNFAGIERAA 10
Db 6 WNFAGIERAA 15

RESULT 47
ABG30951
ID ABG30951 standard; peptide; 15 AA.
XX
XX ABG30951;
AC
XX
XX 21-OCT-2002 (first entry)
DT
XX
XX Mycobacterium tuberculosis ESAT-6 residues 1-15.
DE
XX
XX ESAT-6; mycobacterial infection; tuberculosis; pulmonary tuberculosis;
KW tuberculosis lymphadenitis; extrapulmonary tuberculosis.
KW
XX
XX Mycobacterium tuberculosis.
OS
XX
XX WO200254072-A2.
PN
XX
XX 11-JUL-2002.
PD
XX
XX 08-JAN-2002; 2002WO-GB0000055.
PF
XX
XX 08-JAN-2001; 2001GB-00000432.
PR
XX 08-JAN-2001; 2001US-0259868P.
PR
XX
XX (ISIS-) ISIS INNOVATION LTD.
PA
XX
XX Lalvani A;
PI
XX
XX WPI; 2002-583633/62.
DR
XX
XX Determining the progress of a mycobacterial infection, by direct ex vivo
PT quantitation of ESAT-6-specific T cells.
PT
XX
XX Example 2; Page 40; 53pp; English.
PS
XX
XX The invention describes a method of determining the efficacy of treatment
CC for mycobacterial infection (such as pulmonary tuberculosis, tuberculosis
CC lymphadenitis and extrapulmonary tuberculosis). The method involves
CC determining the level of T cells specific for a mycobacterial antigen
CC that has decreased after the treatment and therefore determining the

CC efficacy of the treatment. The method is useful for determining the
 CC efficacy of treatment for mycobacterial infection, the mycobacterial
 CC infection is Mycobacterium tuberculosis or M.bovis infection. The
 CC invention also describes a method useful for determining the presence of
 CC a latent infection in a sample from the individual for the presence of T
 CC cells specific for a mycobacterial antigen. Also described in a method
 CC for determining the effect of an intervention on a mycobacterial
 CC infection in an individual an a method for treating an individual
 CC infected by a mycobacterium. This sequence represents a peptide of
 CC Mycobacterium tuberculosis ESAT-6, the mycobacterial antigen measured in
 CC the invention
 CC
 XX
 SQ Sequence 15 AA;

Query Match 70.1%; Score 54; DB 5; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.033;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WNFAGIEAAA 10
 DB 6 WNFAGIEAAA 15
 |||||

RESULT 48
 AAO17432
 ID AAO17432 standard; peptide; 15 AA.
 XX
 AC AAO17432;
 XX
 DT 11-JUL-2002 (first entry)
 XX
 DE Early secreted antigenic target 6 T cell epitope #1.

XX
 KW Tuberculosis; TB; vaccination; vaccine; CD4+ T cell immune response;
 KW poxvirus vector; HIV; malaria; Helicobacter pylori; influenza; hepatitis;
 KW viral infection; leprosy; protozoan parasite; cancer; tuberculosstatic;
 KW anti-HIV; protozoicide; antibacterial; virucide; hepatotropic;
 KW antiinflammatory; antileprotic; cytostatic; epitope.

XX
 OS Mycobacterium tuberculosis.

XX
 PN WO200224224-A2.

XX
 PD 28-MAR-2002.

XX
 PF 13-SEP-2001; 2001WO-GB004116.

XX
 PR 21-SEP-2000; 2000GB-00023203.

XX
 PA (OXXO-) OXXON PHARMACEUTICALS LTD.

XX
 PI Hill AVS, Meshane H, Gilbert S, Reece W, Schneider J;

XX
 XX WPI; 2002-394098/42.

XX
 DR Inducing CD4+ T-cell response against target antigen by administering a
 PT composition comprising a source of CD4+ epitopes which is a non-
 PT replicating or replication impaired recombinant poxvirus vector.

XX
 PS Example 1; Page 21; 50pp; English.

XX
 CC The present invention relates to a method of inducing a CD4+ T-cell
 CC response against a target antigen, by administering two different
 CC compositions comprising a source of CD4+ T-cell epitope(s) of the target
 CC antigen, where the second composition further includes an epitope which
 CC is same as the epitope of the first composition, where the source of the
 CC epitopes for the compositions is a non-replicating or replication
 CC impaired recombinant poxvirus vector. The methods are useful for inducing
 CC CD4+ T-cell immune responses against diseases such as tuberculosis, human
 CC immunodeficiency virus (HIV) (persistent viral infection), malaria,
 CC Helicobacter pylori, influenza, hepatitis (chronic hepatitis B and C),
 CC cytomegalovirus (CMV), viral infection, herpes virus-induced disease,
 CC leprosy and diseases caused by non-malarial protozoan parasite such as

CC toxoplasma and cancer. The present sequence is an epitope from
 CC Mycobacterium tuberculosis useful in the method of the invention
 XX
 SQ Sequence 15 AA;

Query Match 70.1%; Score 54; DB 5; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.033;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAAA 10
 DB 6 WNFAGIEAAA 15
 |||||

RESULT 49
 ADI33341
 ID ADI33341 standard; peptide; 15 AA.

XX
 AC ADI33341;

XX
 DT 22-APR-2004 (first entry)

XX
 DE Mycobacterium tuberculosis ESAT-6 peptide epitope #1.

XX
 KW pathogen; vaccine; cellular response; HPV; HIV; SIV; HCV; chlamydia; HBV;
 KW EBV; CMV; VZV; HSV; Legionella; Leishmaniasis; influenza;
 KW foot and mouth virus; Toxoplasma; Brucella; Cryptococcus; Candida;
 KW Aspergillus; Mycobacterium; T cell; ESAT-6; CFP10; virucide; protozoide;
 KW antibacterial; fungicide; epitope.

XX
 OS Mycobacterium tuberculosis.

XX
 PN WO2004005925-A2.

XX
 PD 15-JAN-2004.

XX
 PF 07-JUL-2003; 2003WO-GB002936.

XX
 PR 05-JUL-2002; 2002GB-00015710.

XX
 PA (ISIS-) ISIS INNOVATION LTD.

XX
 PI Lalvani A, Ewer K;

XX
 DR WPI; 2004-143006/14.

XX
 CC Diagnosing in an individual recent exposure to an agent, useful in
 PT treating a disease caused by a pathogen, by determining in vitro or in
 PT vivo whether the T cells of recognize a protein having at least 30 amino
 PT acids.

XX
 PS Claim 16; Page 33; 48pp; English.

XX
 CC The invention relates to a novel method for diagnosing in an individual
 CC recent exposure to an agent which is a pathogen, vaccine or any other
 CC moiety, which induces a cellular response. The pathogen can include: HPV,
 CC HIV, SIV, HCV, chlamydia species, HBV, EBV, CMV, VZV, HSV, Legionella, S,
 CC typhi, P. falciparum, Leishmaniasis, M. leprae, influenza virus, foot and
 CC mouth virus, a Toxoplasma species, a Brucella species, a Cryptococcus
 CC species, a Candida species, an Aspergillus species, or Mycobacterium
 CC tuberculosis. The invention also provides a vaccine against any of the
 CC above pathogens. The method comprises determining in vitro or in vivo
 CC whether the T cells of the individual recognize a protein from the agent
 CC having a length of at least 30 amino acids. The invention also comprises
 CC a protein or epitope peptide which is from ESAT-6 or CFP10. The vaccines
 CC of the invention have: virucide, protozoide, antibacterial, and fungicide
 CC activity. The method is useful in diagnosing in an individual recent
 CC exposure to an agent which is a pathogen, vaccine or any other moiety
 CC which induces a cellular response. The protein described above, the
 CC product which prevents or treats a condition caused by a pathogen or the
 CC antigen or its analogue is useful in the manufacturing of a medicament
 CC for diagnosing and treating an individual recently exposed to a pathogen.
 CC This sequence represents a peptide epitope of the invention for

CC recognition by a T cell relating to the invention.

Sequence 15 AA:

Query Match 70.1%; Score 54; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 10; Conservative 0; Mismatches 0; Indels

Qy 1 WNFAGIEAAA 10
||| ||| ||| |||
Db 6 WNFAGIEAAA 15

RESULT 50

AEB45088

AM513000
ID AEB45088 standard; peptide; 15 AA.

AC AEB45088;

06-OCT-2005 (first entry)

XX
DE M. tuberculosis ESAT6 peptide fragment SEQ ID NO 218.

xx immunogenicity; viral infection; infection, bacterial infection; cancer; neoplasia; autoimmune disease; immune disorder; inflammation; allergy; Anti-bacterial; Virucide; Fungicide; Anti-HIV; Hepatotropic; Antiparasitic; Cytostatic; immunosuppressive; antiarthritic; antirheumatic; neuroprotective; antidiabetic; gastrointestinal-Gen.; anti-inflammatory; antitumor; antipoxiatic; dermatological; antiasthmatic; antiallergic; immunomodulator.

OS Mycobacterium tuberculosis.

XX PN WO2005070959-A2.

04-AUG-2005.

24--JAN-2005: 2005W0-IIS002251-XX PF

XX
PR 23-JAN-2004: 2004IIS-0538713P.

PR 06-OCT-2004; 2004US-0616855P.
YY

PA (VIEV-) VIEVAX CORP.
yy

PI Mahairas GG;
yy

DR WPI; 2005-542270/55.

PT Immune response altering agent useful for treating autoimmune diseases.
PT comprises first domain having T/B cell epitopes or Toll-like receptor-
PT binding proteins, and second domain having heterologous target molecule.
PT

PS Claim 65: SEO ID NO 218: 130pp: English, XX

The invention relates to an immune response altering agent (I) which comprises a first domain having one or more components chosen from T cell epitopes, B cell epitopes, and Toll-like receptor (TLR)-binding proteins or its TLR-binding domains, and a second domain having heterologous target molecule against which an immune response is desired. (I) is useful for altering or inducing an immune response to a target. (I) is also useful for treating viral infections (e.g., HIV and hepatitis C virus), bacterial infections (e.g., *Staphylococcus* and *Pseudomonas*), parasites (e.g., *Leishmania*), fungal infections (e.g., *Candida*), cancer (e.g., non-Hodgkin's lymphoma, Hodgkin's disease and leukemia), and autoimmune diseases such as rheumatoid arthritis, multiple sclerosis, insulin dependent diabetes, Addison's disease, celiac disease, inflammatory bowel disease, ulcerative colitis, Crohn's disease, systemic lupus erythematosus, psoriasis, Sjogren's syndrome, etc. (I) is useful for treating inflammatory and hyperproliferative skin diseases, and allergic reactions such as asthma, bronchitis, allergic rhinitis etc. (I) alters an immune response generated against the heterologous target molecule. (I) can be applied to wide range of species such as humans, non-human primates, horses, etc. The present sequence represents the amino

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OM protein - protein search, using sw model

Run on: May 4, 2006, 15:13:52 ; Search time 24 Seconds
(without alignments)
60.135 Million cell updates/sec

Title: US-09-830-839-6

Perfect score: 77

Sequence: 1 MNFAGIEAAASAIQ 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

PIR 80:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77	100.0	95	2 A70803	early secretory an
2	47	61.0	714	2 G86844	hypothetical prote
3	44	57.1	225	2 T50707	urease accessory p
4	43	55.8	476	2 H95313	NoeA host specific
5	43	55.8	476	2 S71360	noeA protein - Rhi
6	42.5	55.2	141	2 H83229	conserved hypotet
7	42	54.5	369	2 G72069	conserved hypotet
8	42	54.5	369	2 E86554	Fe-S oxidoreductas
9	41	53.2	384	2 A69622	ferrichrome ABC tr
10	41	53.2	445	2 D82342	probable cadaverin
11	41	53.2	540	2 F86745	ABC transporter pe
12	40	51.9	294	2 I41220	glyceraldehyde-3-p
13	40	51.9	323	2 B97457	BH3305 conserved h
14	40	51.9	323	2 AD2675	conserved hypotet
15	40	51.9	330	2 H69020	probable Na+/Ca2+
16	40	51.9	493	2 F95940	probable xanthine
17	40	51.9	536	2 B84349	hypothetical prote
18	40	51.9	761	2 T51912	hypothetical prote
19	39	50.6	101	2 F71059	hypothetical prote
20	39	50.6	287	2 E71063	hypothetical prote
21	39	50.6	379	2 S58457	ubiquinol-cytochro
22	39	50.6	379	2 S58462	ubiquinol-cytochro
23	39	50.6	445	2 AF1022	probable amino aci
24	39	50.6	445	2 B65221	probable amino aci
25	39	50.6	445	2 A91266	probable amino aci
26	39	50.6	445	2 F86106	probable amino aci
27	39	50.6	448	2 T05591	tyrosine transamin
28	39	50.6	715	2 B83518	pimeloyl-CoA synth
29	39	50.6	745	2 B33856	hypothetical 80K p

30	50.6	990	1	TQSC26	transposase - Esch
31	49.4	95	2	T10031	early secretory an
32	49.4	98	2	A75393	conserved hypotet
33	49.4	195	2	T36975	hypothetical prote
34	49.4	219	2	AG2036	hypothetical prote
35	49.4	303	2	AI2211	hypothetical prote
36	49.4	313	2	AB3052	hypothetical prote
37	49.4	313	2	B98234	hypothetical prote
38	49.4	399	2	F87356	hypothetical prote
39	49.4	422	2	T05592	tyrosine transamin
40	49.4	425	2	S69796	pectate lyase (EC
41	49.4	443	2	AE0826	probable cadaverin
42	49.4	444	2	H86108	transport of lysin
43	49.4	444	2	A41842	lysine/cadaverine
44	49.4	444	2	B91268	transport protein
45	49.4	444	2	AE0147	probable amino aci
46	49.4	844	2	B84773	probable mitochond
47	49.4	923	2	T38398	hypothetical GPas
48	49.4	988	1	TQSC21	transposase - Esch
49	48.1	172	2	H87253	hypothetical prote
50	48.1	178	2	G82977	hypothetical prote
51	48.1	182	2	S71353	Coq7 protein homol
52	48.1	256	2	G70666	hypothetical prote
53	48.1	260	2	S72748	Blf77-F3_136 prote
54	48.1	261	2	A22224	cobalamin 5'-phosp
55	48.1	335	2	T39033	hypothetical prote
56	48.1	343	2	H95879	probable sugar ABC
57	48.1	413	2	G95965	conserved hypotet
58	48.1	472	2	D87321	succinylglutamic s
59	48.1	475	1	CZCLCA	cellulase (EC 3.2.
60	48.1	490	2	C86879	arginine/ornitine
61	48.1	492	2	S32951	regulatory protein
62	48.1	497	2	G86878	arginine/ornitine
63	48.1	507	2	S06272	photosystem II chl
64	48.1	509	2	JA0148	photosystem II chl
65	48.1	509	2	AB1824	photosystem II CP4
66	48.1	509	2	T06855	photosystem II pro
67	48.1	553	2	AE1140	probable sulfate t
68	48.1	553	2	AI1498	probable sulfate t
69	48.1	655	2	T00768	polyadenylate-bind
70	48.1	1223	2	S62011	PH085 protein - Ye
71	48.1	1438	2	T17402	dihydroaeruginoin
72	48.1	1649	2	C86822	hypothetical prote
73	36.5	47.4	371	2 C70626	hypothetical prote
74	36	46.8	125	1 CCRFCP	cytochrome c' - Rh
75	36	46.8	145	2 F70698	hypothetical prote
76	36	46.8	158	2 S68978	Na+/Ca2+, K+-exchan
77	36	46.8	188	2 C97467	hypothetical prote
78	36	46.8	188	2 AF2685	conserved hypotet
79	36	46.8	192	1 S75273	hypothetical prote
80	36	46.8	245	2 F95420	conserved hypotet
81	36	46.8	247	2 H90825	hypothetical prote
82	36	46.8	248	2 S77407	hypothetical prote
83	36	46.8	302	2 AD3308	cobalt-zinc-cadmiu
84	36	46.8	314	2 C87514	5,10-methylenetet
85	36	46.8	341	2 T35426	probable oxidorede
86	36	46.8	369	2 T24793	hypothetical prote
87	36	46.8	384	2 T51423	formate dehydrogen
88	36	46.8	412	2 C87686	ferredoxin reducta
89	36	46.8	413	2 AC1045	putrescine permease
90	36	46.8	427	2 F97790	putrescine-ornithi
91	36	46.8	429	2 F71651	putrescine-ornithi
92	36	46.8	450	2 AG2281	hypothetical prote
93	36	46.8	456	2 S62331	phosphotransferase
94	36	46.8	523	2 T07834	hydroxymethylpyrim
95	36	46.8	533	2 AB7710	hypothetical prote
96	36	46.8	547	2 AD2250	acetolactate synth
97	36	46.8	651	2 S44257	phosphotransferase
98	36	46.8	721	2 A95144	hypothetical prote
99	36	46.8	721	2 G98011	hypothetical prote
100	36	46.8	730	2 E75387	NADH dehydrogenase
101	36	46.8	731	2 T19721	hypothetical prote
102	36	46.8	739	2 I56187	transcription fact

103	36	46.8	770	1	S30293	transcription fact	176	35	45.5	627	2	S14683	Ig mu chain precu
104	36	46.8	797	2	C85164	hypothetical prote	177	35	45.5	666	2	T40172	hypothetical prote
105	36	46.8	797	2	H71412	hypothetical prote	178	35	45.5	832	2	S76815	conserved hypotet
106	36	46.8	898	2	A10283	probable membrane	179	35	45.5	879	2	H82192	leucyl-tRNA synthe
107	36	46.8	1120	2	F90693	mechanosensitive c	180	35	45.5	887	2	E82590	hypothetical prote
108	36	46.8	1120	2	B85476	probable membrane	181	35	45.5	913	2	T15278	hypothetical prote
109	36	46.8	1120	2	H64776	hypothetical prote	182	35	45.5	1068	2	A10519	integral membrane
110	36	46.8	2154	2	A84669	probable adhesin y	183	35	45.5	1100	2	T40561	5-methyltetrahydro
111	36	46.8	3295	2	AE0074	rifamycin polyketi	184	35	45.5	1253	2	T42376	RNA polymerase III
112	36	46.8	3413	2	T17467	protein T21E12.4 [185	35	45.5	1289	2	E90098	hypothetical prote
113	36	46.8	4464	2	D87755	hypothetical prote	186	35	45.5	1421	2	A60338	cell surface antigen
114	35.5	46.1	264	2	AG3354	aminotransferase [187	35	45.5	1528	2	A43607	sex comb protein -
115	35.5	46.1	402	2	C87133	protein Flm21.12 [188	35	45.5	1566	2	T13748	hemagglutinin/hemo
116	35.5	46.1	493	2	F96696	glucose-6-phosphat	189	35	45.5	1668	2	T17421	hypothetical prote
117	35.5	46.1	539	2	E87276	glucose-inhibited	190	35	45.5	1774	2	B81192	vesicular transport
118	35.5	46.1	628	1	BWASGA	hypothetical prote	191	35	45.5	1975	2	B81044	probable GTPase-ac
119	35.5	46.1	656	2	A84018	hypothetical prote	192	35	45.5	2015	2	B81989	hypothetical prote
120	35.5	46.1	676	2	G69154	conserved hypotet	193	35	45.5	2550	2	B53435	hypothetical prote
121	35.5	46.1	692	2	A83488	hypothetical prote	194	35	45.5	3079	1	RGBY12	probable GTPase-ac
122	35.5	46.1	692	2	A83488	hypothetical prote	195	35	45.5	3079	1	RGBY12	hypothetical prote
123	35.5	46.1	692	2	A83488	hypothetical prote	196	35	45.5	3079	1	RGBY12	conserved hypotet
124	35.5	46.1	692	2	A83488	hypothetical prote	197	35	45.5	3079	1	RGBY12	hypothetical prote
125	35	45.5	172	2	H91194	hypothetical prote	198	34.5	44.8	334	2	C86426	hypothetical prote
126	35	45.5	172	2	H91194	hypothetical prote	199	34.5	44.8	334	2	C86426	hypothetical prote
127	35	45.5	211	2	AB2645	conserved hypotet	200	34	44.2	100	2	B72399	probable short cha
128	35	45.5	224	2	H82658	carboxylesterase x	201	34	44.2	113	2	AP1538	hypothetical prote
129	35	45.5	230	2	S51274	terminal protein -	202	34	44.2	133	2	S55555	ribosomal protein
130	35	45.5	245	2	QJ0337	gene F41 protein -	203	34	44.2	141	2	B97287	hypothetical prote
131	35	45.5	257	2	S16865	ribosomal protein	204	34	44.2	162	2	D70721	hypothetical prote
132	35	45.5	267	2	A87404	hypothetical prote	205	34	44.2	184	2	A42556	hypothetical prote
133	35	45.5	271	2	G87429	hypothetical prote	206	34	44.2	200	2	A71539	probable recombin
134	35	45.5	280	2	T25829	hypothetical prote	207	34	44.2	204	2	T36466	mutf domain-contai
135	35	45.5	283	2	T51091	hypothetical prote	208	34	44.2	214	2	T19247	probable methytra
136	35	45.5	288	2	A86042	hypothetical prote	209	34	44.2	215	2	T36466	thioesterase II BH
137	35	45.5	309	2	T41203	WD repeat protein	210	34	44.2	229	2	F83879	probable permease
138	35	45.5	312	2	B97427	hypothetical prote	211	34	44.2	232	2	H83122	probable short cha
139	35	45.5	319	2	A61500	hypothetical prote	212	34	44.2	244	2	C95901	hypothetical prote
140	35	45.5	326	2	D97743	hypothetical prote	213	34	44.2	261	2	S74566	probable permease
141	35	45.5	326	2	B71681	pyruvate dehydroge	214	34	44.2	262	2	E83605	2-oxo-hepta-3-ene
142	35	45.5	331	2	H95279	probable ABC trans	215	34	44.2	267	2	AF3526	hypothetical prote
143	35	45.5	339	2	B83496	hypothetical prote	216	34	44.2	268	2	AF2167	hypothetical prote
144	35	45.5	363	2	F84360	threonine synthase	217	34	44.2	269	2	S73999	hemK protein limpo
145	35	45.5	372	2	T11100	ubiquinol-cytochro	218	34	44.2	277	2	A84950	probable membrane
146	35	45.5	379	2	S58459	ubiquinol-cytochro	219	34	44.2	286	2	H97056	hypothetical prote
147	35	45.5	379	2	S58458	ubiquinol-cytochro	220	34	44.2	291	2	AG1065	hypothetical prote
148	35	45.5	381	2	G72601	acetyl-CoA acetyl	221	34	44.2	316	2	C73369	conserved hypotet
149	35	45.5	399	2	G75332	collagenase - Aqu	222	34	44.2	317	2	H95143	chitinase (EC 3.2.
150	35	45.5	400	2	A87700	hypothetical prote	223	34	44.2	318	2	S65019	chitinase (EC 3.2.
151	35	45.5	409	2	F70387	hypothetical prote	224	34	44.2	318	2	T03026	oligopeptide trans
152	35	45.5	420	2	T31285	hypothetical prote	225	34	44.2	332	2	T34758	probable isomerase
153	35	45.5	420	2	S76691	hypothetical prote	226	34	44.2	334	2	H87192	probable membrane
154	35	45.5	421	2	D72677	hypothetical prote	227	34	44.2	335	2	G64817	hypothetical prote
155	35	45.5	423	2	S47761	probable transport	228	34	44.2	335	2	G85589	hypothetical prote
156	35	45.5	423	2	G86027	probable transport	229	34	44.2	335	2	E90739	leucine dehydrogen
157	35	45.5	423	2	C91181	keratin, 47K type	230	34	44.2	339	2	C86978	hypothetical prote
158	35	45.5	429	2	A25145	conserved hypotet	231	34	44.2	341	2	F81217	hypothetical prote
159	35	45.5	440	2	C82410	hydroxymethylpyrim	232	34	44.2	350	2	E81236	hypothetical prote
160	35	45.5	445	2	A84410	probable amino aci	233	34	44.2	350	2	F69112	conserved hypotet
161	35	45.5	451	2	E83418	putrescine/ornithi	234	34	44.2	356	2	G95298	cuticle-degrading
162	35	45.5	452	2	G95306	glucokinase (EC 2.	235	34	44.2	385	1	YKXT	hypothetical prote
163	35	45.5	455	2	JC7550	hypothetical prote	236	34	44.2	388	1	S22387	hypothetical prote
164	35	45.5	459	2	AC2116	glucokinase (EC 2.	237	34	44.2	393	2	AH2150	hypothetical prote
165	35	45.5	467	2	JC7551	ABC transporter (a	238	34	44.2	398	2	H64534	azarene carbazole
166	35	45.5	469	2	D70048	hypothetical prote	239	34	44.2	409	2	JW0101	hypothetical prote
167	35	45.5	477	2	T45722	probable aldehyde	240	34	44.2	412	2	D71972	carboxypeptidase [
168	35	45.5	487	2	D95687	DNA-directed RNA p	241	34	44.2	412	2	G87553	hypothetical prote
169	35	45.5	508	2	S26724	probable thiamin b	242	34	44.2	435	2	T30114	hypothetical prote
170	35	45.5	525	2	E86363	noxk protein Bra	243	34	44.2	437	2	H83143	hypothetical prote
171	35	45.5	566	2	S35231	ribulokinase (EC 2	244	34	44.2	452	2	T35729	probable oxidoredu
172	35	45.5	569	2	A24984	L-ribulokinase [m	245	34	44.2	453	2	A87047	putrescine/ornithi
173	35	45.5	569	2	AD0515	probable long-chal	246	34	44.2	455	2	T44519	
174	35	45.5	601	2	H69274	peptide transporte	247	34	44.2				
175	35	45.5	624	2	T48587		248	34	44.2				

Ig mu chain precu
 glucose inhibited
 hypothetical prote
 conserved hypotet
 leucyl-tRNA synthe
 hypothetical prote
 hypothetical prote
 integral membrane
 5-methyltetrahydro
 RNA polymerase III
 hypothetical prote
 cell surface antigen
 sex comb protein -
 polyketide synthase
 hemagglutinin/hemo
 hemagglutinin/hemo
 hypothetical prote
 vesicular transport
 probable GTPase-ac
 hypothetical 17.8K
 hypothetical prote
 conserved hypotet
 rnfB-related prote
 E. coli SugE prote
 E. coli SugE prote
 ribosomal protein
 ribosomal protein
 hypothetical prote
 hypothetical prote
 hypothetical prote
 probable recombin
 mutf domain-contai
 hypothetical prote
 thioesterase II BH
 probable permease
 probable short cha
 hypothetical prote
 probable permease
 2-oxo-hepta-3-ene
 hypothetical prote
 hypothetical prote
 hemK protein limpo
 probable membrane
 hypothetical prote
 hypothetical prote
 conserved hypotet
 chitinase (EC 3.2.
 chitinase (EC 3.2.
 oligopeptide trans
 probable isomerase
 probable membrane
 hypothetical prote
 hypothetical prote
 leucine dehydrogen
 hypothetical prote
 hypothetical prote
 conserved hypotet
 cuticle-degrading
 (si)-synth
 hypothetical prote
 hypothetical prote
 azarene carbazole
 hypothetical prote
 carboxypeptidase [

249	34	44.2	462	2	C84591	probable tyrosine	322	33.5	43.5	439	2	D82384	putrescine-ornithi
250	34	44.2	465	1	JC1318	triacylglycerol li	323	33.5	43.5	616	2	T14235	NADH2 dehydrogenas
251	34	44.2	470	2	C69725	phosphotransferase	324	33	42.9	28	2	A56499	brevicin-27 - Lact
252	34	44.2	475	2	T46745	arginine/ornithine	325	33	42.9	57	2	AG3105	conserved hypoteth
253	34	44.2	484	2	T36427	probable rhamnose	326	33	42.9	69	2	T45354	hypothetical prote
254	34	44.2	508	2	T07277	photosystem II chl	327	33	42.9	82	2	G70765	hypothetical prote
255	34	44.2	514	2	E71974	flagellin B - Heli	328	33	42.9	102	2	B87150	conserved hypoteth
256	34	44.2	514	2	C64534	ferulate-5-hydroxy	329	33	42.9	102	2	D70631	hypothetical prote
257	34	44.2	520	2	T04591	amino acid permeas	330	33	42.9	111	2	E98181	hypothetical prote
258	34	44.2	521	2	A95549	conserved membrane	331	33	42.9	119	2	B72701	ribosomal protein
259	34	44.2	527	2	G87082	probable homeobox	332	33	42.9	120	2	B64450	hypothetical prote
260	34	44.2	532	2	T05281	hypothetical prote	333	33	42.9	125	2	A97598	conserved hypoteth
261	34	44.2	556	2	A70560	methylmalonyl-CoA	334	33	42.9	125	2	AI2819	cytochrome c' [val
262	34	44.2	561	1	D75425	probable membrane	335	33	42.9	131	1	CCRKV	envelope protein -
263	34	44.2	561	2	S63388	unknown protein, 6	336	33	42.9	138	2	S24078	ribosomal protein
264	34	44.2	594	2	E96667	TPR domain protein	337	33	42.9	144	2	G75323	hypothetical prote
265	34	44.2	596	2	D87710	carbon starvation	338	33	42.9	152	2	B84409	probable plasma me
266	34	44.2	598	2	A69609	methyl-accepting c	339	33	42.9	158	2	B86418	transcription regu
267	34	44.2	599	2	G87322	probable carbon st	340	33	42.9	158	2	F87545	hypothetical prote
268	34	44.2	605	2	AG0460	alpha-amylase [imp	341	33	42.9	163	2	G72707	signal peptidase I
269	34	44.2	620	2	AH1827	DnaK-related prote	342	33	42.9	164	1	ZPECL	4-carboxymuconolac
270	34	44.2	631	2	F82206	hypothetical prote	343	33	42.9	164	2	C75424	hypothetical prote
271	34	44.2	650	2	T32897	RNA helicase prh75	344	33	42.9	165	2	S74709	conserved hypoteth
272	34	44.2	685	2	T09159	conserved hypoteth	345	33	42.9	165	2	AF2862	hypothetical prote
273	34	44.2	711	2	S68443	double-stranded RN	346	33	42.9	165	2	E97639	hypothetical prote
274	34	44.2	721	2	D82496	prolyl oligopeptid	347	33	42.9	180	2	AD3485	hypothetical prote
275	34	44.2	723	2	B87706	probable disease r	348	33	42.9	184	2	B84259	hypothetical prote
276	34	44.2	741	2	T05250	probable enzyme [i	349	33	42.9	195	2	D72254	glycerol uptake op
277	34	44.2	751	2	T42597	DNA helicase/prima	350	33	42.9	206	2	JC2574	hypothetical 22K p
278	34	44.2	761	2	C64813	YbhJ protein - Esc	351	33	42.9	211	2	G75533	ribosomal protein
279	34	44.2	761	2	G90728	probable enzyme [i	352	33	42.9	239	2	F87580	sugar fermentation
280	34	44.2	761	2	H85579	probable enzyme yb	353	33	42.9	244	2	S37984	conserved purine nu
281	34	44.2	764	2	S49849	aconitate hydratase	354	33	42.9	251	2	H87692	flagellar biosynth
282	34	44.2	809	2	S55344	outer envelope mem	355	33	42.9	255	2	H71966	flagellar biosynth
283	34	44.2	835	2	T05259	probable disease r	356	33	42.9	255	2	E64541	ubiquinol-cytochro
284	34	44.2	876	2	F97688	leucyl-tRNA synthet	357	33	42.9	262	2	S24723	acetyltransferase (EC
285	34	44.2	876	2	AC2914	aconitate hydratase	358	33	42.9	262	2	S24723	hypothetical prote
286	34	44.2	878	2	A97854	probable membrane	359	33	42.9	266	2	T30913	hypothetical prote
287	34	44.2	879	1	B64945	conserved hypoteth	360	33	42.9	267	2	E89870	probable secreted
288	34	44.2	879	2	AI0728	hypothetical prote	361	33	42.9	271	2	T37222	NAD(P)H2 dehydroge
289	34	44.2	879	2	D85795	hypothetical prote	362	33	42.9	274	1	A30879	hypothetical prote
290	34	44.2	879	2	H90946	aconitate hydratase	363	33	42.9	276	2	D70618	hypothetical prote
291	34	44.2	890	2	AH0270	aconitate hydratase	364	33	42.9	284	2	E82868	hypothetical prote
292	34	44.2	891	2	AH0654	aconitate hydratase	365	33	42.9	285	2	G97303	uncharacterized co
293	34	44.2	891	2	B48642	aconitate hydratase	366	33	42.9	287	2	S77309	hypothetical prote
294	34	44.2	891	2	A90860	aconitate hydratase	367	33	42.9	290	2	C87208	conserved hypoteth
295	34	44.2	891	2	E85759	aconitate hydratase	368	33	42.9	292	2	I59266	water channel prot
296	34	44.2	891	2	G64875	aconitate hydratase	369	33	42.9	294	2	I41222	glyceraldehyde-3-p
297	34	44.2	895	2	AI3483	aconitate hydratase	370	33	42.9	295	2	AB0462	sn-glycerol-3-phos
298	34	44.2	897	2	AD2906	aconitate hydratase	371	33	42.9	295	2	B83433	translocator prote
299	34	44.2	897	2	E97681	cytoplasmic aconit	372	33	42.9	301	2	AC0262	LYSR-family transc
300	34	44.2	898	2	B84471	aconitate hydratase	373	33	42.9	306	2	S77133	homoserine kinase
301	34	44.2	898	2	T04693	aconitate hydratase	374	33	42.9	313	2	F64851	flagellar protein
302	34	44.2	898	2	T10101	aconitate hydratase	375	33	42.9	313	2	C90811	flagellar basal bo
303	34	44.2	901	2	A48653	phage infection pr	376	33	42.9	313	2	G85670	lytB protein [impo
304	34	44.2	901	2	F86833	phage infection pr	377	33	42.9	319	2	A84947	hypothetical prote
305	34	44.2	903	2	AH7704	aconitate hydratase	378	33	42.9	325	2	H70925	hypothetical prote
306	34	44.2	907	2	T04820	aconitate hydratase	379	33	42.9	325	2	D87733	hypothetical prote
307	34	44.2	908	2	G82824	aconitate xF0290 [380	33	42.9	325	2	T32940	protein W03D8.9 [i
308	34	44.2	910	2	B83451	aconitate hydratase	381	33	42.9	326	2	A41862	C-S lyase (ORF326)
309	34	44.2	913	2	F70873	aconitate hydratase	382	33	42.9	328	2	A96944	transcription regu
310	34	44.2	944	2	G87135	conserved hypoteth	383	33	42.9	328	2	J50459	gene H protein - p
311	34	44.2	1152	2	D87046	gene ei protein -	384	33	42.9	330	2	D95879	probable dihydroxy
312	34	44.2	1188	2	S48861	lysobactin synthet	385	33	42.9	332	2	T52069	GTPase-activating
313	34	44.2	1575	2	T18545	hypothetical prote	386	33	42.9	333	2	T05187	chitinase [EC 3.2.
314	34	44.2	1891	2	T13594	gene hindsight pro	387	33	42.9	333	2	T20106	hypothetical prote
315	34	44.2	1920	2	T13893	protein-tyrosine-p	388	33	42.9	338	1	A64063	UDP-glucose 4-epime
316	33.5	43.5	150	2	E97254	hypothetical prote	389	33	42.9	338	2	XUECTG	UDP-glucose 4-ep
317	33.5	43.5	251	2	C81816	hypothetical prote	390	33	42.9	338	2	C90727	UDP-galactose-4-ep
318	33.5	43.5	290	2	T48880	beta-lactamase (EC	391	33	42.9	338	2	D85578	UDP-glucose 4-ep
319	33.5	43.5	357	2	AB3044	oxidoreductase Atu	392	33	42.9	338	2	F82419	UDP-glucose 4-epim
320	33.5	43.5	357	2	B98242	hypothetical prote	393	33	42.9	343	2	S74438	iron(III) dicitrat
321	33.5	43.5	435	2	E64079	putrescine/ornithi	394	33	42.9	347	2	S11223	UDPglucose 4-epime

395	33	42.9	347	2	D96033	probable sugar upt	468	33	42.9	510	2	B70368	L-aspartate oxidas
396	33	42.9	350	2	T10498	mpglucose 4-epime	469	33	42.9	512	2	B87804	protein K04F10.2 [
397	33	42.9	352	2	S76739	sulfate-binding pr	470	33	42.9	513	2	T44290	biotin carboxylase
398	33	42.9	354	1	S73697	probable X-pro dip	471	33	42.9	517	2	E95920	probable per type
399	33	42.9	355	2	T34711	uroporphyrinogen d	472	33	42.9	525	2	B83913	hypothetical prote
400	33	42.9	355	2	T40321	upr. glucose NAD de	473	33	42.9	530	2	T20360	hypothetical prote
401	33	42.9	356	2	S58529	alpha-complex prot	474	33	42.9	537	2	E96681	protein F1E22.4 [i
402	33	42.9	362	2	S78515	single-stranded nu	475	33	42.9	538	1	C98308	hypothetical prote
403	33	42.9	365	2	S42471	hnNP protein E2 -	476	33	42.9	551	1	S26857	aldehyde dehydrog
404	33	42.9	366	2	T32598	hypothetical prote	477	33	42.9	552	2	A12256	seed biotin contai
405	33	42.9	369	2	F81674	conserved hypotet	478	33	42.9	557	1	R3EC1	hypothetical prote
406	33	42.9	369	2	B71516	probable Fe-S oxid	479	33	42.9	557	1	AC0614	30S ribosomal prot
407	33	42.9	371	2	B84615	probable D-amino a	480	33	42.9	557	2	B90753	30S ribosomal subu
408	33	42.9	372	2	G69600	citrate (si)-synth	481	33	42.9	557	2	H85616	30S ribosomal subu
409	33	42.9	372	2	H84044	citrate synthase I	482	33	42.9	557	2	AB0170	30S ribosomal prot
410	33	42.9	377	2	C87503	acyl-CoA dehydrog	483	33	42.9	557	2	AD2832	DNA repair protein
411	33	42.9	378	2	AF32507	3-dehydroquinat s	484	33	42.9	557	2	H97609	DNA repair protein
412	33	42.9	379	2	T19069	hypothetical prote	485	33	42.9	565	2	B82761	extracellular endo
413	33	42.9	380	2	G97969	hypothetical prote	486	33	42.9	565	2	T50536	succinate dehydrog
414	33	42.9	380	2	F95101	aminotransferase,	487	33	42.9	571	2	T20359	hypothetical prote
415	33	42.9	383	2	C87481	peptidase, M23/M37	488	33	42.9	571	2	T37858	probable dihydroxy
416	33	42.9	383	2	B83922	short-chain-specif	489	33	42.9	598	2	AH2184	hypothetical prote
417	33	42.9	385	2	S53838	ubiquinol-cytochro	490	33	42.9	599	2	AH0388	alpha-glucosidase
418	33	42.9	387	1	VC9643	acetate / acetoin	491	33	42.9	609	2	A49656	estrogen-responsiv
419	33	42.9	388	1	VC9643	coat protein - art	492	33	42.9	630	2	A49656	hypothetical prote
420	33	42.9	388	2	S24926	coat protein, 41k	493	33	42.9	630	2	T48369	NADH2 dehydrogenas
421	33	42.9	388	2	VC5437	spliceosome-associ	494	33	42.9	633	2	B70946	ABC transporter, H
422	33	42.9	389	2	D26395	homeotic protein U	495	33	42.9	643	2	C87412	short-chain alcoh
423	33	42.9	390	2	JE0212	hypothetical 44k P	496	33	42.9	657	2	S77543	hypothetical prote
424	33	42.9	390	2	JE0211	hypothetical 44k P	497	33	42.9	658	2	B96740	hypothetical prote
425	33	42.9	394	2	AH0362	nucleoside permeas	498	33	42.9	670	2	T09205	hypothetical prote
426	33	42.9	398	2	AI3231	conjugal transfer	499	33	42.9	684	2	AS2004	hypothetical prote
427	33	42.9	399	2	T48267	probable zinc fing	500	33	42.9	684	1	WZB886	77.8k DNA helicase
428	33	42.9	412	2	H72741	probable thiazole	501	33	42.9	716	1	S63392	probable membrane
429	33	42.9	416	2	AB0081	probable permeal	502	33	42.9	719	2	T12453	hypothetical prote
430	33	42.9	417	2	JC7693	soluble-type glyco	503	33	42.9	754	2	A56234	hypothetical prote
431	33	42.9	417	2	B59392	wnt10a protein pro	504	33	42.9	768	2	H69430	probable formate C
432	33	42.9	418	2	H71331	probable cell divi	505	33	42.9	776	1	H69430	hypothetical prote
433	33	42.9	418	2	S56369	hypothetical 44.8k	506	33	42.9	777	2	T08659	hypothetical prote
434	33	42.9	418	2	H86109	probable transport	507	33	42.9	881	1	A64040	hypothetical prote
435	33	42.9	418	2	B98269	probable transport	508	33	42.9	885	2	A84373	leucine-tRNA synth
436	33	42.9	422	2	JX0078	putidaredoxin redu	509	33	42.9	900	2	AI1279	aconitate hydratase
437	33	42.9	425	2	F95886	probable protein f	510	33	42.9	900	2	AI1642	aconitate hydratase
438	33	42.9	426	2	JC5086	polytopic cytoplas	511	33	42.9	901	2	F89910	H+-exporting ATPase
439	33	42.9	426	2	AI0586	putrescine/ornithi	512	33	42.9	905	2	S75035	phosphotransferase
440	33	42.9	439	2	B40839	putrescine/ornithi	513	33	42.9	908	2	F64207	aconitate hydratase
441	33	42.9	439	2	H90718	putrescine transpo	514	33	42.9	909	2	G69599	cation-transportin
442	33	42.9	439	2	H85568	putrescine transpo	515	33	42.9	911	2	AD2271	probable plasma me
443	33	42.9	444	2	F81367	probable transmemb	516	33	42.9	931	2	F84637	seizure-related pr
444	33	42.9	446	2	B81367	MARA efflux family	517	33	42.9	977	2	I52657	env polyprotein -
445	33	42.9	453	2	B95135	conserved hypotet	518	33	42.9	985	1	VCLJSP	RNA i protein - Cu
446	33	42.9	453	2	D98003	L-serine/ornithine	519	33	42.9	993	1	PLVXOM	ATP-dependent RNA
447	33	42.9	455	2	E75505	hypothetical prote	520	33	42.9	993	2	E71392	RNA i protein - Cu
448	33	42.9	461	2	H64087	hypothetical prote	521	33	42.9	993	2	JA0074	hypothetical prote
449	33	42.9	466	2	D91069	gamma-aminobutyrat	522	33	42.9	1063	2	D86731	heterocyst glycoli
450	33	42.9	466	2	H65045	hypothetical prote	523	33	42.9	1108	2	T31335	hypothetical prote
451	33	42.9	466	2	H82321	arginine/ornithine	524	33	42.9	1109	2	AC2475	carbamoylphosphate
452	33	42.9	468	2	H82321	hypothetical prote	525	33	42.9	1123	2	AD2045	hypothetical prote
453	33	42.9	471	2	E69435	probable amino aci	526	33	42.9	1162	2	A12843	hypothetical prote
454	33	42.9	472	2	H83497	hypothetical prote	527	33	42.9	1186	2	B97621	hypothetical prote
455	33	42.9	474	2	T34389	conserved hypotet	528	33	42.9	1201	2	A83007	O-antigen biosynth
456	33	42.9	477	2	D71333	probable amino aci	529	33	42.9	1275	2	T18556	conserved hypotet
457	33	42.9	481	1	I64144	arginine/ornithine	530	33	42.9	1291	2	E82325	BUD3 protein - yea
458	33	42.9	481	2	D86612	hypothetical prote	531	33	42.9	1367	2	S74285	probable ABC trans
459	33	42.9	482	2	T23532	probable arginine/	532	33	42.9	1413	2	G84790	immediate-early pr
460	33	42.9	483	2	G71523	probable arginine/	533	33	42.9	1446	1	A45344	protein F57C12.4 [
461	33	42.9	484	2	T36538	probable transmemb	534	33	42.9	1494	2	E89447	beta transducin-li
462	33	42.9	484	2	T36538	arginine/ornithine	535	33	42.9	1693	2	S76086	extracellular nucl
463	33	42.9	485	2	A72006	aldehyde dehydrog	536	33	42.9	1879	2	S74915	hypothetical prote
464	33	42.9	487	2	AH2374	sodium-dependent n	537	33	42.9	1882	2	S73484	hypothetical prote
465	33	42.9	492	2	F64464	L-lysine transport	538	33	42.9	1888	2	T14273	zinc finger protei
466	33	42.9	501	2	S18573	Photosystem II rea	539	33	42.9	1898	2	T42440	phospholipase C ho
467	33	42.9	508	2	T07985		540	33	42.9				

541	33	42.9	1922	2	T21581	hypothetical prote	614	32	41.6	274	2	T36347	hypothetical prote
542	33	42.9	3519	2	S43048	polyketide synthas	615	32	41.6	281	2	A65219	pnmJ protein - Esc
543	33	42.9	3828	2	T13857	trithorax protein	616	32	41.6	281	2	A91264	phosphonate metabo
544	33	42.9	4967	2	S72269	ryanodine receptor	617	32	41.6	286	2	F86104	phosphonate metabo
545	33	42.9	4969	2	A37113	ryanodine receptor	618	32	41.6	286	2	T19460	hypothetical prote
546	32.5	42.2	120	2	G70895	probable PE protei	619	32	41.6	287	2	AH3492	hydroxymethylgluta
547	32.5	42.2	169	2	AD1120	different proteins	620	32	41.6	288	2	T24066	exonuclease III ho
548	32.5	42.2	169	2	AD1481	different proteins	621	32	41.6	290	2	S76202	hypothetical prote
549	32.5	42.2	200	1	A34319	superoxide dismuta	622	32	41.6	291	2	ME2000	hypothetical prote
550	32.5	42.2	200	2	H84774	superoxide dismuta	623	32	41.6	295	1	AMECUA	sn-Glycerol-3-phos
551	32.5	42.2	200	2	T50043	superoxide dismuta	624	32	41.6	295	2	AE0993	glycerol-3-phospha
552	32.5	42.2	310	2	D75471	probable proline d	625	32	41.6	295	2	B91166	hypothetical prote
553	32.5	42.2	370	2	T05598	hypothetical prote	626	32	41.6	295	2	B86012	hypothetical prote
554	32.5	42.2	435	2	F84674	probable AAA-type	627	32	41.6	296	2	AG3388	exodeoxyribonuclea
555	32.5	42.2	547	2	H75632	Na(+)-linked D-ala	628	32	41.6	296	2	T35345	chitinase - Strept
556	32.5	42.2	551	2	S51941	prunin 1 precursor	629	32	41.6	302	2	G84053	hybrid-endo-beta-1
557	32.5	42.2	601	2	F83471	hypothetical prote	630	32	41.6	313	2	H71341	conserved hypoteth
558	32.5	42.2	608	2	F83397	probable peptidase	631	32	41.6	320	2	AG2387	hypothetical prote
559	32.5	42.2	625	2	T02847	probable membrane	632	32	41.6	321	1	LNH0ER	19E Fc receptor II
560	32	41.6	26	2	S65140	photosystem II D1	633	32	41.6	325	2	T06214	probable b-keto ac
561	32	41.6	70	2	AC0344	conserved phosphat	634	32	41.6	328	2	A70145	proliporotein dia
562	32	41.6	98	2	S75869	ribose-5-phosphate	635	32	41.6	328	2	C97268	uncharacterized pr
563	32	41.6	113	2	AG1587	hypothetical prote	636	32	41.6	329	2	C83506	probable oxidoredu
564	32	41.6	113	2	AD1652	hypothetical prote	637	32	41.6	333	1	D69812	ferrichrome ABC tr
565	32	41.6	115	2	S68316	hypothetical prote	638	32	41.6	335	2	T36304	probable anthranil
566	32	41.6	122	2	A86530	iron regulatory pr	639	32	41.6	335	2	T37280	probable cathepsin
567	32	41.6	122	2	B72093	acyl-carrier prote	640	32	41.6	338	2	E86465	hypothetical prote
568	32	41.6	124	2	D71025	probable ribosomal	641	32	41.6	352	2	H87236	probable integral
569	32	41.6	127	2	H72566	probable ribosomal	642	32	41.6	353	2	A11859	leucine dehydrogen
570	32	41.6	128	2	C75109	lsu ribosomal prot	643	32	41.6	353	2	B47045	uroporphyrinogen d
571	32	41.6	131	2	S18540	hypothetical prote	644	32	41.6	354	2	G75619	probable hemin ABC
572	32	41.6	133	2	I23725	ubiquinol-cytochro	645	32	41.6	357	2	D83685	nicotinate-nucleot
573	32	41.6	134	2	I46090	ubiquinol-cytochro	646	32	41.6	358	2	H72666	hypothetical prote
574	32	41.6	134	2	I46091	ubiquinol-cytochro	647	32	41.6	358	2	H95398	probable ABC trans
575	32	41.6	138	2	S41384	hypothetical 15K p	648	32	41.6	369	2	C97484	outer membrane pro
576	32	41.6	142	2	AC3345	LSU ribosomal prot	649	32	41.6	369	2	AC2702	probable membrane
577	32	41.6	142	2	C75344	conserved hypoteth	650	32	41.6	369	2	A69802	A/G-specific adeni
578	32	41.6	151	2	S37013	transposase (clone	651	32	41.6	370	2	F96002	probable sugar upt
579	32	41.6	154	2	A89962	6,7-dimethyl-8-rib	652	32	41.6	373	2	AG1270	citrate synthase c
580	32	41.6	154	2	F83415	hypothetical prote	653	32	41.6	378	2	B98272	hypothetical prote
581	32	41.6	156	2	E84230	hypothetical prote	654	32	41.6	379	1	S33572	ubiquinol-cytochro
582	32	41.6	158	2	S49918	hypothetical prote	655	32	41.6	379	2	AS3077	ubiquinol-cytochro
583	32	41.6	158	2	AD3583	riboflavin synthas	656	32	41.6	380	2	B82634	threonine dehydrat
584	32	41.6	159	2	A72660	hypothetical prote	657	32	41.6	381	2	T11440	ubiquinol-cytochro
585	32	41.6	165	2	AC0894	conserved hypoteth	658	32	41.6	384	2	T35407	conserved hypoteth
586	32	41.6	166	2	AB2147	hypothetical prote	659	32	41.6	384	2	T00625	branched-chain ami
587	32	41.6	168	2	AB3498	diacylglycerol kina	660	32	41.6	385	1	CBNC	ubiquinol-cytochro
588	32	41.6	169	2	A10058	signal peptidase I	661	32	41.6	385	2	S53087	ubiquinol-cytochro
589	32	41.6	170	2	A75333	hypothetical prote	662	32	41.6	386	2	T14243	ubiquinol-cytochro
590	32	41.6	170	2	C86652	hypothetical prote	663	32	41.6	386	2	E97196	probable glycosylt
591	32	41.6	173	2	G90351	hypothetical prote	664	32	41.6	387	1	CBASN	ubiquinol-cytochro
592	32	41.6	173	2	B65097	hypothetical 20.9	665	32	41.6	387	2	AC3190	hypothetical prote
593	32	41.6	179	2	B85969	hypothetical prote	666	32	41.6	389	2	T04612	tyrosine transamin
594	32	41.6	179	2	G91124	hypothetical prote	667	32	41.6	391	2	H97491	alanine racemase (
595	32	41.6	179	2	F83305	hypothetical prote	668	32	41.6	391	2	AG2709	alanine racemase [
596	32	41.6	182	2	B56274	sulfur-regulated p	669	32	41.6	398	2	S53054	NADH2 dehydrogenas
597	32	41.6	191	2	B82104	phosphoheptose iso	670	32	41.6	398	2	C87491	NADH dehydrogenase
598	32	41.6	194	2	D82956	conserved hypoteth	671	32	41.6	398	2	B75254	acetate kinase - D
599	32	41.6	195	2	T46072	DNA binding protei	672	32	41.6	399	2	C83563	tyrosyl-tRNA synth
600	32	41.6	200	2	AE2902	conserved hypoteth	673	32	41.6	400	2	C85899	hypothetical prote
601	32	41.6	202	2	T35126	hypothetical prote	674	32	41.6	400	2	H91054	hypothetical prote
602	32	41.6	204	2	H72256	conserved hypoteth	675	32	41.6	400	2	E65031	hypothetical prote
603	32	41.6	211	2	S21864	probable cyateine	676	32	41.6	400	2	AE0808	nucleoside permeas
604	32	41.6	215	2	AE3012	conserved hypoteth	677	32	41.6	402	2	S58477	rdsl protein - fis
605	32	41.6	222	2	H69055	conserved hypoteth	678	32	41.6	405	2	JC5175	probable glutamate
606	32	41.6	235	2	S25538	phenylalanine.ammo	679	32	41.6	421	2	T38764	probable storage prote
607	32	41.6	240	2	S13498	repressor protein	680	32	41.6	422	2	C70582	aureobasidin a res
608	32	41.6	240	2	AI1677	metal cations ABC	681	32	41.6	423	2	C70582	probable PPE prote
609	32	41.6	241	2	F97706	3-oxoacyl-l-acyl-ca	682	32	41.6	424	2	A54964	pectate lyase (EC
610	32	41.6	242	2	T36850	hypothetical prote	683	32	41.6	425	2	JC7271	hypothetical prote
611	32	41.6	254	2	AH0407	stationary-phase s	684	32	41.6	425	2	A83071	hypothetical prote
612	32	41.6	258	2	B96718	probable sterol de	685	32	41.6	432	2	T04712	probable formamida
613	32	41.6	269	1	S74490	type IV prepilin p	686	32	41.6	434	2	C95362	probable aminopept

687 32 41.6 440 2 D83805 hypothetical prote
688 32 41.6 444 2 D35794 probable 4-aminobu
689 32 41.6 448 2 B71319 probable acetate k
690 32 41.6 449 2 S03127 gene cob intron pr
691 32 41.6 450 2 A64408 conserved hypotet
692 32 41.6 461 2 S74414 Na+/H+-exchanging
693 32 41.6 462 2 AH3621 chloride channel p
694 32 41.6 462 2 S61332 IGA-specific metal
695 32 41.6 464 2 A28631 amylase precursor,
696 32 41.6 465 2 G96655 unknown protein, 2
697 32 41.6 475 2 A47674 alpha-amylase (EC
698 32 41.6 476 2 A90071 arginine/ornithin
699 32 41.6 476 2 H87352 hypothetical prote
700 32 41.6 479 2 J00781 sucrose uptake pro
701 32 41.6 479 2 F82432 PTS system, sucros
702 32 41.6 480 2 S39978 scrA protein - Sta
703 32 41.6 481 2 D64883 Aminobenzoyl-gluta
704 32 41.6 481 2 A90869 hypothetical prote
705 32 41.6 481 2 H85749 hypothetical prote
706 32 41.6 483 2 E83359 chitinase PA2300 (
707 32 41.6 484 1 Q08E77 HVLf3 protein - hu
708 32 41.6 484 2 T34016 hypothetical prote
709 32 41.6 485 2 T34016 Na+/H+-exchanging
710 32 41.6 488 1 QXASB1 mRNA maturase bi
711 32 41.6 490 2 I52410 cytochrome P450 2C
712 32 41.6 490 2 A36122 cytochrome P450 2C
713 32 41.6 494 1 S22687 intercellular spre
714 32 41.6 500 2 T03387 polyamine oxidase
715 32 41.6 502 2 T21935 hypothetical prote
716 32 41.6 508 2 S33774 photosystem II chl
717 32 41.6 508 2 B81594 hypothetical prote
718 32 41.6 508 2 E86549 hypothetical prote
719 32 41.6 508 2 C72074 hypothetical prote
720 32 41.6 511 2 T15629 hypothetical prote
721 32 41.6 512 2 S78887 hypothetical prote
722 32 41.6 514 2 S48730 Cry j II protein -
723 32 41.6 514 2 JC2498 second major aller
724 32 41.6 522 2 F75391 2-isopropylmalate
725 32 41.6 528 2 T12309 permealase I - como
726 32 41.6 528 2 G96553 hypothetical prote
727 32 41.6 538 2 E85438 step II splicing f
728 32 41.6 541 2 A90666 probable exported
729 32 41.6 542 2 T30493 hypothetical prote
730 32 41.6 550 2 A41468 60K heat shock pro
731 32 41.6 551 2 S58238 DR38 protein - fr
732 32 41.6 552 1 S19647 T-complex protein
733 32 41.6 553 2 S53080 hypothetical prote
734 32 41.6 556 2 G70503 probable cycA prot
735 32 41.6 557 2 E90170 hypothetical prote
736 32 41.6 560 2 F81423 L-lactate permease
737 32 41.6 603 2 AB2678 conserved hypotet
738 32 41.6 603 2 G97459 hypothetical prote
739 32 41.6 615 2 S24761 Cpo 61.1 protein -
740 32 41.6 615 2 JC7576 transcription fact
741 32 41.6 616 2 A46230 RNA-binding protei
742 32 41.6 618 2 D87651 prolly oligopeptid
743 32 41.6 619 2 F81324 glucose inhibited
744 32 41.6 621 2 H71713 glucose inhibited
745 32 41.6 622 2 D97710 glucose inhibited
746 32 41.6 626 2 I49100 msdc6 precursor -
747 32 41.6 638 2 S37085 polyadenylate-bind
748 32 41.6 641 2 A12524 hypothetical prote
749 32 41.6 647 2 T23407 hypothetical prote
750 32 41.6 652 2 S52683 probable membrane
751 32 41.6 659 2 T40383 hypothetical prote
752 32 41.6 661 1 A69048 ferrous iron trans
753 32 41.6 679 2 S28366 recombination repa
754 32 41.6 690 2 D75487 v-type ATP synthas
755 32 41.6 694 2 G01161 thymopietin alpha
756 32 41.6 707 2 A13290 transketolase (EC
757 32 41.6 710 2 T44753 hypothetical prote
758 32 41.6 721 2 T20010 hypothetical prote
759 32 41.6 732 2 AB0991 heavy metal-transp

760 32 41.6 733 2 A87168 conserved hypotet
761 32 41.6 738 2 I40719 isocitrate dehydro
762 32 41.6 752 2 AD2076 methyl-accepting c
763 32 41.6 757 2 T02884 D-(-)-3-hydroxybut
764 32 41.6 768 2 F33060 hypothetical prote
765 32 41.6 795 2 D64343 hypothetical prote
766 32 41.6 805 2 A64453 H+-exporting ATPas
767 32 41.6 823 2 B35963 protein-tyrosine k
768 32 41.6 824 2 S4108 protein-tyrosine k
769 32 41.6 848 2 G86708 hypothetical prote
770 32 41.6 860 2 F86349 alanine-tRNA ligas
771 32 41.6 867 2 H70411 hypothetical prote
772 32 41.6 870 2 E72541 probable aconitase
773 32 41.6 887 2 T27868 hypothetical prote
774 32 41.6 889 1 A44153 aconitase hydratase
775 32 41.6 889 2 A44154 aconitase hydratase
776 32 41.6 889 2 S26403 aconitase hydratase
777 32 41.6 889 2 S18720 aconitase hydratase
778 32 41.6 906 2 G75362 aconitase hydratase
779 32 41.6 916 2 D83093 aconitase hydratase
780 32 41.6 940 2 S73950 secretion protein
781 32 41.6 1028 2 B24785 phosphotransferase
782 32 41.6 1050 2 T36395 hypothetical prote
783 32 41.6 1091 2 A29553 hypothetical prote
784 32 41.6 1091 2 G98329 DNA polymerase III
785 32 41.6 1135 2 T42723 probable DNA-ditec
786 32 41.6 1135 2 T42368 DNA-directed RNA p
787 32 41.6 1206 2 A21140 hypothetical prote
788 32 41.6 1214 2 T21315 hypothetical prote
789 32 41.6 1271 2 T49009 protein kinase lik
790 32 41.6 1316 2 B86240 protein F20824.12
791 32 41.6 1317 2 B85189 disease resistance
792 32 41.6 1328 2 T43060 agrin - electric r
793 32 41.6 1442 2 T42607 transcription acti
794 32 41.6 1450 2 T45888 ABC transporter-11
795 32 41.6 1551 2 AB2410 WD-repeat protein
796 32 41.6 1613 2 G64488 reverse gyrase (in
797 32 41.6 1959 1 AGCH agrin precursor -
798 32 41.6 1959 1 AGRT agrin - rat
799 32 41.6 2467 2 D71437 probable resistanc
800 32 41.6 3063 2 S55505 fatty-acid synthase
801 32 41.6 3229 2 S27852 probable cell-surf
802 32 41.6 4836 2 T14346 herc2 protein - mo
803 32 41.6 4848 2 T30289 pristinamycin I sy
804 31.5 40.9 111 2 D87500 hypothetical prote
805 31.5 40.9 271 2 J00950 ICP 18.5 protein -
806 31.5 40.9 406 2 AG3021 murein hydrolase (I
807 31.5 40.9 436 2 C98263 conserved hypotet
808 31.5 40.9 433 2 F82298 conserved hypotet
809 31.5 40.9 580 2 B72457 probable phenylala
810 31.5 40.9 580 2 A46538 ig heavy chain, se
811 31.5 40.9 592 2 S51956 endo-1,4-beta-gluc
812 31.5 40.9 593 2 S51956 peptidase, M20/M25
813 31.5 40.9 805 2 G87662 beta-catenin - Hyd
814 31.5 40.9 806 2 JC4835 probable PEG prote
815 31.5 40.9 1159 2 E70741 hypothetical prote
816 31.5 40.9 2204 2 A70524 protein Tln15.13 (I
817 31 40.3 76 2 G97077 conserved membrane
818 31 40.3 83 2 A82386 hypothetical prote
819 31 40.3 84 2 A96525 aspergillopepsin I
820 31 40.3 87 2 E95371 hypothetical prote
821 31 40.3 101 2 H95962 hypothetical prote
822 31 40.3 108 2 JN0368 aspergillopepsin I
823 31 40.3 115 2 A12743 hypothetical prote
824 31 40.3 119 2 E72744 hypothetical prote
825 31 40.3 121 2 E82336 ribosomal protein
826 31 40.3 123 2 H81235 50S ribosomal prot
827 31 40.3 124 2 A81226 conserved hypotet
828 31 40.3 129 2 T35780 ribosomal protein
829 31 40.3 130 2 S74799 probable secreted
830 31 40.3 131 2 A12329 30S ribosomal prot
831 31 40.3 131 2 A12329 30S ribosomal prot
832 31 40.3 131 2 AG3198 hypothetical prote

833	31	40.3	133	2	F75552	ribosomal protein	906	31	40.3	290	2	S44091	oxoglutarate/malat
834	31	40.3	138	1	H64434	hypothetical prote	907	31	40.3	292	2	T22236	hypothetical prote
835	31	40.3	138	2	S24105	envelope protein -	908	31	40.3	294	2	E69462	probable pyruvate
836	31	40.3	138	2	H97524	hypothetical prote	909	31	40.3	294	2	C72378	sugar ABC transpor
837	31	40.3	141	2	A86875	50S ribosomal prot	910	31	40.3	296	1	A69693	integrase/recombin
838	31	40.3	141	2	G83664	ribosomal protein	911	31	40.3	296	2	H87508	phosphoserine phos
839	31	40.3	141	2	S39860	ribosomal protein	912	31	40.3	298	1	C64333	probable pyruvate
840	31	40.3	143	2	F87328	ribosomal protein	913	31	40.3	301	2	H70890	hypothetical prote
841	31	40.3	145	1	GGICE8	globin CTT-VIIB -	914	31	40.3	302	2	E84421	probable phosphati
842	31	40.3	152	2	T04611	hypothetical prote	915	31	40.3	302	2	T05233	hypothetical prote
843	31	40.3	156	1	JN0456	H+-exporting ATPas	916	31	40.3	305	2	S58822	probable membrane
844	31	40.3	156	2	A56680	H+-exporting ATPas	917	31	40.3	305	2	T02851	probable membrane
845	31	40.3	156	2	B83844	6,7-dimethyl-8-rib	918	31	40.3	306	2	T51705	methyleneretrahydr
846	31	40.3	156	2	F75141	hypothetical prote	919	31	40.3	307	2	AX02017	glycerol-3-phospha
847	31	40.3	159	1	S42878	H+-exporting ATPas	920	31	40.3	313	2	JX0096	lectin precursor,
848	31	40.3	163	2	AC1939	peptide methionine	921	31	40.3	314	1	G64658	probable pyruvate
849	31	40.3	168	2	S22102	fimbrial protein M	922	31	40.3	314	2	A71858	pyruvate ferredoxi
850	31	40.3	168	2	A69708	signal peptidase I	923	31	40.3	317	1	S26208	glucose kinase - S
851	31	40.3	169	2	S76933	hypothetical prote	924	31	40.3	317	2	F96810	hypothetical prote
852	31	40.3	174	2	T13538	hypothetical prote	925	31	40.3	319	2	E75068	dipeptide abc tran
853	31	40.3	174	2	F84338	hypothetical prote	926	31	40.3	320	2	G72762	probable acetylpol
854	31	40.3	185	2	AC1218	bifunctional cobal	927	31	40.3	321	2	D81018	iron(III) ABC tran
855	31	40.3	191	2	G71835	ribosomal protein	928	31	40.3	321	2	E81962	probable membrane
856	31	40.3	191	2	G64684	ribosomal protein	929	31	40.3	321	2	F71163	probable oligopept
857	31	40.3	193	1	HIBPA4	internal protein I	930	31	40.3	322	2	E69009	cation antporter
858	31	40.3	194	2	S39798	adenylate kinase (931	31	40.3	322	2	D75142	oligopeptide trans
859	31	40.3	196	2	AC3300	probable membrane-	932	31	40.3	323	2	D87573	inosine-uridine pr
860	31	40.3	198	2	T35915	hypothetical prote	933	31	40.3	326	2	D84412	glucose kinase [im
861	31	40.3	203	2	D87567	conserved hypotet	934	31	40.3	328	2	T40013	thiazole biosynthe
862	31	40.3	209	2	H81056	iron-starvation pr	935	31	40.3	329	2	T45849	peroxidase ATP2la
863	31	40.3	213	2	G84828	hypothetical prote	936	31	40.3	329	2	AG2951	hypothetical prote
864	31	40.3	214	2	S15326	fimbrial protein M	937	31	40.3	329	2	F98331	probable oligopept
865	31	40.3	214	2	AB2705	conserved hypotet	938	31	40.3	336	2	E72359	rod shape-determin
866	31	40.3	214	2	B97487	hypothetical prote	939	31	40.3	337	2	H87491	conserved hypotet
867	31	40.3	220	2	D69797	hypothetical prote	940	31	40.3	338	2	B82499	hypothetical prote
868	31	40.3	220	2	G72716	hypothetical prote	941	31	40.3	340	2	F75557	oxidoreductase, sh
869	31	40.3	224	2	G70851	probable gid prote	942	31	40.3	341	2	AE2652	exopolysphatase
870	31	40.3	226	2	F83184	conserved hypotet	943	31	40.3	344	2	G97253	undecaprenyl-phosp
871	31	40.3	226	2	AD2198	hypothetical prote	944	31	40.3	344	2	H45252	PilV constant regi
872	31	40.3	227	2	T35395	probable transfera	945	31	40.3	345	2	AE2914	conserved hypotet
873	31	40.3	229	2	H82719	NonF-related prote	946	31	40.3	345	2	H97688	hypothetical prote
874	31	40.3	230	2	H81820	heme utilisation p	947	31	40.3	346	2	AH3293	holliday junction
875	31	40.3	231	2	C83179	conserved hypotet	948	31	40.3	347	2	JC7178	chitinase (EC 3.2.
876	31	40.3	232	2	S70211	hypothetical prote	949	31	40.3	349	2	T00526	UDP-N-acetylpyruvo
877	31	40.3	236	2	F64964	yeep protein - Esc	950	31	40.3	351	2	G82541	photosystem II pro
878	31	40.3	236	2	T17705	hypothetical prote	951	31	40.3	352	2	JT0321	cathapsin B-like c
879	31	40.3	239	2	C84994	hypothetical prote	952	31	40.3	353	2	T06466	probable methylgal
880	31	40.3	239	2	AB1689	conserved hypotet	953	31	40.3	354	2	F71312	hypothetical 40K p
881	31	40.3	241	2	C71711	acetoacetyl-COA re	954	31	40.3	355	2	A41314	hypothetical prote
882	31	40.3	242	2	F87640	exsB protein [impo	955	31	40.3	357	2	T24137	peptide chain rele
883	31	40.3	245	2	AI3412	ribonuclease II (956	31	40.3	359	2	D97987	peptide chain rele
884	31	40.3	253	2	B71547	probable cryptopha	957	31	40.3	359	2	P95117	apurinic/aprimidi
885	31	40.3	253	2	B87476	ABC transporter, A	958	31	40.3	361	2	S68268	conserved hypotet
886	31	40.3	255	2	AB3280	membrane-bound lyt	959	31	40.3	364	2	A70474	probable phosphori
887	31	40.3	256	2	T46597	hypothetical prote	960	31	40.3	370	2	A75569	probable sideropho
888	31	40.3	256	2	AD1115	hypothetical prote	961	31	40.3	370	2	B95420	probable pepQ - My
889	31	40.3	257	2	AE1476	hypothetical prote	962	31	40.3	372	1	C70658	adp-glucose pyroph
890	31	40.3	258	2	T02819	probable membrane	963	31	40.3	372	2	H97175	probable binding p
891	31	40.3	260	2	G64690	type IIS restricti	964	31	40.3	374	2	C83032	gamma-D-glutamyl-L
892	31	40.3	260	2	G70619	probable 23S rnam	965	31	40.3	376	1	E69957	homocitrate syntha
893	31	40.3	260	2	D81191	hypothetical prote	966	31	40.3	377	2	AD1982	sulfate starvation
894	31	40.3	264	2	T30224	3-oxoacyl-(acyl ca	967	31	40.3	378	2	D69817	ubiquinol-cytochro
895	31	40.3	264	2	S22090	catechol O-methyl	968	31	40.3	379	2	I48132	ubiquinol-cytochro
896	31	40.3	264	2	AG2095	hypothetical prote	969	31	40.3	379	2	I48135	ubiquinol-cytochro
897	31	40.3	269	2	C81197	mutr protein NMB04	970	31	40.3	379	2	I48399	ubiquinol-cytochro
898	31	40.3	269	2	C81833	MutT-related prote	971	31	40.3	379	2	I49400	ubiquinol-cytochro
899	31	40.3	271	2	T35065	tryptophan synthas	972	31	40.3	379	2	I48134	ubiquinol-cytochro
900	31	40.3	271	2	S42418	probable antibioti	973	31	40.3	380	2	T11033	ubiquinol-cytochro
901	31	40.3	272	2	E64379	prephenate dehydra	974	31	40.3	380	2	H69485	DNA-directed RNA p
902	31	40.3	273	2	S67622	hypothetical prote	975	31	40.3	381	2	A86692	pyridoxal-phospha
903	31	40.3	276	2	AE3336	sulfate transport	976	31	40.3	381	2	F87684	hypothetical prote
904	31	40.3	289	2	E84098	prolipoprotein dia	977	31	40.3	386	2	S87684	aminotransferase p
905	31	40.3	289	2	F86404	unknown protein [i	978	31	40.3	387	2	S32934	

979 31 40.3 387 2 B84313 aminomethyltransfe
980 31 40.3 387 2 G84190 hypothetical prote
981 31 40.3 387 2 C96720 hypothetical prote
982 31 40.3 388 2 AC3216 isomerase/lactoniz
983 31 40.3 389 2 S62597 ubiquinol-cytochro
984 31 40.3 390 2 S78188 ubiquinol-cytochro
985 31 40.3 390 2 A83622 probable chemotaxi
986 31 40.3 392 2 A82572 aminotransferase,
DNA-directed RNA p
987 31 40.3 393 2 S25365 pyrimidine nucleos
988 31 40.3 393 2 S49456 probable PPE prote
989 31 40.3 393 2 G70929 outer mitochondria
990 31 40.3 393 2 S48398 xylose isomerase (
991 31 40.3 395 1 S16214 hypothetical prote
992 31 40.3 395 2 F69148 hyaluronan synthas
993 31 40.3 395 2 A48755 aspartate aminotra
994 31 40.3 395 2 D83782 hypothetical prote
995 31 40.3 395 2 T09373 NADH2 dehydrogenas
996 31 40.3 396 2 S78164 DNA-directed RNA p
997 31 40.3 397 2 C75182 probable DNA-direc
998 31 40.3 397 2 G71031 membrane-bound lyt
999 31 40.3 398 2 AC3322 probable transamin
1000 31 40.3 399 2 S39740

ALIGNMENTS

RESULT 1
A70803
early secretory antigen target esat6 - Mycobacterium tuberculosis (strain H37Rv)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: A70803; S49174
R:Colle, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A>Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: A70803
A>Title: nucleic acid sequence not shown; translation not shown
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-95 <COL>
A:Cross-references: UNIPROT:Q57165; UNIPARC:UPI0000036DD3; GB:AL123456; NID
A:Experimental source: strain H37Rv
R:Soerensen, A.L.; Nagai, S.; Houen, G.; Andersen, P.; Andersen, A.B.
submitted to the EMBL Data Library, June 1994
A:Reference number: S49174
A:Accession: S49174
A:Molecule type: DNA
A:Residues: 1-13, 'R', 15-22, 'S', 24-95 <SOE>
A:Cross-references: UNIPARC:UPI000017AUSF; EMBL:X79562; NID:gs531708
C:Genetics:
A:Gene: esat6

Query Match 100.0%; Score 77; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 3.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WNFAGIEAAASAIQ 15
|||||
Db 6 WNFAGIEAAASAIQ 20
|||||
RESULT 2
G86844
hypothetical protein glnp [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C:Species: Lactococcus lactis subsp. lactis
C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puller, A.; Abola, P.; Barloy-Hubler
C:Accession: G86844
R:Solotkin, A.; Wincker, P.; Manger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001

A>Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: G86844
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-714 <SO>
A:Cross-references: UNIPROT:Q9CRS5; UNIPARC:UPI00000D44A5; GB:AB005176; PID:g12724781; I
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: glnp

Query Match 61.0%; Score 47; DB 2; Length 714;
Best Local Similarity 50.0%; Pred. No. 4.4;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAIQ 14
|||||
Db 303 WNFIFQAAVDSVQ 316
|||||

RESULT 3
T50707
urease accessory protein D [imported] - Rhodobacter sphaeroides
C:Species: Rhodobacter sphaeroides
C>Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 31-Dec-2004
C:Accession: T50707
R:Choudhary, M.; Kaplan, S.
Nucleic Acids Res. 28, 862-867, 2000
A>Title: DNA sequence analysis of the photosynthesis region of Rhodobacter sphaeroides
A:Reference number: 225222; MUID:20115911; PMID:10648776
A:Accession: T50707
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-225 <CH>
A:Cross-references: UNIPROT:Q9RPF6; UNIPARC:UPI00000B5484; EMBL:AF195122; PIDN:AAF24251
A:Experimental source: strain 2.4.1
C:Genetics:
A:Gene: ureD
C:Superfamily: urease accessory protein UreD

Query Match 57.1%; Score 44; DB 2; Length 225;
Best Local Similarity 75.0%; Pred. No. 4.4;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 AGIEAAASAIQ 15
|||||
Db 178 AGVEAAASAFDG 189
|||||

RESULT 4
H95313
NoeA host specific nodulation protein [imported] - Sinorhizobium meliloti (strain 1021)
C:Species: Sinorhizobium meliloti
C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: H95313
R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bow
; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A>Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilo
A:Reference number: A95262; MUID:21396509; PMID:11481432
A:Accession: H95313
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-476 <KUR>
A:Cross-references: UNIPROT:Q52892; UNIPARC:UPI000013032A; GB:AE006469; PIDN:AAK5074.1
A:Experimental source: strain 1021, megaplasmid pSymA
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puller, A.; Abola, P.; Barloy-Hubler
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A>Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A;Reference number: A96039; MUID:21368234; PMID:11474104

A;Contents: annotation

C;Genetics:

A;Gene: noeA

A;Genome: plasmid

C;Superfamily: Rhizobium meliloti noeA protein

Query Match 55.8%; Score 43; DB 2; Length 476;

Best Local Similarity 70.0%; Pred. No. 14;

Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAAA 10

|||:|||||

Db 101 WSPAGLKAAA 110

RESULT 5

S71360 noeA protein - Rhizobium meliloti

C;Species: Rhizobium meliloti

C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C;Accession: S71360; S71358

R;Ardourel, M.; Lortet, G.; Maillet, F.; Roche, P.; Truchet, G.; Prome, J.C.; Rosenberg,

submitted to the EMBL Data Library, May 1995

A;Reference number: S71360

A;Accession: S71360

A;Molecule type: DNA

A;Residues: 1-476 <ARD>

A;Cross-references: UNIPROT:Q52892; UNIPARC:UPI000013032A; EMBL:U26430; NID:gl326068; PT

A;Experimental source: strain RCR2011

R;Ardourel, M.; Lortet, G.; Maillet, F.; Roche, P.; Truchet, G.; Prome, J.C.; Rosenberg,

Mol. Microbiol. 17, 687-699, 1995

A;Title: In Rhizobium meliloti, the operon associated with the nod box n5 comprises nodI

A;Reference number: S71357; MUID:96111489; PMID:8801423

A;Accession: S71358

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 304-339 <ARW>

A;Cross-references: UNIPARC:UPI00001792D2; EMBL:U26430

A;Experimental source: strain RCR2011 (=SU47)

C;Genetics:

A;Gene: noeA

C;Superfamily: Rhizobium meliloti noeA protein

C;Keywords: nodulation

Query Match 55.8%; Score 43; DB 2; Length 476;

Best Local Similarity 70.0%; Pred. No. 14;

Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAAA 10

|||:|||||

Db 101 WSPAGLKAAA 110

RESULT 6

H83229

conserved hypothetical protein PA3332 [imported] - Pseudomonas aeruginosa (strain PA01)

C;Species: Pseudomonas aeruginosa

C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004

C;Accession: H83229

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lm,

; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A;Reference number: A82950; MUID:20437337; PMID:10984043

A;Accession: H83229

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-141 <STO>

A;Cross-references: UNIPROT:Q9HYR3; UNIPARC:UPI00000C59BA; GB:AE004755; GB:AE004091; NID

A;Experimental source: strain PA01

C;Genetics:

A;Gene: PA3332

C;Superfamily: Bacillus subtilis hypothetical protein yseE

Query Match 55.2%; Score 42.5; DB 2; Length 141;

Best Local Similarity 40.9%; Pred. No. 4.8;

Matches 9; Conservative 2; Mismatches 4; Indels 7; Gaps 1;

QY 1 WN-----FAGIEAAASAIQ 15

|||:|||||

Db 119 WNPRLHLEALGGVEAAAKIVQ 140

RESULT 7

G72069

conserved hypothetical protein CP0240 [imported] - Chlamydophila pneumoniae (strains CW

N;Alternate names: fe-s oxidoreductase

C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C;Accession: G72069; F81599

R;Kallman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J. J.

Nature Genet. 21, 385-389, 1999

A;Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.

A;Reference number: A72000; MUID:99206606; PMID:10192388

A;Accession: G72069

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-369 <ARN>

A;Cross-references: UNIPROT:Q52839; UNIPARC:UPI00000D403D; GB:AE001636; GB:AE001363; N1

A;Experimental source: strain CW1029

R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,

, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg

Nucleic Acids Res. 28, 1397-1406, 2000

A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.

A;Reference number: A81500; MUID:20150255; PMID:10684935

A;Accession: F81599

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-369 <REA>

A;Cross-references: UNIPARC:UPI00000D403D; GB:AE002184; GB:AE002161; NID:G7189156; PIDN

A;Experimental source: strain AR39, HL cells

C;Genetics:

A;Gene: CPN0513; CP0240

C;Superfamily: hypothetical protein AF0390

Query Match 54.5%; Score 42; DB 2; Length 369;

Best Local Similarity 77.8%; Pred. No. 16;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WNFAGIEAAA 9

|||:|||||

Db 305 WNYLGIEAA 313

RESULT 8

E86554

Fe-S oxidoreductase [imported] - Chlamydophila pneumoniae (strain J138)

C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: E86554

R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; I

Nucleic Acids Res. 28, 2311-2314, 2000

A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.

A;Reference number: A86491; MUID:20330349; PMID:10871362

A;Accession: E86554

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-369 <STO>

A;Cross-references: UNIPROT:Q92839; UNIPARC:UPI00000D403D; GB:BA000008; NID:G8978883; F

A;Experimental source: strain J138

C;Genetics:

A;Gene: CPJ0513

C;Superfamily: hypothetical protein AF0390

Query Match 54.5%; Score 42; DB 2; Length 369;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 1; Mismatches 0; Gaps 0;

QY 1 WNPAGIEAAA 9
||:|||||
DB 305 WNYLGIEAA 313

RESULT 9
A69622
ferrichrome ABC transporter (permease) fhbB - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: A69622
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertoni, R.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chakrabarti, A.; Ehrlich, S.D.; Emmerman, P.T.; Entian, K.D.; Errington, J.; Fabbet, C.; Ferrari, E.; Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallet, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koester, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Laubet, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y.; M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, R.; Rieger, M.; Rivolta, C.; Roche, B.; Roche, M.; Sadaie, Y.; Sato, T.; Scallan, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serron, akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: A69622
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-384 <KUN>
A:Cross-references: UNIPROT:P49936; UNIPARC:UPI000060A52; GB:Z99121; GB:AL009126; NID:9384377
A:Experimental source: strain 168
C:Genetics:
A:Gene: fhbB
C:Superfamily: vitamin B12 transport protein btuB

Query Match 53.2%; Score 41; DB 2; Length 384;
Best Local Similarity 46.7%; Pred. No. 25;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 WNPAGIEAAAATG 15
||:|||||
DB 174 WSPAGAGLCASTVMG 188

RESULT 10
D82342
probable cadaverine/lysine antiporter CadB VC0280 [imported] - Vibrio cholerae (strain N5)
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004
C:Accession: D82342
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F.; L., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: D82342
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-445 <HEI>
A:Cross-references: UNIPROT:Q9KV76; UNIPARC:UPI00000C2C57; GB:AE004116; GB:AE003852; NID:10952301
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC0280
A:Map position: 1
C:Superfamily: ecotropic retrovirus receptor protein

Query Match 53.2%; Score 41; DB 2; Length 445;
Best Local Similarity 60.0%; Pred. No. 30;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 WNPAGIEAAA 10
||:|||||
DB 199 WSPGVESAA 208

RESULT 11
F86745
ABC transporter permease protein yjyD [imported] - Lactococcus lactis subsp. lactis (str. C)
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C:Accession: F86745
R:Boletín, A.; Winkler, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich, A.; Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. A.
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: F86745
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-540 <STO>
A:Cross-references: UNIPROT:Q9CGX6; UNIPARC:UPI00000C6961; GB:AE005176; PID:g12723906; 1
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: yjyD

Query Match 53.2%; Score 41; DB 2; Length 540;
Best Local Similarity 69.2%; Pred. No. 36;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 FAGIEAASAIQ 15
||:|||||
DB 339 FVGNATAAIRG 351

RESULT 12
I41220
glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - Escherichia I
C:Species: Escherichia blattae
C:Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C:Accession: I41220; I41223; I41226
R:Lawrence, J.G.; Ochman, H.; Hartl, D.L.
J. Gen. Microbiol. 137, 1911-1921, 1991
A:Title: Molecular and evolutionary relationships among enteric bacteria.
A:Reference number: I40701; MUID:92065252; PMID:1955870
A:Accession: I41220
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-294 <RES>
A:Cross-references: UNIPROT:P24749; UNIPARC:UPI000012AEAA; GB:M63358; NID:g146076; PIDN:141220
A:Accession: I41223
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-294 <RES>
A:Cross-references: UNIPARC:UPI000012AEAA; GB:M63359; NID:g146108; PIDN:AAA23852.1; PID:141226
A:Experimental source: ATCC 33429
A:Accession: I41226
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-294 <RES>
A:Cross-references: UNIPARC:UPI000012AEAA; GB:M63360; NID:g146114; PIDN:AAA23855.1; PID:141226
A:Experimental source: ATCC 33430
C:Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C:Keywords: oxidoreductase

Query Match 51.9%; Score 40; DB 2; Length 294;
Best Local Similarity 58.3%; Pred. No. 29;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 WNPAGIEAASA 12

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Db          70 WNEAGVEVWAE 81
|||||
RESULT 13
B97457
BH3305 conserved hypothetical [imported] - Agrobacterium tumefaciens (strain C58, Cereon
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: B97457
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, D.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: B97457
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-323 <KUR>
A;Cross-references: UNIPROT:Q8UH81; UNIPARC:UPI000000D1928; GB:AE007869; PIDN:AAK86611.1;
C;Genetics:
A;Gene: AGR_C_1468
A;Map position: circular chromosome

Query Match          51.9%; Score 40; DB 2; Length 323;
Best Local Similarity 61.5%; Pred. No. 31;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 FAGIEAASAIQ 15
|||||
Db 11 FAGISCAATALAG 23

RESULT 14
AD2675
conserved hypothetical protein Atu0802 [imported] - Agrobacterium tumefaciens (strain C5
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AD2675
R;Wood, D.W.; Secubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AD2675
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-323 <KUR>
A;Cross-references: UNIPROT:Q8UH81; UNIPARC:UPI000000D1928; GB:AE008688; PIDN:AAL41818.1;
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu0802
A;Map position: circular chromosome

Query Match          51.9%; Score 40; DB 2; Length 323;
Best Local Similarity 61.5%; Pred. No. 31;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 FAGIEAASAIQ 15
|||||
Db 11 FAGISCAATALAG 23

RESULT 15
H69020
probable Na+/Ca2+-exchanging protein - Methanobacterium thermoautotrophicum (strain D
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: H69020
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;

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; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: H69020
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-330 <WTH>
A;Cross-references: UNIPROT:O27223; UNIPARC:UPI00000066638; GB:AE000885; GB:AE000666; NI
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH1155
A;Start codon: TTG

Query Match          51.9%; Score 40; DB 2; Length 330;
Best Local Similarity 46.7%; Pred. No. 32;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WNPAGIEAASAIQ 15
|||||
Db 95 WNIAGILGISSVVAG 109

RESULT 16
F95940
probable xanthine dehydrogenase (EC 1.1.1.204) [imported] - Sinorhizobium meliloti (str
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 31-Dec-2004
C;Accession: F95940
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Herna
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing end
A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: F95940
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-493 <KUR>
A;Cross-references: UNIPROT:Q92VB8; UNIPARC:UPI000000CB669; GB:AL591985; PIDN:CAC49190.1
A;Experimental source: strain 1021, megaplasmid pSymB
R;Gallier, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure
heault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: xdhA1; SMD21286
A;Genome: plasmid
C;Superfamily: xanthine dehydrogenase, small subunit
C;Keywords: oxidoreductase

Query Match          51.9%; Score 40; DB 2; Length 493;
Best Local Similarity 50.0%; Pred. No. 49;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 WNPAGIEAASAIQ 14
|||||
Db 433 WNDAAIEAGVAALE 446

RESULT 17
B84349
hypothetical protein Vng1985c [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: B84349
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky,
; Leithauer, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl
Jung, K.H.; Alam, M.; Freitas, T.

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Best Local Similarity 50.0%; Pred. No. 56;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 WNFAGIEAASAIQ 14
    ||| : ||| : |||
DB 31 WNFGLLAACLAQ 44

RESULT 22
S58462
ubiquinol-cytochrome-c reductase (EC 1.10.2.2) cytochrome b - Stellar sea lion mitochondrion
C;Species: mitochondrion Eumecoptas jubatus (Stellar sea lion)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S58462
R;Arnasen, U.; Bodin, K.; Gullberg, A.; Ledje, C.; Mouchaty, S.
J. Mol. Evol. 40, 78-85, 1995
A;Title: A molecular view of pinniped relationships with particular emphasis on the true
A;Reference number: S58447; MUID:95230701; PMID:7714914
A;Accession: S58462
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-379 <ARN>
A;Cross-references: UNIPROT:Q34471; UNIPARC:UPI000008PBB9; EMBL:X82311; NID:g693959; PID
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1994
C;Genetics:
A;Genome: mitochondrion
A;Genetic code: SGCI
C;Superfamily: cytochrome b; cytochrome b homology; cytochrome b6 homology; plastoquinol
C;Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; mitochondrion;
F;11-339/Domain: cytochrome b6 homology <CBH>
F;11-209/Domain: cytochrome b6 homology <CB6>
F;36-53/Domain: transmembrane #status predicted <TM1>
F;81-99/Domain: transmembrane #status predicted <TM2>
F;117-133/Domain: transmembrane #status predicted <TM3>
F;142-146/Region: ubiquinone binding #status predicted <TM4>
F;178-200/Domain: transmembrane #status predicted <TM5>
F;221-339/Domain: plastoquinol-plastocyanin reductase 17K protein homology <17K>
F;229-245/Domain: transmembrane #status predicted <TM6>
F;288-304/Domain: transmembrane #status predicted <TM7>
F;323-343/Domain: transmembrane #status predicted <TM8>
F;353-369/Domain: transmembrane #status predicted <TM9>
F;83,182/Binding site: heme iron (His) (axial ligands) (low potential) #status predicted
F;97,196/Binding site: heme iron (His) (axial ligands) (high potential) #status predicted

Query Match 50.6%; Score 39; DB 2; Length 379;
Best Local Similarity 50.0%; Pred. No. 56;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 WNFAGIEAASAIQ 14
    ||| : ||| : |||
DB 31 WNFGLLAACLAQ 44

RESULT 23
AF1022
Probable amino acid permease STY4493 [imported] - Salmonella enterica subsp. enterica se
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 05-Oct-2004
C;Accession: AF1022
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Comerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AF1022
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-445 <PAR>
A;Cross-references: UNIPARC:UPI000005A86C; GB:AL513382; PIDN:CAD09279.1; PID:g16505283;
C;Genetics:
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A;Gene: STY4493
C;Superfamily: ecotropic retrovirus receptor protein

Query Match 50.6%; Score 39; DB 2; Length 445;
Best Local Similarity 50.0%; Pred. No. 66;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 WNFAGIEAASAA 12
    | : | : | : |
DB 202 WSFIGVESASVA 213

RESULT 24
B65221
Probable amino acid/amine transport protein [similarity] - Escherichia coli (strain K-12)
N;Alternate names: hypothetical protein f326a
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
C;Accession: B65221; S56344
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: B65221
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-445 <BLAT>
A;Cross-references: UNIPROT:P60061; UNIPARC:UPI000013B545; GB:AE000484; GB:U00096; NID:
A;Experimental source: strain K-12, substrain MGI655
R;Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
Nucleic Acids Res. 23, 2105-2119, 1995
A;Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92
A;Reference number: S56314; MUID:95334362; PMID:7610040
A;Accession: S56344
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-321, 'SQWR', 326 <BUR>
A;Cross-references: UNIPARC:UPI000016F6C5; EMBL:U14003; NID:g1263172; PIDN:AAA97015.1;
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
C;Superfamily: ecotropic retrovirus receptor protein

Query Match 50.6%; Score 39; DB 2; Length 445;
Best Local Similarity 50.0%; Pred. No. 66;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 WNFAGIEAASAA 12
    | : | : | : |
DB 202 WSFIGVESASVA 213

RESULT 25
A91266
Probable amino acid/amine transport protein ECs5097 [imported] - Escherichia coli (stra
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004
C;Accession: A91266
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: A91266
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-445 <HAY>
A;Cross-references: UNIPROT:P60063; UNIPARC:UPI000013B545; GB:BA000007; PIDN:BAB38520.1
A;Experimental source: strain O157:H7, substrain RMD 050952
C;Genetics:
A;Gene: ECs5097
C;Superfamily: ecotropic retrovirus receptor protein

Query Match 50.6%; Score 39; DB 2; Length 445;
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Best Local Similarity 50.0%; Pred. No. 66; Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;	
QY 1 WNPAGIEAAASA 12 : : : : :	
Db 202 WSPGIVGESASVA 213	
RESULT 26	
F86106	
probable amino acid/amine transport protein [similarity] - Escherichia coli (strain O157:H7)	
C:Species: Escherichia coli	
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004	
C:Accession: F86106	
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001	
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.	
A:Reference number: A85480; MUID:21074935; PMID:11206551	
A:Accession: F86106	
A:Status: preliminary	
A:Molecule type: DNA	
A:Residues: 1-445 <STO>	
A:Cross-references: UNIPROT:P60063; UNIPARC:UPI0000138545; GB:AE005174; NID:G12519085; E	
A:Experimental source: strain O157:H7, substrain EDL933	
C:Genetics:	
A:Gene: YJGE	
C:Superfamily: ecotropic retrovirus receptor protein	
Query Match 50.6%; Score 39; DB 2; Length 445; Best Local Similarity 50.0%; Pred. No. 66; Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;	
QY 1 WNPAGIEAAASA 12 : : : : :	
Db 202 WSPGIVGESASVA 213	
RESULT 27	
T05591	
tyrosine transaminase homolog F9D16.60 - Arabidopsis thaliana	
C:Species: Arabidopsis thaliana (mouse-ear cress)	
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004	
C:Accession: T05591	
R:Bevan, M.; Wedler, H.; Wedler, E.; Wambutt, R.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F. submitted to the Protein Sequence Database, February 1999	
A:Reference number: Z15419	
A:Accession: T05591	
A:Molecule type: DNA	
A:Residues: 1-448 <BEV>	
A:Cross-references: UNIPROT:Q9SUR7; UNIPARC:UPI000009DEB1; EMBL:AL035394	
A:Experimental source: cultivar Columbia; BAC clone F9D16	
C:Genetics:	
A:Map position: 4	
A:Introns: 84/2; 197/3; 272/3; 300/3; 352/3; 398/1	
A:Note: F9D16.60	
C:Superfamily: tyrosine transaminase	
Query Match 50.6%; Score 39; DB 2; Length 448; Best Local Similarity 50.0%; Pred. No. 66; Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;	
QY 1 WNPAGIEAAASIO 14 : : : : :	
Db 9 WQPSGDAAEKAAQ 22 : : : : :	
RESULT 28	
B83518	
pmeIoy1-CoA synthetase PA1017 [imported] - Pseudomonas aeruginosa (strain PA01)	
C:Species: Pseudomonas aeruginosa	
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004	
C:Accession: B83518	

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V	
Nature 406, 959-964, 2000	
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho gen	
A:Reference number: A82950; MUID:20437337; PMID:10984043	
A:Accession: B83518	
A:Status: preliminary	
A:Molecule type: DNA	
A:Residues: 1-715 <STO>	
A:Cross-references: UNIPROT:Q91AV6; UNIPARC:UPI00000C5206; GB:AE004534; GB:AE004091; NFI	
A:Experimental source: strain PA01	
C:Genetics:	
A:Gene: PA1017	
C:Superfamily: hypothetical protein MJ0590	
Query Match 50.6%; Score 39; DB 2; Length 715; Best Local Similarity 66.7%; Pred. No. 1.1e+02; Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;	
QY 4 AGIEAAASAIQG 15 : : : : :	
Db 504 AGIESNAENVLG 515 : : : : :	
RESULT 29	
B33856	
hypothetical 80K protein - Bacillus sphaericus	
C:Species: Bacillus sphaericus	
C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 30-Sep-1993	
C:Accession: B33856	
R:Bowditch, R.D.; Baumann, P.; Yousten, A.A. J. Bacteriol. 171, 4178-4188, 1989	
A:Title: Cloning and sequencing of the gene encoding a 125-kilodalton surface-layer prot ein	
A:Reference number: A33856; MUID:89327128; PMID:2666389	
A:Accession: B33856	
A:Status: preliminary; not compared with conceptual translation	
A:Molecule type: DNA	
A:Residues: 1-745 <BOW>	
A:Cross-references: UNIPARC:UPI000017ACA5	
Query Match 50.6%; Score 39; DB 2; Length 745; Best Local Similarity 58.3%; Pred. No. 1.1e+02; Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;	
QY 2 NFANGIEAAASAI 13 : : : : :	
Db 662 NFPAVNAARAAV 673 : : : : :	
RESULT 30	
T0EC26	
transposase - Escherichia coli transposon Tn3926	
C:Species: Escherichia coli	
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004	
C:Accession: S03285	
R:Turner, A.K.; Grinstead, J. Nucleic Acids Res. 17, 1757, 1989	
A:Title: DNA sequence of the transposase gene of the class II transposon, Tn3926.	
A:Reference number: S03285; MUID:89160328; PMID:2537961	
A:Accession: S03285	
A:Molecule type: DNA	
A:Residues: 1-950 <TUR>	
A:Cross-references: UNIPROT:P13694; UNIPARC:UPI00001370DA; EMBL:X14236; NID:G48216; PID	
C:Genetics:	
A:Gene: tnpA	
C:Superfamily: transposase Tn21	
C:Keywords: DNA binding; DNA replication	
Query Match 50.6%; Score 39; DB 1; Length 990; Best Local Similarity 46.7%; Pred. No. 1.5e+02; Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;	

Qy 1 WNFAGIEAAASAIQG 15
Dd 927 WNTVYLERATSALRG 941

RESULT 31

Tl0031
early secretory antigen target 6 protein homolog - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C:Accession: Tl0031
R:Englmeier, K.; Honore, N.; Woods, S.A.; Caudron, B.; Cole, S.T.
Mol. Microbiol. 7, 197-206, 1993
A:Title: Use of an ordered cosmid library to deduce the genomic organization of Mycobact
A:Reference number: Z16917; MUID:93188700; PMID:8446027
A:Accession: Tl0031
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-95 <EIG>
A:Cross-references: UNIPROT:Q50206; UNIPARC:UPI0000012A1A0; EMBL:Y14967; NID:g2370268; PT
C:Genetics:
A:Gene: esx

```

Query Match      49.4%; Score 38; DB 2; Length 95;
Best Local Similarity 33.3%; Pred. No. 19;
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

```

Qy

1 WNFAGIEAAASAIQG 15
| : | : | : ||
Dd

5 WHFPALOGAVNELOG 19

RESULT 32

conserved hypothetical protein - Deinococcus radiodurans (strain R1)
 A75393
 C:Species: Deinococcus radiodurans
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C:Accession: A75393
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

Query Match 49.4%; Score 38; DB 2; Length 98;
Best Local Similarity 58.3%; Pred. No. 20;
Matches 7: Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 WNFAGIEAAASA 12
| | | : | | |
Db 87 WRFLGLEFALSA 98

RESULT 33

T336975
hypochemical protein SCU11.04 - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T336975
R:Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1999
A:Reference number: Z21618
A:Accession: T336975

A;Status: preliminary; translated from GB/EMBL/DDBB
A;Molecule type: DNA
A;Residues: 1-195 <OLI>
A;Cross-references: UNIPROT:Q9RIAR; UNIPARC:UPI000000
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SCJ11.04

Query Match	49.4%;	Score 38;	DB 2;	Length 195;
Best Local Similarity	63.6%;	Pred. No. 41;		
Matches	7;	Conservative	3;	Mismatches 1; Indels 0; Gaps 0;

Qy 5 GIEAASAIQG 15
||| : :
Db 147 GIEAAAKVEG 157

RESULT 34

AG2036
hypothetical protein alr1845 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-May-2004
C:Accession: AG2036
F:Kazaki, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuguch
Nakanishi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AG2036
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-219 <KUR>
A:Cross-references: UNIPARC:UPI0000CE21F; GB:BA000019; PIDN:BAB73544.1; PID:g17130935;
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr1845
C:Superfamily: tRNA (guanine-N(7)-)-methyltransferase

Query Match 49.4%; Score 38; DB 2; Length 219;
Best Local Similarity 46.2%; Pred. No. 46;
Matches 6: Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 WNFAGIEAAASAI 13
|||:|
Db 66 WNFGLGIEIRSLV 78

RESULT 35

AI2211
hypothetical protein alr3248 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AI2211
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigunch
Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AI2211
A:Status: preliminary
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-303 <KUR>
A:Cross-references: UNIPROT:Q8YS43; UNIPARC:UPI00000CE709; GB:BA000019; PIDN:BA074947.1
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr3248

Query Match 49.4%; Score 38; DB 2; Length 303;
Best Local Similarity 46.7%; Pred. No. 65;
Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

A;Accession: T36975

QY 1 WNFAGIEAAASAIQG 15
| | | | | : | | | | |
Db 58 WIFGGIAAGTVVLQG 72

RESULT 36

AB3052
Hypothetical protein Atu4031 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AB3052
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan
Science 294, 2317-2323, 2001
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AB3052
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-313 <KUR>
A:Cross-references: UNIPROT:Q8U8Q9; UNIPARC:UPI00000D2401; GB:AE008689; PIDN:AAI44832.1;
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu4031
A:Map position: linear chromosome

Query Match 49.4%; Score 38; DB 2; Length 313;
Best Local Similarity 46.7%; Pred. No. 68;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAIQG 15
| | | | | : | | | | |
Db 197 WSVVGIRAAATPALAG 211

RESULT 37

B98234
Hypothetical protein AGR_L_1644 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C:Species: Agrobacterium tumefaciens
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: B98234
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, P.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: B97359; MUID:21608551; PMID:11743194
A:Accession: B98234
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-313 <KUR>
A:Cross-references: UNIPROT:Q8U8Q9; UNIPARC:UPI00000D2401; GB:AE007870; PIDN:AAK89396.1;
C:Genetics:
A:Gene: AGR_L_1644
A:Map position: linear chromosome

Query Match 49.4%; Score 38; DB 2; Length 313;
Best Local Similarity 46.7%; Pred. No. 68;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAIQG 15
| | | | | : | | | | |
Db 197 WSVVGIRAAATPALAG 211

RESULT 38

F87356
Hypothetical protein CC0865 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 05-Oct-2004
C:Accession: F87356

R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: F87356
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-399 <STO>
A:Cross-references: UNIPROT:Q9A9U6; UNIPARC:UPI00000C71CA; GB:AE005673; NID:G13422124; I
C:Genetics:
A:Gene: CC0865
C:Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase III

Query Match 49.4%; Score 38; DB 2; Length 399;
Best Local Similarity 46.7%; Pred. No. 87;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAIQG 15
| | | | | : | | | | |
Db 249 WAGAGLASHAALDG 263

RESULT 39

T05592
Tyrosine transaminase homolog F9D16.70 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T05592
R:Bevan, M.; Wedler, H.; Wedler, E.; Wambutt, R.; Hobeisel, J.; Mewes, H.W.; Mayer, K.F.
submitted to the Protein Sequence Database, February 1999
A:Reference number: Z15419
A:Accession: T05592
A:Molecule type: DNA
A:Residues: 1-422 <BEV>
A:Cross-references: UNIPROT:Q9SUR6; UNIPARC:UPI0000051PE7; EMBL:AL035394
A:Experimental source: cultivar Columbia; BAC clone F9D16
C:Genetics:
A:Map position: 4
A:Introns: 84/2; 197/3; 270/3; 290/3; 342/3; 374/1
A:Note: F9D16.70
C:Superfamily: tyrosine transaminase

Query Match 49.4%; Score 38; DB 2; Length 422;
Best Local Similarity 58.3%; Pred. No. 93;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASA 12
| | | | | : | | | | |
Db 9 WQFSGSEAAKDA 20

RESULT 40

S69796
pectate lyase (EC 4.2.2.2) precursor - Erwinia chrysanthemi
C:Species: Erwinia chrysanthemi
C>Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S69796
R:Lojkowska, E.; Masciaux, C.; Boccara, M.; Robert-Baudouy, J.; Hugouvieux-Cotte-Pattat,
Mol. Microbiol. 16, 1183-1195, 1995
A:Title: Characterization of the pect lyase encoding a novel pectate lyase of Erwinia ch
A:Reference number: S69796; MUID:96020649; PMID:8577252
A:Accession: S69796
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-425 <LOJ>
A:Cross-references: UNIPROT:Q47473; UNIPARC:UPI000016F3BA; EMBL:X81136; NID:G1262764; P:
C:Genetics:
A:Gene: pect

C:Keywords: carbon-oxygen lyase
F1-25/Domain: signal sequence #status predicted <SIG>
F126-425/Product: pectate lyase #status predicted <MAT>

Query Match 49.4%; Score 38; DB 2; Length 425;
 Best Local Similarity 40.0%; Pred. No. 93;
 Matches 6; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 WNPAGIEAAASATQ 15
 |||:|:|
 Db 142 WYFKGVETRAGYQ 156
 |||:|:|

RESULT 41
 AE0826
 probable cadaverine/lysine antiporter [imported] - Salmonella enterica subsp. enterica s
 C:Species: Salmonella enterica subsp. enterica serovar Typhi
 A:Note: this species has also been called Salmonella typhi
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 05-Oct-2004
 C:Accession: AE0826
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-443 <PAR>
 A:Cross-references: UNIPARC:UPI0000059A81; GB:AL513382; PIDN:CAD02761.1; PID:g16503771;
 C:Genetics:
 A:Gene: STY2805
 C:Superfamily: ecotropic retrovirus receptor protein

Query Match 49.4%; Score 38; DB 2; Length 443;
 Best Local Similarity 60.0%; Pred. No. 98;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WNPAGIEAAA 10
 |||:|:|
 Db 198 WAFVGVESAA 207
 |||:|:|

RESULT 42
 H86108
 transport of lysine/cadaverine [imported] - Escherichia coli (strain O157:H7, substrain
 C:Species: Escherichia coli
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
 C:Accession: H86108
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: H86108
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-444 <STO>
 A:Cross-references: UNIPARC:UPI00001659E5; GB:AE0005174; NID:g12519112; PIDN:AAG59332.1;
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: cadB
 C:Superfamily: ecotropic retrovirus receptor protein

Query Match 49.4%; Score 38; DB 2; Length 444;
 Best Local Similarity 60.0%; Pred. No. 98;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WNPAGIEAAA 10
 |||:|:|
 Db 198 WAFVGVESAA 207
 |||:|:|

RESULT 43

A41842
 lysine/cadaverine antiporter membrane protein cadB - Escherichia coli (strain K-12)
 C:Species: Escherichia coli
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Oct-2004
 C:Accession: A41842; B41968; S56361; C65223
 R:Meng, S.Y.; Bennett, G.N.
 J. Bacteriol. 174, 2659-2669, 1992
 A:Title: Nucleotide sequence of the Escherichia coli cad operon: a system for neutraliz
 A:Reference number: A41842; MUID:92210511; PMID:1556085
 A:Accession: A41842
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-444 <MEN>
 A:Cross-references: UNIPROT:P23891; UNIPARC:UPI0000001701; GB:M76411; NID:g145455; PIDN
 R:Watson, N.; Dunyak, D.S.; Rosey, E.L.; Slonczewski, J.L.; Olson, E.R.
 J. Bacteriol. 174, 530-540, 1992
 A:Title: Identification of elements involved in transcriptional regulation of the Esche
 A:Reference number: A41968; MUID:92105022; PMID:1370290
 A:Accession: B41968
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-444 <WAT>
 A:Cross-references: UNIPARC:UPI0000001701; GB:M67452; NID:g145451; PIDN:AAA23532.1; PID
 A:Note: sequence extracted from NCBI backbone (NCBI:75631, NCSIP:75633)
 R:Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
 Nucleic Acids Res. 23, 2105-2119, 1995
 A:Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92
 A:Reference number: S56361; MUID:95334362; PMID:7610040
 A:Accession: S56361
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-444 <BUR>
 A:Cross-references: UNIPARC:UPI0000001701; EMBL:U14003; NID:g1263172; PIDN:AAA97032.1;
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C
 .A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A:Title: The complete genome sequence of Escherichia coli K-12.
 A:Reference number: A64720; MUID:97426617; PMID:9278503
 A:Accession: C65223
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-444 <BLAT>
 A:Cross-references: UNIPARC:UPI0000001701; GB:AE000486; GB:U00096; NID:g1790574; PIDN:A
 A:Experimental source: strain K-12, substrain MG1655
 C:Genetics:
 A:Gene: cadB
 C:Superfamily: ecotropic retrovirus receptor protein
 C:Keywords: membrane protein

Query Match 49.4%; Score 38; DB 2; Length 444;
 Best Local Similarity 60.0%; Pred. No. 98;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WNPAGIEAAA 10
 |||:|:|
 Db 198 WAFVGVESAA 207
 |||:|:|

RESULT 44
 B91268
 transport protein of lysine/cadaverine ECs5114 [imported] - Escherichia coli (strain O1
 C:Species: Escherichia coli
 C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004
 C:Accession: B91268
 R:Hayaashi, T.; Makino, K.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G
 gawara, N.; Yasunaga, T.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
 A:Reference number: A99629; MUID:21156231; PMID:11258796
 A:Accession: B91268
 A:Status: preliminary
 A:Molecule type: DNA

A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: H87253
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-172 <STO>
A;Cross-references: UNIPROT:Q9AC27; UNIPARC:UPI000000C6EF2; GB:AE005673; NID:g13421132; F
C;Genetics:
A;Gene: CC0040

Query Match 48.1%; Score 37; DB 2; Length 172;
Best Local Similarity 33.3%; Pred. No. 54;
Matches 5; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAIQG 15
| : : : : :
Db 157 WRLSGFDASAANLRG 171

RESULT 50

G82977
hypothetical protein PA5357 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: G82977
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: G82977
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-178 <STO>
A;Cross-references: UNIPROT:Q9HTK1; UNIPARC:UPI000000CSFC0; GB:AE004947; GB:AE004091; NID
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA5357
C;Superfamily: Escherichia coli 4-hydroxybenzoate synthetase

Query Match 48.1%; Score 37; DB 2; Length 178;
Best Local Similarity 53.3%; Pred. No. 56;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAIQG 15
| : : : : :
Db 84 WVFARVARSALLEG 98

Search completed: May 4, 2006, 15:17:42
Job time : 54 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 15:00:31 ; Search time 155 Seconds
(without alignments)
68.277 Million cell updates/sec

Title: US-09-830-839-6

Perfect score: 77

Sequence: 1 WNFAGIEAAASAIQG 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	77	100.0	94	1	ESXA_MYCBO
2	77	100.0	94	1	P0A565 mycobacteri
3	77	100.0	95	2	Q5A0D8 MYCTU
4	64	83.1	56	2	Q5G541 MYCUL
5	64	83.1	56	2	Q5G545 MYCUL
6	64	83.1	72	2	Q4VQH8 MYCOO
7	47	61.0	714	2	Q4KSH1 LACLC
8	47	61.0	714	2	Q9CES5 LACLA
9	46	59.7	377	2	Q8H746 PHYCI
10	46	59.7	454	2	Q8H749 PHYCI
11	46	59.7	2348	2	Q5Z1P8 NOCPA
12	45	58.4	495	2	Q4WZC2 ASPFU
13	45	58.4	715	2	Q82VB0 NITEU
14	44	57.1	61	2	Q57DJ6 BRUAB
15	44	57.1	61	2	Q8G115 BRUSU
16	44	57.1	225	2	Q9RF66 RHOSH
17	44	57.1	517	2	Q86G78 LEIHO
18	44	57.1	517	2	Q4FW28 LEIMA
19	44	57.1	1460	2	Q6KHL9 MYCMA
20	43	55.8	476	1	NOEA RHIME
21	43	55.8	476	2	Q6PW80 RHIME
22	43	55.8	508	2	Q6BN69 DEBHA
23	43	55.8	540	2	Q5V3L9 HALMA
24	43	55.8	717	2	Q5B2P0 EMENI
25	43	55.8	833	2	Q870X8 NEUCR
26	43	55.8	953	2	Q5P997 ANAMM
27	42.5	55.2	141	2	Q9HYR3 PSEAE
28	42	54.5	146	1	Y1312 BIFLO
29	42	54.5	369	2	Q9Z839 CHLPN
30	42	54.5	384	2	Q7VP24 CHLPN
31	42	54.5	476	2	Q518C5_ENTHI

32	42	54.5	773	2	Q5WEB7_BACSK	Q5web7 bacillus cl
33	42	54.5	2028	1	Q7XL20_ORYSA	Q7xl20 oryza sativ
34	41	53.2	384	2	FRUB_BACSU	P49936 bacillus su
35	41	53.2	402	1	DGTL1_BRAJA	Q89kz0 bradyrhizob
36	41	53.2	404	2	Q6N5W5_RHOPA	Q6n5w5 rhodopseudo
37	41	53.2	440	2	Q9PAD1_MORJA	Q9fad1 moritella j
38	41	53.2	443	2	Q9AMK7_VIBVU	Q9amk7 vibrio vuln
39	41	53.2	444	2	Q5E343_VIBF1	Q5e343 vibrio fisc
40	41	53.2	445	2	Q8DAX6_VIBVU	Q8dax6 vibrio vuln
41	41	53.2	445	2	Q8KV76_VIBCH	Q8kv76 vibrio chol
42	41	53.2	447	2	Q75VK9_VIBPA	Q75vk9 vibrio para
43	41	53.2	447	2	Q87KT5_VIBPA	Q87kt5 vibrio para
44	41	53.2	452	2	Q7MIY1_VIBVY	Q7miy1 vibrio vuln
45	41	53.2	463	2	Q82D65_STRAW	Q82d65 streptomyce
46	41	53.2	465	2	Q5E2K7_LACRE	Q5e2k7 lactobacill
47	41	53.2	494	2	Q62AX2_BURMA	Q62ax2 burkholderi
48	41	53.2	528	2	Q63K00_BURPS	Q63k00 burkholderi
49	41	53.2	540	2	Q9CGX6_LACLA	Q9c9x6 lactococcus
50	41	53.2	751	2	Q5WI16_BACSK	Q5wi16 bacillus cl
51	41	53.2	783	2	Q524F9_MAGGR	Q524f9 magnaporth
52	41	53.2	803	2	Q5C8V6_LEIMA	Q5c8v6 leishmania
53	41	53.2	913	2	Q87W23_PSESM	Q87w23 pseudomonas
54	41	53.2	961	2	Q58KD3_9BACT	Q58kd3 leptospiril
55	41	53.2	989	2	Q58KG4_9BACT	Q58kg4 leptospiril
56	41	53.2	4331	2	Q41YL2_AZOVI	Q41yl2 azotobacter
57	40	51.9	84	2	Q4VUY2_9CHIR	Q4vuy2 brachyphyll
58	40	51.9	134	2	Q9XMD1_PTEPA	Q9xmd1 pteronotus
59	40	51.9	134	2	Q9XMD0_PTEDV	Q9xmd0 pteronotus
60	40	51.9	142	2	Q4VUX6_9CHIR	Q4vux6 brachyphyll
61	40	51.9	145	2	Q4VUX5_9CHIR	Q4vux5 brachyphyll
62	40	51.9	294	1	G3P_ESCBL	P24749 escherichia
63	40	51.9	297	2	Q7UZ85_RHOBA	Q7uz85 rhodopirell
64	40	51.9	323	2	Q8UH81_AGRTH	Q8uh81 agrobacteri
65	40	51.9	330	2	Q27223_METTH	Q27223 methanobact
66	40	51.9	332	2	Q5GRX0_WOLTR	Q5grx0 wolbachia s
67	40	51.9	332	2	Q73HS0_WOLPM	Q73hs0 wolbachia p
68	40	51.9	376	2	Q6PX86_BRACV	Q6px86 brachyphyll
69	40	51.9	379	1	CYB_PTEGV	Q9bin0 pteronotus
70	40	51.9	379	1	CYB_PTEGY	Q9b0e2 pteronotus
71	40	51.9	379	1	CYB_PTEMA	Q9b106 pteronotus
72	40	51.9	379	1	CYB_PTEPR	Q8wdk6 pteronotus
73	40	51.9	379	1	CYB_PTEQR	Q9b165 pteronotus
74	40	51.9	379	1	Q9B372_PTEPA	Q9b0y1 pteronotus
75	40	51.9	379	2	Q9B376_PTEPA	Q9b372 pteronotus
76	40	51.9	379	2	Q9B367_PTEPR	Q9b376 pteronotus
77	40	51.9	379	2	Q9B364_PTEPR	Q9b367 pteronotus
78	40	51.9	379	2	Q9B368_PTEPR	Q9b364 pteronotus
79	40	51.9	379	2	Q9B366_PTEPR	Q9b368 pteronotus
80	40	51.9	379	2	Q9B375_PTEPA	Q9b366 pteronotus
81	40	51.9	379	2	Q9B373_PTEPA	Q9b375 pteronotus
82	40	51.9	379	2	Q9B374_PTEPA	Q9b373 pteronotus
83	40	51.9	379	2	Q6PX96_BRACV	Q9b374 pteronotus
84	40	51.9	379	2	Q6PX87_BRACV	Q6px96 brachyphyll
85	40	51.9	379	2	Q6PX87_BRACV	Q6px87 brachyphyll
86	40	51.9	379	2	Q6PX85_BRACV	Q6px87 brachyphyll
87	40	51.9	379	2	Q6PX83_BRACV	Q6px85 brachyphyll
88	40	51.9	379	2	Q9B0U6_PTEPA	Q9b0u6 pteronotus
89	40	51.9	379	2	Q6PX92_BRACV	Q6px92 brachyphyll
90	40	51.9	379	2	Q53AK0_9CHIR	Q53ak0 pteronotus
91	40	51.9	379	2	Q53AJ9_9CHIR	Q53aj9 pteronotus
92	40	51.9	379	2	Q53AJ6_PTEQU	Q53aj6 pteronotus
93	40	51.9	379	2	Q53AJ5_PTEQU	Q53aj5 pteronotus
94	40	51.9	379	2	Q53AJ3_PTEMA	Q53aj3 pteronotus
95	40	51.9	379	2	Q9B377_PTEPA	Q53aj3 pteronotus
96	40	51.9	379	2	Q4VUW5_BRACV	Q9b377 pteronotus
97	40	51.9	379	2	Q4VUW1_BRACV	Q4vuw5 brachyphyll
98	40	51.9	379	2	Q4VUW0_BRACV	Q4vuw1 brachyphyll
99	40	51.9	379	2	Q4VUY6_9CHIR	Q4vuw0 brachyphyll
100	40	51.9	379	2	Q4VYD22_BRACV	Q4vuy6 brachyphyll
101	40	51.9	379	2	Q4VUX0_BRACV	Q7ydz2 brachyphyll
102	40	51.9	379	2	Q6PX82_BRACV	Q4vux0 brachyphyll
103	40	51.9	379	2	Q6PX82_BRACV	Q6px82 brachyphyll
104	40	51.9	379	2	Q6PX91_BRACV	Q6px91 brachyphyll

105	40	51.9	379	2	Q4VUY0_9CHIR	Q4VUY0 brachyphyl	178	39	50.6	475	2	Q51WV1_MAGGR	Q51WV1 magnaporthe
106	40	51.9	380	2	Q5HSD3_XANOR	Q5HSD3 xanthomonas	179	39	50.6	486	2	Q5WIY8_BACSK	Q5WIY8 bacillus cl
107	40	51.9	387	2	Q52IX6_CHICK	Q52IX6 gallus gall	180	39	50.6	486	2	Q5N2P3_SYNP6	Q5N2P3 synechococc
108	40	51.9	419	2	Q94LJ5_ORYSA	Q94LJ5 oryza sativ	181	39	50.6	510	2	Q4SCN6_TYNGP	Q4SCN6 tetraodon n
109	40	51.9	419	2	Q7X987_ORYSA	Q7X987 oryza sativ	182	39	50.6	514	1	TBL1R_HUMAN	Q8BZK7 homo sapien
110	40	51.9	455	2	Q53LD6_ORYSA	Q53LD6 oryza sativ	183	39	50.6	514	1	TBL1R_HUMAN	Q8BZK7 homo sapien
111	40	51.9	493	2	Q92VB8_RHIME	Q92VB8 rhizobium m	184	39	50.6	514	1	TBL1R_HUMAN	Q8BZK7 homo sapien
112	40	51.9	536	2	Q9HNR2_HALSA	Q9HNR2 halobacteri	185	39	50.6	522	2	Q7SZM9_XENLA	Q6GPC6 xenopus lae
113	40	51.9	561	2	Q6QTF9_TRICR	Q6QTF9 trypanosoma	186	39	50.6	522	2	Q6GPC6_XENLA	Q6GPC6 xenopus lae
114	40	51.9	610	2	Q6GPP0_XENLA	Q6GPP0 xenopus lae	187	39	50.6	522	2	Q6GPC6_XENLA	Q6GPC6 xenopus lae
115	40	51.9	761	2	Q87J3ES_NEUCR	Q87J3ES neurospora	188	39	50.6	522	2	Q6GPC6_XENLA	Q6GPC6 xenopus lae
116	40	51.9	785	2	Q7NH88_GLOVI	Q7NH88 gloeobacter	189	39	50.6	653	2	Q8F8F6_PSEPK	Q8F8F6 pseudomonas
117	40	51.9	916	2	Q5KW46_GEOKA	Q5KW46 geobacillus	190	39	50.6	653	2	Q8F8F6_PSEPK	Q8F8F6 pseudomonas
118	40	51.9	988	2	Q6BE29_AERPU	Q6BE29 aeromonas p	191	39	50.6	668	2	Q8F8F6_PSEPK	Q8F8F6 pseudomonas
119	40	51.9	988	2	Q6WB26_ALCPA	Q6WB26 alcaligenes	192	39	50.6	674	2	Q8F8F6_PSEPK	Q8F8F6 pseudomonas
120	40	51.9	989	2	Q4WIS8_PSEAE	Q4WIS8 pseudomonas	193	39	50.6	715	2	Q9I4V6_PSEAE	Q9I4V6 pseudomonas
121	40	51.9	1005	2	Q9Q937_9POXV	Q9Q937 rabbit fibr	194	39	50.6	715	2	Q9I4V6_PSEAE	Q9I4V6 pseudomonas
122	40	51.9	1056	2	Q9Q8R2_9POXV	Q9Q8R2 myxoma viru	195	39	50.6	728	2	Q8DUT7_STRMU	Q8DUT7 streptococc
123	40	51.9	1556	2	Q4Q626_LEIMA	Q4Q626 leishmania	196	39	50.6	728	2	Q8DUT7_STRMU	Q8DUT7 streptococc
124	40	51.9	2002	2	Q71S06_HUMAN	Q71S06 homo sapien	197	39	50.6	753	2	Q8E240_STRAS	Q8E240 streptococc
125	40	51.9	2555	2	Q91ZE6_MOUSE	Q91ZE6 mus musculu	198	39	50.6	765	2	Q8E7J9_STRAT	Q8E7J9 streptococc
126	40	51.9	2561	2	Q8VTE5_MOUSE	Q8VTE5 mus musculu	199	39	50.6	775	2	Q5LXV2_STRTR	Q5LXV2 streptococc
127	40	51.9	2564	1	SPTN4_HUMAN	Q8VTE5 mus musculu	200	39	50.6	784	2	Q8DS45_STRMU	Q8DS45 streptococc
128	40	51.9	2564	2	Q71S07_HUMAN	Q71S07 homo sapien	201	39	50.6	807	2	Q5M2F4_STRTR	Q5M2F4 streptococc
129	39	51.3	1084	2	Q4NXT0_9BELT	Q4NXT0 anaeromyxob	202	39	50.6	837	2	Q7SD25_NEUCR	Q7SD25 neurospora
130	39	50.6	98	2	Q5OWV0_IDILO	Q5OWV0 idiomarina	203	39	50.6	870	2	Q4JVF5_CORJK	Q4JVF5 corynebacte
131	39	50.6	101	2	Q58924_PVRHO	Q58924 pyrococcus	204	39	50.6	887	2	Q4JVF5_CORJK	Q4JVF5 corynebacte
132	39	50.6	120	2	Q8WCZ3_ARCPH	Q8WCZ3 arctoccephal	205	39	50.6	989	2	Q6U505_KLEPN	Q6U505 klebsiella
133	39	50.6	120	2	Q8WCZ4_ARCPH	Q8WCZ4 arctoccephal	206	39	50.6	990	1	TNP7_ECOLI	P13694 escherichia
134	39	50.6	120	2	Q8WCZ5_ARCPH	Q8WCZ5 arctoccephal	207	39	50.6	990	2	Q5W3I3_SALTY	Q5W3I3 salmonella
135	39	50.6	120	2	Q8WCZ6_EUMJU	Q8WCZ6 eumetopias	208	39	50.6	990	2	Q9F3V7_PSEAE	Q9F3V7 pseudomonas
136	39	50.6	120	2	Q8W853_EUMJU	Q8W853 eumetopias	209	39	50.6	990	2	Q5I4V3_SALCH	Q5I4V3 salmonella
137	39	50.6	120	2	Q8W817_ARCTO	Q8W817 arctoccephal	210	39	50.6	990	2	Q6G5I2_ENTCL	Q6G5I2 enterobacte
138	39	50.6	125	2	Q36265_ZALCA	Q36265 zalophus ca	211	39	50.6	990	2	Q6G5I2_ENTCL	Q6G5I2 enterobacte
139	39	50.6	125	2	Q7GGU6_EUMJU	Q7GGU6 eumetopias	212	39	50.6	990	2	Q4AH91_KLEFN	Q4AH91 klebsiella
140	39	50.6	138	2	Q4TR91_98PHN	Q4TR91 erythroba	213	39	50.6	1051	2	Q7AQU8_SALTY	Q7AQU8 salmonella
141	39	50.6	155	1	RIFK_MOUSE	Q8CFV9 mus musculu	214	39	50.6	1051	2	Q6CW80_KLUJA	Q6CW80 kluveromyc
142	39	50.6	155	2	Q5JSG9_HUMAN	Q5JSG9 homo sapien	215	39	50.6	1172	2	Q521Q4_MAGGR	Q521Q4 magnaporthe
143	39	50.6	155	2	Q6AYAT_RAT	Q6AYAT rattus norv	216	39	50.6	1401	2	Q4Q480_LEIMA	Q4Q480 leishmania
144	39	50.6	161	2	Q9F434_KLEPN	Q9F434 klebsiella	217	39	50.6	1424	2	Q4P656_STRMU	Q4P656 ustilago ma
145	39	50.6	162	1	RIFK_HUMAN	Q9G696 homo sapien	218	38.5	50.0	1866	2	Q86W13_HUMAN	Q86W13 homo sapien
146	39	50.6	189	2	Q6YXG6_MACNE	Q6YXG6 macaca neme	219	38.5	50.0	109	2	Q5P669_AZOSE	Q5P669 azoarcus sp
147	39	50.6	199	2	Q87PV4_VTBPA	Q87PV4 vibrio para	220	38.5	50.0	393	2	Q9EWU0_STRCO	Q9EWU0 streptomyce
148	39	50.6	202	2	Q9FTZ5_ORYSA	Q9FTZ5 oryza sativ	221	38.5	50.0	398	2	Q4LJW8_9BURK	Q4LJW8 burkholderi
149	39	50.6	227	2	Q8D876_VIBVU	Q8D876 vibrio vuln	222	38.5	50.0	433	2	Q5LTV3_MAGGR	Q5LTV3 magnaporthe
150	39	50.6	232	2	Q6G518_ECOLI	Q6G518 escherichia	223	38.5	50.0	525	2	Q5P8K4_AZOSE	Q5P8K4 azoarcus sp
151	39	50.6	240	2	Q7MM97_VIBVY	Q7MM97 vibrio vuln	224	38.5	50.0	913	2	Q4ZN28_PSESY	Q4ZN28 pseudomonas
152	39	50.6	243	1	PYRF_XENCP	Q8P3D7 xanthomonas	225	38	49.4	56	2	Q4THO0_TETNG	Q4THO0 tetraodon n
153	39	50.6	243	2	Q4UNV9_XANCP	Q4UNV9 xanthomonas	226	38	49.4	92	2	Q4VHG1_PLABE	Q4VHG1 plasmodium
154	39	50.6	254	2	Q4R044_ERICE	Q4R044 epirates c	227	38	49.4	95	1	ESXA_MYCLE	ESXA0206 mycobacteri
155	39	50.6	265	2	Q5KZF9_GEOXA	Q5KZF9 geobacillus	228	38	49.4	98	2	Q6NJ54_CORDI	Q6NJ54 corynebacte
156	39	50.6	270	2	Q3FNL9_LACAC	Q3FNL9 lactobacillu	229	38	49.4	98	2	Q7OKR0_ANOGA	Q7OKR0 anopheles g
157	39	50.6	278	2	Q85U06_9SAUR	Q85U06 natator-9pp	230	38	49.4	115	2	Q9RUD3_DEIRA	Q9RUD3 deinococcus
158	39	50.6	281	2	Q8VL07_AZOBH	Q8VL07 azospirillu	231	38	49.4	133	2	Q9EK26_PSEFL	Q9EK26 pseudomonas
159	39	50.6	324	2	Q58895_PYRHO	Q58895 pyrococcus	232	38	49.4	133	2	Q9EK26_PSEFL	Q9EK26 pseudomonas
160	39	50.6	370	1	CYB_EPICE	Q5ZBF5 oryza sativ	233	38	49.4	136	2	Q7PQ54_ANOGA	Q7PQ54 anopheles g
161	39	50.6	370	1	CYB_EPICE	Q8H19 oligodon ci	234	38	49.4	147	2	Q81885_ANOGA	Q81885 anopheles g
162	39	50.6	379	1	CYB_FUNJU	Q34471 eumetopias	235	38	49.4	147	2	Q81885_ECOLI	Q81885 escherichia
163	39	50.6	379	1	CYB_FUNJU	Q84471 eumetopias	236	38	49.4	177	2	Q8G885_ECOLI	Q8G885 escherichia
164	39	50.6	386	2	Q92S22_RHIME	Q92S22 rhizobium m	237	38	49.4	177	2	Q6N4S8_RHOFA	Q6N4S8 rhodospseudo
165	39	50.6	424	2	Q8VYP2_ARATH	Q8VYP2 arabidopsis	238	38	49.4	195	2	Q9RIA0_STRCO	Q9RIA0 streptomyce
166	39	50.6	425	1	PELL_ERWCH	Q47473 erwina chr	239	38	49.4	197	2	Q5P7T3_AZOSE	Q5P7T3 azoarcus sp
167	39	50.6	425	1	ADIC_EGOS7	Q5B5D7 aspergillus	240	38	49.4	212	1	THIE_CHLCV	THIE0165 chlamydomo
168	39	50.6	445	2	ADIC_EGOS7	Q5B5D7 aspergillus	241	38	49.4	212	1	THIE_CHLCV	THIE0165 chlamydomo
169	39	50.6	445	1	ADIC_EGOL6	P60062 escherichia	242	38	49.4	224	1	TRNB_ANASP	TRNB0144 anabaena sp
170	39	50.6	445	1	ADIC_ECOLI	P60062 escherichia	243	38	49.4	224	1	TRNB_ANASP	TRNB0144 anabaena sp
171	39	50.6	445	1	ADIC_ECOLI	P60061 escherichia	244	38	49.4	233	2	Q8P5P9_BRAJA	Q8P5P9 bradyrhizob
172	39	50.6	445	1	ADIC_SALTY	P60065 salmonella	245	38	49.4	254	2	Q48078_9SAUR	Q48078 eryx johni
173	39	50.6	445	1	ADIC_SALTY	P60065 salmonella	246	38	49.4	254	2	Q48078_9SAUR	Q48078 eryx johni
174	39	50.6	445	1	ADIC_SALTY	P60065 salmonella	247	38	49.4	255	2	Q07294_PSEFL	Q07294 pseudomonas
175	39	50.6	445	2	Q57GT3_SALCH	Q57GT3 salmonella	248	38	49.4	270	2	Q89NH9_BRAJA	Q89NH9 bradyrhizob
176	39	50.6	445	2	Q5R024_SALPA	Q5R024 salmonella	249	38	49.4	273	2	Q5WL32_BACSK	Q5WL32 bacillus cl
177	39	50.6	448	2	Q9SUK7_ARATH	Q9SUK7 arabidopsis	250	38	49.4	280	2	Q5LGU3_BACFN	Q5LGU3 bacteroides
												Q64XP6_BACFR	Q64XP6 bacteroides

251	38	49.4	285	2	Q8EIE7_SHEON	Q8EIE7 shewanella	324	38	49.4	988	2	Q9WTH3_9ZZZZ	Q9WTH3 plasmid r10
252	38	49.4	303	2	Q8Y543_ANASP	Q8Y543 anabaena sp	325	38	49.4	988	2	Q573P1_9BACT	Q573P1 uncultured
253	38	49.4	313	2	Q8U809_AGRT5	Q8U809 agrobacteri	326	38	49.4	988	2	Q58A17_9BURK	Q58A17 ralstonia m
254	38	49.4	326	2	Q8OWM5_MOUSE	Q8OWM5 mus musculus	327	38	49.4	988	2	Q79PA6_KLEPN	Q79PA6 klebsiella
255	38	49.4	331	2	Q5YVH5_NOCPA	Q5YVH5 nocardia fa	328	38	49.4	988	2	Q7BP61_SHIFL	Q7BP61 shigella fl
256	38	49.4	336	2	Q6AU58_ORYSA	Q6AU58 oryza sativ	329	38	49.4	989	2	Q6TFR3_COMAC	Q6TFR3 comamonas a
257	38	49.4	336	2	Q5FS66_GLOOX	Q5FS66 gluconobact	330	38	49.4	989	2	Q5NU20_9BURK	Q5NU20 ralstonia m
258	38	49.4	341	2	Q9XIV5_ORYSA	Q9XIV5 oryza sativ	331	38	49.4	989	2	Q8W60_NITEU	Q8W60 nitrosomona
259	38	49.4	345	2	Q7WU04_ECOLI	Q7WU04 escherichia	332	38	49.4	1062	2	Q96X97_SULTO	Q96X97 sulfolobus
260	38	49.4	350	2	Q7UAM4_SHIFL	Q7UAM4 shigella fl	333	38	49.4	1062	2	Q4J7S9_SULAC	Q4J7S9 sulfobus
261	38	49.4	350	2	Q83P45_SHIFL	Q83P45 shigella fl	334	38	49.4	1141	1	NOL6_HUMAN	Q8R5K4 mus musculu
262	38	49.4	365	2	Q5LIV9_MAGGR	Q5LIV9 magnaporthe	335	38	49.4	1146	1	NOL6_HUMAN	Q8R5K4 mus sapien
263	38	49.4	372	2	Q69AU3_PYSAR	Q69AU3 pyas korro	336	38	49.4	1196	2	Q6FTP3_CANGA	Q6FTP3 candida gla
264	38	49.4	395	2	Q5B4Q4_EMENI	Q5B4Q4 aspergillus	337	38	49.4	1863	2	Q6AU96_ORYSA	Q6AU96 oryza sativ
265	38	49.4	399	2	Q9A9U6_CAUCR	Q9A9U6 caulobacter	338	38	49.4	1905	2	Q5W669_ORYSA	Q5W669 oryza sativ
266	38	49.4	413	2	Q62E45_BURMA	Q62E45 burkholderi	339	38	49.4	1963	2	Q7XFZ7_ORYSA	Q7XFZ7 oryza sativ
267	38	49.4	413	2	Q63J31_BURPS	Q63J31 burkholderi	340	38	49.4	1963	2	Q94HV2_ORYSA	Q94HV2 oryza sativ
268	38	49.4	415	2	Q68820_9HEPC	Q68820 hepaticis c	341	38	49.4	1973	2	Q7NP45_GLOVI	Q7NP45 gloebacter
269	38	49.4	418	2	Q9WXF6_LACCA	Q9WXF6 lactobacill	342	38	49.4	1992	2	Q7XWS1_ORYSA	Q7XWS1 oryza sativ
270	38	49.4	422	2	Q9SUR6_ARATH	Q9SUR6 arabidopsis	343	38	49.4	2015	2	Q7XT04_ORYSA	Q7XT04 oryza sativ
271	38	49.4	428	2	Q4LS94_9BURK	Q4LS94 burkholderi	344	38	49.4	2026	2	Q7XE40_ORYSA	Q7XE40 oryza sativ
272	38	49.4	432	2	Q4NU15_9DELT	Q4NU15 anaeromyxob	345	38	49.4	2026	2	Q84T73_ORYSA	Q84T73 oryza sativ
273	38	49.4	443	2	Q57LFP3_SALCH	Q57LFP3 salmonella	346	38	49.4	2027	2	Q60EK1_ORYSA	Q60EK1 oryza sativ
274	38	49.4	443	2	Q5PIH7_SALPA	Q5PIH7 salmonella	347	38	49.4	2027	2	Q65WY4_ORYSA	Q65WY4 oryza sativ
275	38	49.4	443	2	Q8Z4M1_SALTI	Q8Z4M1 salmonella	348	38	49.4	2027	2	Q7XLL4_ORYSA	Q7XLL4 oryza sativ
276	38	49.4	443	2	Q8ZN34_SALTY	Q8ZN34 salmonella	349	38	49.4	2027	2	Q7XNC3_ORYSA	Q7XNC3 oryza sativ
277	38	49.4	444	1	ADIC_VERPE	Q8ZGS9 yersinia pe	350	38	49.4	2027	2	Q53QC3_ORYSA	Q53QC3 oryza sativ
278	38	49.4	444	1	CADB_ECOLI	Q23891 escherichia	351	38	49.4	2028	2	Q7XQ56_ORYSA	Q7XQ56 oryza sativ
279	38	49.4	444	2	Q7B9X2_ECOLI	Q7B9X2 escherichia	352	38	49.4	2697	2	Q4Q1E1_LEIMA	Q4Q1E1 leishmania
280	38	49.4	444	2	Q66D09_YERPS	Q66D09 yersinia ps	353	38	49.4	3216	2	Q8FKQ3_ECOLD	Q8FKQ3 escherichia
281	38	49.4	451	2	Q8NAH4_HUMAN	Q8NAH4 homo sapien	354	38	49.4	3242	2	Q8G9X9_ECOLI	Q8G9X9 escherichia
282	38	49.4	454	2	Q8JW84_ECOLI	Q8JW84 escherichia	355	37.5	48.7	145	2	Q5DYS6_VIBF1	Q5DYS6 vibrio fisc
283	38	49.4	460	2	Q5LWZ9_SILPO	Q5LWZ9 silicibacte	356	37.5	48.7	372	2	Q62AF1_BURMA	Q62AF1 burkholderi
284	38	49.4	461	2	Q60414_METCA	Q60414 methylococ	357	37.5	48.7	393	2	Q63MZ0_BURPS	Q63MZ0 burkholderi
285	38	49.4	464	2	Q7WX73_ALCEU	Q7WX73 alcaligenes	358	37.5	48.7	408	2	Q8LKV4_ORYSA	Q8LKV4 oryza sativ
286	38	49.4	473	2	Q7SA78_ASHGO	Q7SA78 ashbya goss	359	37.5	48.7	434	2	Q8XEA8_MESCR	Q8XEA8 mesenteriant
287	38	49.4	474	2	Q4WC17_ASPFU	Q4WC17 aspergillus	360	37.5	48.7	525	2	Q8XDY8_RALSO	Q8XDY8 ralstonia s
288	38	49.4	474	2	Q4LIL3_9BURK	Q4LIL3 burkholderi	361	37.5	48.7	864	2	Q7RWY4_NEUCR	Q7RWY4 neurospora
289	38	49.4	530	2	Q5A4H0_CANAL	Q5A4H0 candida alb	362	37.5	48.7	1329	2	Q5WJ22_BACSC	Q5WJ22 bacillus cl
290	38	49.4	536	2	Q8FIZ4_ECOLD	Q8FIZ4 escherichia	363	37	48.1	40	2	Q91K02_9HEPC	Q91K02 hepaticis c
291	38	49.4	543	2	Q60A65_METCA	Q60A65 methylococ	364	37	48.1	50	2	Q539Z4_CHEMA	Q539Z4 cheirogaleu
292	38	49.4	557	2	Q4KDE4_PSEF5	Q4KDE4 pseudomonas	365	37	48.1	69	2	Q53A06_CHEMA	Q53A06 cheirogaleu
293	38	49.4	561	2	Q7R716_PLAYO	Q7R716 plasmodium	366	37	48.1	75	1	PO2F1_MACEU	Q28466 macropus eu
294	38	49.4	568	2	Q93NB1_9GAMM	Q93NB1 halomonas s	367	37	48.1	81	2	Q4JNA3_9HEPC	Q4JNA3 hepaticis c
295	38	49.4	583	2	Q4NZL3_9DELT	Q4NZL3 anaeromyxob	368	37	48.1	81	2	Q4JNA4_9HEPC	Q4JNA4 hepaticis c
296	38	49.4	595	2	Q4RK39_TETNG	Q4RK39 tetraodon n	369	37	48.1	81	2	Q4JNA7_9HEPC	Q4JNA7 hepaticis c
297	38	49.4	616	2	Q6C7L1_YARLI	Q6C7L1 yarrowia li	370	37	48.1	119	2	Q8W9P0_CHEMA	Q8W9P0 cheirogaleu
298	38	49.4	641	2	Q7SLG6_ORYSA	Q7SLG6 oryza sativ	371	37	48.1	131	2	Q5E0P0_VIBF1	Q5E0P0 vibrio fisc
299	38	49.4	642	2	Q4S3J1_TETNG	Q4S3J1 tetraodon n	372	37	48.1	133	2	Q51NH8_MAGGR	Q51NH8 magnaporthe
300	38	49.4	688	2	Q7X155_ORYSA	Q7X155 oryza sativ	373	37	48.1	134	2	Q4T727_TETNG	Q4T727 tetraodon n
301	38	49.4	706	2	Q5KLL0_CRYNE	Q5KLL0 cryptococcu	374	37	48.1	149	2	Q9K2L8_9ENTR	Q9K2L8 brenneria q
302	38	49.4	706	2	Q55YD1_CRYNE	Q55YD1 cryptococcu	375	37	48.1	149	2	Q9K3A3_9ENTR	Q9K3A3 brenneria q
303	38	49.4	713	2	Q4WEC1_ASPPU	Q4WEC1 aspergillus	376	37	48.1	149	2	Q9L9T7_9ENTR	Q9L9T7 brenneria l
304	38	49.4	718	2	Q5KY66_GEOKA	Q5KY66 geobacillus	377	37	48.1	149	2	Q9L9T8_9ENTR	Q9L9T8 brenneria l
305	38	49.4	728	2	Q5N1I4_SYNP6	Q5N1I4 synecococc	378	37	48.1	149	2	Q9L9T9_9ENTR	Q9L9T9 brenneria q
306	38	49.4	731	2	Q51VG6_MAGGR	Q51VG6 magnaporthe	379	37	48.1	149	2	Q9L9U0_9ENTR	Q9L9U0 brenneria q
307	38	49.4	733	2	Q8A6K3_BACTN	Q8A6K3 bacteroides	380	37	48.1	153	2	Q98GG4_RHILO	Q98GG4 rhizobium l
308	38	49.4	751	2	Q4SEK4_TETNG	Q4SEK4 tetraodon n	381	37	48.1	155	2	Q4HKC2_CAMLA	Q4HKC2 campylobact
309	38	49.4	811	2	Q4S2Y4_TETNG	Q4S2Y4 tetraodon n	382	37	48.1	172	2	Q4NZE3_9DELT	Q4NZE3 anaeromyxob
310	38	49.4	823	2	Q8VZP7_ARATH	Q8VZP7 arabidopsis	383	37	48.1	172	2	Q9AC27_CAUCR	Q9AC27 caulobacter
311	38	49.4	844	2	Q9SJ70_ARATH	Q9SJ70 arabidopsis	384	37	48.1	178	2	Q9HTK1_PSEAE	Q9HTK1 pseudomonas
312	38	49.4	909	2	Q7XQ66_ORYSA	Q7XQ66 oryza sativ	385	37	48.1	183	2	Q9FFG5_ARATH	Q9FFG5 arabidopsis
313	38	49.4	923	1	YAUA_SCHPO	Q10165 schizosacch	386	37	48.1	185	2	Q60U07_MYCHY	Q60U07 mycoplasma
314	38	49.4	934	2	Q6KDD4_ECOLI	Q6KDD4 escherichia	387	37	48.1	191	2	Q5DUN2_KLROX	Q5DUN2 klebsiella
315	38	49.4	962	1	ARVC_HUMAN	Q00192 homo sapien	388	37	48.1	191	2	Q8TFC0_9HEPC	Q8TFC0 hepaticis c
316	38	49.4	962	1	ARVC_MOUSE	P98203 mus musculu	389	37	48.1	196	1	RBWMS_XENLA	Q9Y9P5 xenopus lae
317	38	49.4	981	2	Q75D19_ASHGO	Q75D19 ashbya goss	390	37	48.1	196	2	Q4V877_XENLA	Q4V877 xenopus lae
318	38	49.4	983	2	Q7T071_CHICK	Q7T071 gallus gall	391	37	48.1	197	2	Q5PAY7_XENLA	Q5PAY7 anaplasm m
319	38	49.4	988	1	TNP2_ECOLI	P06694 escherichia	392	37	48.1	197	2	Q66IX3_XENLA	Q66IX3 xenopus lae
320	38	49.4	988	2	Q70S13_5PSED	Q70S13 pseudomonas	393	37	48.1	210	2	Q69PA9_ORYSA	Q69PA9 oryza sativ
321	38	49.4	988	2	Q7BT65_ECOLI	Q7BT65 escherichia	394	37	48.1	211	2	Q53A02_CHEMA	Q53A02 cheirogaleu
322	38	49.4	988	2	Q8GGX4_ECOLI	Q8GGX4 escherichia	395	37	48.1	211	2	Q53922_9PRIM	Q53922 cheirogaleu
323	38	49.4	988	2	Q8RSK8_9BACT	Q8RSK8 uncultured	396	37	48.1	218	2	Q4NUG9_9DELT	Q4NUG9 anaeromyxob

397	37	48.1	235	2	Q4N9D4_THEPA	Q4n9d4 theileria p	470	37	48.1	424	2	Q4NYNA_9DELT	Q4nyN4 anaeromyxob
398	37	48.1	253	2	Q32816_LACLC	Q32816 lactococcus	471	37	48.1	435	2	Q5B850_EMENI	Q5b850 aspergillus
399	37	48.1	256	2	Q7X2Y6_9BACT	Q7x2y6 uncultured	472	37	48.1	446	2	Q6A1D3_LACFE	Q6a1d3 bacteroides
400	37	48.1	256	2	Q7XZP2_MYCBO	Q7xzp2 mycobacteri	473	37	48.1	450	1	G6P1_LACFE	Q6p1 lactobacill
401	37	48.1	256	2	P95152_MYCTU	P95152 mycobacteri	474	37	48.1	452	2	Q8EVF6_MYCPE	Q8evf6 mycoplasma
402	37	48.1	259	2	Q7NNW8_GLOVI	Q7nnw8 mycobacteri	475	37	48.1	459	2	Q8KGV3_LACIA	Q8kgv3 lactococcus
403	37	48.1	260	2	Q49657_MYCLE	Q49657 mycobacteri	476	37	48.1	462	2	Q9MUC4_PSINU	Q9muc4 psilotum nu
404	37	48.1	261	1	COBS_VIBCH	Q9k818 vibrio chol	477	37	48.1	462	2	Q7NOS1_CHRVO	Q7nsg1 chromobacte
405	37	48.1	270	2	Q4W54_ASPFU	Q4w54 aspergillus	478	37	48.1	462	2	Q93JL3_STRCO	Q93jl3 streptomyc
406	37	48.1	277	2	Q48034_9SAUR	Q48034 corallus an	479	37	48.1	466	2	Q9AAL5_CAUCR	Q9aal5 caulobacter
407	37	48.1	281	2	Q7NQA7_CHRVO	Q7nqa7 chromobacte	480	37	48.1	472	2	GUNA_CLOC	P17901 clostridium
408	37	48.1	281	2	Q7N4D2_PHOLL	Q7n4d2 phthorhabu	481	37	48.1	475	1	Q6C1A8_YARLI	Q6c1a8 varrowia li
409	37	48.1	290	2	Q6W1Y9_RHISN	Q6w1y9 rhizobium s	482	37	48.1	478	2	Q9CE15_LACIA	Q9ce15 lactococcus
410	37	48.1	293	2	Q6W1Y9_RHISN	Q6w1y9 rhizobium s	483	37	48.1	490	2	Q9CE15_LACIA	Q9ce15 lactococcus
411	37	48.1	294	2	Q92KE0_RHISP	Q92ke0 rhizobium s	484	37	48.1	492	1	HUPR_RHOCA	P26E08 rhodobacter
412	37	48.1	297	2	Q03296_APSAP	Q03296 apalone spi	485	37	48.1	494	2	Q6FC09_ACTIAD	Q6fc09 actinobact
413	37	48.1	307	2	Q7RPH4_PLAYO	Q7rph4 plasmodium	486	37	48.1	497	2	Q9CEB19_LACIA	Q9ceb19 lactococcus
414	37	48.1	311	2	Q53A14_CHEME	Q53a14 cheirogaleu	487	37	48.1	507	1	P8BB_SYNY3	P8bbs2 synchocyst
415	37	48.1	315	2	Q6U8A7_TRIFO	Q6u8a7 tritrichomo	488	37	48.1	508	2	Q8WHZ6_PSINU	Q8whz6 psilotum nu
416	37	48.1	328	2	Q48033_9SAUR	Q48033 corallus an	489	37	48.1	508	2	Q4P5F4_ARATH	Q4p5f4 arabidopsis
417	37	48.1	329	2	Q67QO7_SYMTH	Q67qo7 symbiobacte	490	37	48.1	509	1	P8BB_ANASP	P8bbs1 anabaena sp
418	37	48.1	329	2	Q87PK8_VIBPA	Q87pk8 vibrio para	491	37	48.1	509	1	P8BB_CYPAPA	P8bbs2 cyanophora
419	37	48.1	330	2	Q6NE3_ORYSA	Q6ne3 oryza sativ	492	37	48.1	525	2	Q7MT34_9ACTO	Q7mt34 streptomyc
420	37	48.1	335	1	YD59_SCHPO	Q10312 schizosacch	493	37	48.1	526	2	Q9K574_9LACT	Q9k574 lactococcus
421	37	48.1	336	2	Q83S54_SHIFL	Q83s54 shigella fl	494	37	48.1	526	2	Q4SJT4_TETNG	Q4sjt4 tetraodon n
422	37	48.1	343	2	Q92WM8_RHIME	Q92wm8 rhizobium m	495	37	48.1	529	2	Q35967_9HYST	Q35967 thrichomys
423	37	48.1	346	2	Q8FUT4_XANAC	Q8fut4 xanthomonas	496	37	48.1	534	2	Q4UX20_XANCP	Q4ux20 xanthomonas
424	37	48.1	350	2	Q6GVS2_CABBR	Q6gvs2 caenorhabdi	497	37	48.1	534	2	Q8P735_XANCP	Q8p735 xanthomonas
425	37	48.1	351	2	Q87QU0_VIBPA	Q87qu0 vibrio para	498	37	48.1	536	2	Q7NC10_GLOVI	Q7nc10 gloeobacter
426	37	48.1	356	2	Q5L6N8_CHLAB	Q5l6n8 chlamydophi	499	37	48.1	536	2	Q9ST03_HORVU	Q9st03 hordeum vul
427	37	48.1	370	2	Q824C3_CHLCO	Q824c3 rhizobium l	500	37	48.1	551	2	Q723C6_LISMF	Q723c6 listeria mo
428	37	48.1	371	2	Q988C3_RHILO	Q988c3 rhizobium l	501	37	48.1	553	2	Q8Y9K3_LISIN	Q8y9k3 listeria in
429	37	48.1	379	1	CYB_ALLTR	Q5vj52 allocebus t	502	37	48.1	553	2	Q92ED1_LISIN	Q92ed1 listeria in
430	37	48.1	379	1	CYB_CHEMA	Q34169 cheirogaleu	503	37	48.1	579	2	Q6CB19_YARLI	Q6cb19 varrowia li
431	37	48.1	379	1	CYB_CHEMA	Q5vj55 cheirogaleu	504	37	48.1	597	2	Q3FVU4_RAT	Q3fuv4 rattus norv
432	37	48.1	379	1	CYB_MICBE	Q5vj55 cheirogaleu	505	37	48.1	599	2	Q63UES_BURFS	Q63ues bukkholderi
433	37	48.1	379	1	CYB_MICRF	Q9g120 microcebus	506	37	48.1	608	2	Q5WAJ0_BACSK	Q5waj0 bacillus cl
434	37	48.1	379	1	CYB_MIRCO	Q34972 mirza coque	507	37	48.1	614	2	Q5LX79_SILPO	Q5lx79 silicibacte
435	37	48.1	379	1	CYB_ZAPTR	Q9xnn1 zapus trino	508	37	48.1	652	2	Q4P360_USTWA	Q4p360 ustulago ma
436	37	48.1	379	2	Q9G543_MICMY	Q9g543 microcebus	509	37	48.1	659	2	Q33LH1_ORYSA	Q33lh1 oryza sativ
437	37	48.1	379	2	Q9G945_9PRIM	Q9g945 microcebus	510	37	48.1	660	1	PABP3_ARATH	PABP3 arabidopsis
438	37	48.1	379	2	Q9G942_MICMY	Q9g942 microcebus	511	37	48.1	665	2	Q812A4_RAT	Q812a4 rattus norv
439	37	48.1	379	2	Q9G944_9PRIM	Q9g944 microcebus	512	37	48.1	684	2	Q92JW0_RHIME	Q92jw0 rhizobium m
440	37	48.1	379	2	Q5VJ53_MICMU	Q5vj53 microcebus	513	37	48.1	698	2	Q8XSG8_RALSO	Q8xsg8 ralstonia s
441	37	48.1	379	2	Q8G0X7_MICRF	Q8g0x7 microcebus	514	37	48.1	719	2	Q7XP99_ORYSA	Q7xp99 oryza sativ
442	37	48.1	379	2	Q9G235_MICRV	Q9g235 microcebus	515	37	48.1	736	2	Q8K300_STRAW	Q8k300 streptomyc
443	37	48.1	379	2	Q9G156_9PRIM	Q9g156 microcebus	516	37	48.1	739	2	Q8K8M4_STRP3	Q8k8m4 streptococ
444	37	48.1	379	2	Q9G215_9PRIM	Q9g215 microcebus	517	37	48.1	766	2	Q8P2Y4_STRP8	Q8p2y4 streptococ
445	37	48.1	379	2	Q5F4E3_MINSC	Q5f4e3 miniopterus	518	37	48.1	766	2	Q87907_STRP3	Q87907 streptococ
446	37	48.1	379	2	Q53A15_CHEME	Q5a15 cheirogaleu	519	37	48.1	770	2	Q5XE98_STRP6	Q5xe98 streptococ
447	37	48.1	379	2	Q53A13_CHEME	Q5a13 cheirogaleu	520	37	48.1	770	2	Q9A1U2_STRPY	Q9a1u2 streptococ
448	37	48.1	379	2	Q53A09_CHEME	Q5a09 cheirogaleu	521	37	48.1	770	2	Q9A1U2_STRPY	Q9a1u2 streptococ
449	37	48.1	379	2	Q53A07_CHEMA	Q5a07 cheirogaleu	522	37	48.1	796	2	Q7X2N4_SPHEL	Q7x2n4 sphingomona
450	37	48.1	379	2	Q53A03_CHEMA	Q5a03 cheirogaleu	523	37	48.1	856	2	Q5F0R1_AZOSE	Q5f0r1 erythroba
451	37	48.1	379	2	Q53929_CHEMA	Q53929 cheirogaleu	524	37	48.1	856	2	Q5F0R1_AZOSE	Q5f0r1 azoarcus sp
452	37	48.1	379	2	Q53928_CHEMA	Q53928 cheirogaleu	525	37	48.1	878	2	Q5R5C5_VIBF1	Q5r5c5 vibrio fisc
453	37	48.1	379	2	Q53927_CHEMA	Q53927 cheirogaleu	526	37	48.1	930	2	Q68HC7_DUNSA	Q68hc7 dunaliella
454	37	48.1	379	2	Q53921_9PRIM	Q53921 cheirogaleu	527	37	48.1	989	2	Q8GBR9_PSEYM	Q8gbr9 pseudomonas
455	37	48.1	379	2	Q53926_CHEMA	Q53926 cheirogaleu	528	37	48.1	989	2	Q8BBQ4_PSESM	Q8bbq4 pseudomonas
456	37	48.1	379	2	Q53A11_CHEME	Q5a11 cheirogaleu	529	37	48.1	1040	2	Q6KAZ0_XANMA	Q6kaz0 xanthomonas
457	37	48.1	379	2	Q36128_9HYST	Q36128 trichomys se	530	37	48.1	1040	2	Q6KAZ0_XANMA	Q6kaz0 xanthomonas
458	37	48.1	380	2	Q6X2L1_APAFE	Q6x2l1 apalone fer	531	37	48.1	1040	2	Q6KAZ0_XANMA	Q6kaz0 xanthomonas
459	37	48.1	380	2	Q6X2L0_9SAUR	Q6x2l0 apalone mut	532	37	48.1	1040	2	Q9F240_XANMA	Q9f240 xanthomonas
460	37	48.1	380	2	Q6X2K8_APSAP	Q6x2k8 apalone spi	533	37	48.1	1118	2	Q5NJL6_9BACT	Q5njl6 uncultured
461	37	48.1	384	2	Q7RH85_PLAYO	Q7rh85 plasmodium	534	37	48.1	1220	2	Q67M05_SYMTH	Q67m05 symbiobacte
462	37	48.1	384	2	Q4YR56_PLABE	Q4yr56 campylobact	535	37	48.1	1223	2	Q02979_YEAST	Q02979 saccharomyc
463	37	48.1	394	2	Q4HFA6_CAMUP	Q4hfa6 campylobact	536	37	48.1	1247	2	Q75FU6_LEPIC	Q75fu6 leptospira
464	37	48.1	395	2	Q4H8L1_9DEIO	Q4h8l1 daeinococcus	537	37	48.1	1247	2	Q8EXU9_LEPIN	Q8exu9 leptospira
465	37	48.1	404	1	DGTIA_RHILO	Q81b2 rhizobium l	538	37	48.1	1249	2	Q7S1I4_NEUCR	Q7s1i4 neurospora
466	37	48.1	408	2	Q899U5_CLOTE	Q899u5 clostridium	539	37	48.1	1321	2	Q74ZH9_ASHGO	Q74zh9 ashbya goss
467	37	48.1	413	2	Q92U06_RHIME	Q92u06 rhizobium m	540	37	48.1	1365	2	Q8XON8_NEUCR	Q8xon8 neurospora
468	37	48.1	424	2	Q5NAM0_ORYSA	Q5nam0 oryza sativ	541	37	48.1	1414	2	Q4QE45_LEIMA	Q4qe45 leishmania
469	37	48.1	424	2	Q84UD0_BRAOL	Q84ud0 brassica ol	542	37	48.1	1438	2	Q9RFM8_PSEAE	Q9rfm8 pseudomonas

543	37	48.1	1438	2	085739_PSEAE	085739 pseudomonas	616	36	46.8	206	2	Q85921_9HIV1	Q85921 human immun
544	37	48.1	1512	2	Q688R5_ORYSA	Q688R5 oryza sativ	617	36	46.8	206	2	Q85922_9HIV1	Q85922 human immun
545	37	48.1	1610	2	Q7XR15_ORYSA	Q7XR15 oryza sativ	618	36	46.8	206	2	Q85923_9HIV1	Q85923 human immun
546	37	48.1	1649	2	Q9CPA2_LACIA	Q9CPA2 lactococcus	619	36	46.8	207	2	Q85923_9HIV1	Q85923 human immun
547	37	48.1	1709	2	Q7XIL3_ORYSA	Q7XIL3 oryza sativ	620	36	46.8	207	2	Q85928_9HIV1	Q85928 human immun
548	37	48.1	1741	2	Q8HB99_ORYSA	Q8HB99 oryza sativ	621	36	46.8	211	1	TRMB_SYNY3	F73161 synchocyst
549	37	48.1	1744	2	Q9C3Z2_COCH	Q9C3Z2 cochliobolu	622	36	46.8	211	2	Q6H280_SYNPH	Q5n280 synchococc
550	37	48.1	1751	2	Q7XS98_ORYSA	Q7XS98 oryza sativ	623	36	46.8	212	2	Q6H289_TRIHG	Q6h289 trimeresuru
551	37	48.1	1809	2	Q75LQ3_ORYSA	Q75LQ3 oryza sativ	624	36	46.8	213	1	TRMB_PROMA	Q7vd48 trocholoroco
552	37	48.1	1823	2	Q65XT9_ORYSA	Q65XT9 oryza sativ	625	36	46.8	214	2	Q6H290_TRIHG	Q6h290 trimeresuru
553	37	48.1	1898	2	Q6ATQ5_ORYSA	Q6ATQ5 oryza sativ	626	36	46.8	217	2	Q6H288_TRIHG	Q6h288 trimeresuru
554	37	48.1	1910	2	Q7XU19_ORYSA	Q7XU19 oryza sativ	627	36	46.8	218	2	Q6H288_9SAUR	Q6h288 trimeresuru
555	37	48.1	1926	2	Q5JQ02_ORYSA	Q5JQ02 oryza sativ	628	36	46.8	219	2	Q73X50_MYCPA	Q73X50 mycobacteri
556	37	48.1	1937	2	Q75M23_ORYSA	Q75M23 oryza sativ	629	36	46.8	228	2	Q51HN1_MAGGR	Q51hn1 magnaporth
557	37	48.1	1992	2	Q94LL4_ORYSA	Q94LL4 oryza sativ	630	36	46.8	229	2	Q5U4S6_XENLA	Q5u4s6 xenopus lae
558	37	48.1	2137	2	Q8XP07_RALSO	Q8XP07 ralstonia s	631	36	46.8	231	2	Q6H285_9SAUR	Q6h285 trimeresuru
559	37	48.1	2276	2	Q4FYP0_LEIMA	Q4FYP0 leishmania	632	36	46.8	233	2	Q69TP8_ORYSA	Q69tp8 oryza sativ
560	37	48.1	3331	2	Q7XPS4_ORYSA	Q7XPS4 oryza sativ	633	36	46.8	233	2	Q5LR45_SILPO	Q5lr45 silicibacte
561	37	48.1	3848	2	P94772_ERWCH	P94772 erwina chr	634	36	46.8	234	2	Q6H283_9SAUR	Q6h283 trimeresuru
562	37	48.1	6481	2	Q4Q892_LEIMA	Q4Q892 leishmania	635	36	46.8	238	2	Q03375_9SCIU	Q03375 paraxerus c
563	36.5	47.4	139	2	Q53W77_THET8	Q53W77 thermus the	636	36	46.8	238	2	Q7Y929_AZEPF	Q7y929 azemiops fe
564	36.5	47.4	159	2	Q88BD7_PSEPK	Q88BD7 pseudomonas	637	36	46.8	240	2	Q7MP22_VIBVY	Q7mp22 vibrio vuln
565	36.5	47.4	306	2	Q746L3_THET2	Q746L3 thermus the	638	36	46.8	240	2	Q6H289_9SAUR	Q6h289 trimeresuru
566	36.5	47.4	327	2	Q72U28_THET2	Q72U28 thermus the	639	36	46.8	242	2	Q6H291_9SAUR	Q6h291 trimeresuru
567	36.5	47.4	371	2	Q7U0S8_MYCHO	Q7U0S8 mycobacteri	640	36	46.8	245	2	Q92X12_RHIME	Q92x12 rhizobium m
568	36.5	47.4	371	2	P96353_MYCTU	P96353 mycobacteri	641	36	46.8	247	2	Q8X3F8_ECO57	Q8x3f8 escherichia
569	36.5	47.4	401	2	Q73VAL_MYCPA	Q73VAL mycobacteri	642	36	46.8	248	2	Q6V2C9_9LAMI	Q6v2c9 orobanche c
570	36.5	47.4	489	2	Q8FC58_ECOL6	Q8FC58 escherichia	643	36	46.8	248	2	P73470_SYNY3	P73470 synchocyst
571	36.5	47.4	516	2	Q82BT5_STRAM	Q82BT5 streptomyces	644	36	46.8	248	2	Q83LH0_SHIFL	Q83lh0 shigella fl
572	36.5	47.4	572	2	Q99AR1_9VIRU	Q99AR1 torque teno	645	36	46.8	250	2	Q4NUY2_5MICC	Q4ny2 arthrobacte
573	36.5	47.4	621	2	Q8N7Z2_HUMAN	Q8N7Z2 homo sapien	646	36	46.8	257	2	Q7NRL9_CHRVO	Q7nrl9 chromobacte
574	36.5	47.4	657	2	Q4NUK4_9MICC	Q4NUK4 arthrobacte	647	36	46.8	258	2	Q410U0_GIBZE	Q410u0 gibberella
575	36.5	47.4	856	2	Q73NF9_TREDE	Q73NF9 treponema d	648	36	46.8	260	2	Q6FZB6_BAFUR	Q6fzb6 bartonella
576	36	46.8	97	2	Q942Y2_ORYSA	Q942Y2 oryza sativ	649	36	46.8	260	2	Q6G2V9_BAFUR	Q6g2v9 bartonella
577	36	46.8	119	2	Q8W9K7_HAPGR	Q8W9K7 haplaemur g	650	36	46.8	262	2	Q410X2_GIBZE	Q410x2 gibberella
578	36	46.8	120	2	Q55D70_DICTDI	Q55D70 dictyosteli	651	36	46.8	266	2	Q7X9L3_WHEAT	Q7x9l3 triticum ae
579	36	46.8	127	2	Q8H755_PHYCI	Q8H755 phytophthor	652	36	46.8	267	2	Q6H2U5_AZEPF	Q6h2u5 azemiops fe
580	36	46.8	133	2	Q67WB7_ORYSA	Q67WB7 oryza sativ	653	36	46.8	267	2	Q6H2T0_TRIGA	Q6h2t0 trimeresuru
581	36	46.8	137	2	Q8PKA4_XANAC	Q8PKA4 xanthomonas	654	36	46.8	270	1	LGT1_BACCI	Q72xv7 bacillus ce
582	36	46.8	140	2	Q65ZL3_9MURI	Q65ZL3 mus sp. tgl	655	36	46.8	270	1	LGT_BACAN	Q81x52 bacillus an
583	36	46.8	141	2	Q5PSD9_AZOSE	Q5PSD9 azoarcus sp	656	36	46.8	270	1	LGT_BACCR	Q81x57 bacillus ce
584	36	46.8	145	1	Y008_MYCBO	Y59977 mycobacteri	657	36	46.8	270	1	LGT_BACCC	Q63j11 bacillus ce
585	36	46.8	145	1	Y008_MYCTU	P71577 rhodopseudo	658	36	46.8	270	1	LGT_BACHK	Q4mly5 bacillus th
586	36	46.8	146	1	CYCP_RHOPA	P00149 rhodopseudo	659	36	46.8	273	2	Q8KG59_CHLTE	Q8kg59 chlorobium
587	36	46.8	146	2	Q8RM67_RHOPA	Q8Rme7 rhodopseudo	660	36	46.8	284	2	Q67SJO_SYNTH	Q67sjo symbiobacte
588	36	46.8	155	2	Q7PLU4_ANOGA	Q7p114 anopheles g	661	36	46.8	284	2	Q62BL1_BURMA	Q62bl1 burkholderi
589	36	46.8	155	2	Q656H4_ORYSA	Q656H4 oryza sativ	662	36	46.8	290	2	Q5KR04_SELRU	Q5kr04 selenomonas
590	36	46.8	158	2	Q7PL13_ANOGA	Q7p113 anopheles g	663	36	46.8	292	2	Q8XZM6_RALSO	Q8xzm6 ralstonia s
591	36	46.8	169	2	Q68JF4_ENTCL	Q68j14 enterobacte	664	36	46.8	302	2	Q92J08_RHOFA	Q92j08 rhodococcus
592	36	46.8	170	2	Q61170_DROME	Q61170 drosophila	665	36	46.8	293	2	Q4NL64_9MICC	Q4nl64 arthrobacte
593	36	46.8	172	2	Q6H286_TRIHG	Q6h286 trimeresuru	666	36	46.8	298	2	Q62FY4_ORYSA	Q62fy4 oryza sativ
594	36	46.8	180	2	Q8C4C1_MOUSE	Q8c4c1 mus musculu	667	36	46.8	300	2	Q5KXX3_GEOKA	Q5kxx3 geobacillus
595	36	46.8	183	2	Q85914_9HIV1	Q85914 human immun	668	36	46.8	302	2	Q7SB12_NEUCR	Q7sb12 neurospora
596	36	46.8	185	2	Q6TBW5_9BACT	Q6tbw5 uncultured	669	36	46.8	302	2	Q57BV0_BRUAB	Q57bv0 bruceella ab
597	36	46.8	186	2	Q62GX6_BURMA	Q62gx6 burkholderi	670	36	46.8	302	2	Q8FZC2_STRAP	Q8fzc2 bruceella su
598	36	46.8	188	2	Q8UGZ9_AGR75	Q8ugz9 agrobacteri	671	36	46.8	302	2	Q8YIJ4_BRUME	Q8yij4 bruceella me
599	36	46.8	189	2	Q83TZ1_9RHIZ	Q83tz1 rhizobium g	672	36	46.8	302	2	Q9HI69_THEAC	Q9hi69 thermoplasm
600	36	46.8	189	2	Q84HR1_9RHIZ	Q84hr1 rhizobium g	673	36	46.8	303	2	Q5P2A5_AZOSE	Q5p2a5 azoarcus sp
601	36	46.8	191	2	Q8BBF2_9HEPC	Q8bbf2 hepatitis c	674	36	46.8	303	2	Q5XB63_STRAP	Q5xb63 streptococc
602	36	46.8	192	1	RL3_WOISLU	Q7m844 wolinnella s	675	36	46.8	303	2	Q99Z07_STRPE	Q99z07 streptococc
603	36	46.8	193	2	Q85940_9HIV1	Q85940 human immun	676	36	46.8	303	2	Q8POA3_STRP8	Q8poa3 streptococc
604	36	46.8	196	2	Q5LXH1_SILPO	Q5lxh1 silicibacte	677	36	46.8	303	2	Q8K6V5_STRP3	Q8k6v5 streptococc
605	36	46.8	196	2	Q85936_9HIV1	Q85936 human immun	678	36	46.8	305	2	Q8Z299_PYRAE	Q8z299 pyrobaculum
606	36	46.8	199	2	Q8W520_WAIZE	Q8w520 zea mays (m	679	36	46.8	307	2	Q92T09_RHIME	Q92t09 rhizobium m
607	36	46.8	200	2	Q6H287_9SAUR	Q6h287 trimeresuru	680	36	46.8	314	2	Q5RAD9_PONPY	Q5rad9 pongo pygma
608	36	46.8	202	2	Q8AR56_9HIV1	Q8ar56 human immun	681	36	46.8	314	2	Q9A6F4_CAUCR	Q9a6f4 caulobacter
609	36	46.8	203	2	Q8AR51_9HIV1	Q8ar51 human immun	682	36	46.8	323	2	Q5FS41_GLOUC	Q5fs41 gluconobact
610	36	46.8	203	2	Q8AR54_9HIV1	Q8ar54 human immun	683	36	46.8	341	2	Q9X7Y1_STRCO	Q9x7y1 streptomyce
611	36	46.8	203	2	Q8AR72_9HIV1	Q8ar72 human immun	684	36	46.8	356	2	Q6A7G2_PROAC	Q6a7g2 propionibac
612	36	46.8	204	2	Q85949_9HIV1	Q85949 human immun	685	36	46.8	357	2	Q41FP9_GIBZE	Q41fp9 gibberella
613	36	46.8	204	2	Q85950_9HIV1	Q85950 human immun	686	36	46.8	359	2	RF1_STRMU	Q8du64 streptococc
614	36	46.8	205	2	Q12238_9HIV1	Q12238 human immun	687	36	46.8	369	1	RF1_STRMU	Q18081 caenorhabdi
615	36	46.8	205	2	Q8ARN4_9HIV1	Q8arn4 human immun	688	36	46.8				

689	36	45.8	372	2	Q6U7M0_9SAUR	Q6u7m0 eirenis per	762	36	46.8	524	2	Q73AK7_BACC1	Q73ak7 bacillus ce
690	36	46.8	372	2	Q6U7M0_9SAUR	Q6u7m0 eirenis med	763	36	46.8	524	2	Q63D95_BACCZ	Q63d95 bacillus ce
691	36	46.8	372	2	Q69AV6_9SAUR	Q69av6 hemorrhhois	764	36	46.8	525	1	Y1002_RHIME	Y1002 rhizobium m
692	36	46.8	376	1	FDH_ORISA	Q8axp2 oryza sativ	765	36	46.8	526	2	Q4KJ17_PSEF5	Q4kji17 pseudomonas
693	36	46.8	376	2	Q67U72_ORISA	Q67u72 oryza sativ	766	36	46.8	527	1	MTX1_XANCR	MTX1 xanthomonas
694	36	46.8	377	1	FDH_HORVU	Q67u72 oryza sativ	767	36	46.8	527	1	MTX1_XANCR	MTX1 xanthomonas
695	36	46.8	379	1	CYB_PHAFU	Q67u72 oryza sativ	768	36	46.8	533	2	Q9A2E1_CAUCR	Q9a2e1 caulobacter
696	36	46.8	379	2	Q6FXB4_BRACV	Q6fxb4 brachyphyll	769	36	46.8	534	2	Q4PEG5_USYWA	Q4peg5 usilago ma
697	36	46.8	379	2	Q9GAR5_9RODE	Q9gar5 akodon serr	770	36	46.8	535	2	Q8N2P5_SYNP6	Q8n2p5 synecococc
698	36	46.8	379	2	Q6WRH1_9RODE	Q6wrh1 akodon serr	771	36	46.8	540	2	Q8XR08_RALSO	Q8xr08 ralstonia s
699	36	46.8	379	2	Q6X2K6_9SAUR	Q6x2k6 pelochelys	772	36	46.8	547	2	Q8YR33_ANASP	Q8yr33 anabaena ap
700	36	46.8	380	2	Q9XXM3_9CHON	Q9xxm3 oxyura vitt	773	36	46.8	548	2	Q8YR33_DEBHA	Q8yr33 debaryomyce
701	36	46.8	380	2	Q5XXM3_OXYVI	Q5xxm3 oxyura aust	774	36	46.8	552	2	Q6BX89_BORPE	Q6bx89 bordetella
702	36	46.8	380	2	Q5XMC7_9AVES	Q5xmc7 oxyura leuc	775	36	46.8	557	2	Q7VVC6_BORPE	Q7vvc6 bordetella
703	36	46.8	380	2	Q5XMC7_OXYLE	Q5xmc7 oxyura leuc	776	36	46.8	557	2	Q7W7B3_BORPA	Q7w7b3 bordetella
704	36	46.8	380	2	Q5XMC5_9AVES	Q5xmc5 oxyura leuc	777	36	46.8	560	2	Q7W7B3_BORPA	Q7w7b3 bordetella
705	36	46.8	383	2	Q6NFI5_CORDI	Q6nfi5 oxyura leuc	778	36	46.8	560	2	Q6X3X35_9RYP	Q6x3x35 streptococ
706	36	46.8	384	1	FDH_ARATH	Q6nfi5 oxyura leuc	779	36	46.8	561	2	Q57Y54_9RYP	Q57y54 streptococ
707	36	46.8	384	2	Q57Y29_9RYP	Q57y29 oxyura leuc	780	36	46.8	561	2	Q57Y54_9RYP	Q57y54 streptococ
708	36	46.8	384	2	Q57Y31_9RYP	Q57y31 oxyura leuc	781	36	46.8	564	2	Q97AM4_THEVO	Q97am4 thermophilum
709	36	46.8	385	2	Q57Y33_9RYP	Q57y33 oxyura leuc	782	36	46.8	565	2	Q97AM4_THEVO	Q97am4 thermophilum
710	36	46.8	385	2	Q6YU6_BURPS	Q6yu6 burkholderi	783	36	46.8	565	2	Q4LPX3_9BURK	Q4lpk3 burkholderi
711	36	46.8	385	2	Q7V6M7_PROMM	Q7v6m7 burkholderi	784	36	46.8	568	2	Q9HKY1_THEAC	Q9hky1 thermophilum
712	36	46.8	391	2	Q4H9G4_9DELIO	Q4h9g4 burkholderi	785	36	46.8	572	2	Q7TSC9_MOUSE	Q7tsc9 mus musculu
713	36	46.8	397	2	Q4KM98_HUMAN	Q4km98 burkholderi	786	36	46.8	572	2	Q5BD99_EMENI	Q5bd99 emergillu
714	36	46.8	399	2	Q7PNS_9NOGA	Q7pns burkholderi	787	36	46.8	582	2	Q4LVD4_9BURK	Q4lvd4 burkholderi
715	36	46.8	402	2	Q5YX10_NOCRA	Q5yx10 burkholderi	788	36	46.8	582	2	Q4LVD4_9BURK	Q4lvd4 burkholderi
716	36	46.8	403	2	Q746S0_GOSFL	Q746s0 burkholderi	789	36	46.8	585	2	Q4FR57_9GAMM	Q4fr57 psychrobact
717	36	46.8	404	2	Q7BUD7_9ATMD	Q7bud7 burkholderi	790	36	46.8	585	2	Q4FR57_9GAMM	Q4fr57 psychrobact
718	36	46.8	404	2	Q8E8U1_SHEON	Q8e8u1 burkholderi	791	36	46.8	592	2	Q7F8X4_ORYSA	Q7f8x4 oryza sativ
719	36	46.8	406	2	Q8E8U1_SHEON	Q8e8u1 burkholderi	792	36	46.8	592	2	Q7F8X4_ORYSA	Q7f8x4 oryza sativ
720	36	46.8	411	2	Q9A2N2_CAUCH	Q9a2n2 burkholderi	793	36	46.8	597	2	Q6LTJ2_PHOPR	Q6ltj2 photobacter
721	36	46.8	412	2	Q57GP9_SALCH	Q57gp9 burkholderi	794	36	46.8	597	2	Q6LTJ2_PHOPR	Q6ltj2 photobacter
722	36	46.8	413	2	Q821A4_SALTI	Q821a4 burkholderi	795	36	46.8	599	2	Q87KY4_VIBPA	Q87ky4 vibrio para
723	36	46.8	413	2	Q8ZKC0_SALTY	Q8zkc0 burkholderi	796	36	46.8	612	2	Q5ALH2_CANAL	Q5alh2 candida alb
724	36	46.8	414	2	Q8H747_PHYCI	Q8h747 burkholderi	797	36	46.8	612	2	Q5ALH2_CANAL	Q5alh2 candida alb
725	36	46.8	414	2	Q8H748_PHYCI	Q8h748 burkholderi	798	36	46.8	612	2	Q5ALH2_CANAL	Q5alh2 candida alb
726	36	46.8	414	2	Q8H748_PHYCI	Q8h748 burkholderi	799	36	46.8	612	2	Q5ALH2_CANAL	Q5alh2 candida alb
727	36	46.8	419	2	Q8GH19_9BURK	Q8gh19 burkholderi	800	36	46.8	612	2	Q5ALH2_CANAL	Q5alh2 candida alb
728	36	46.8	427	2	Q7P801_RICSI	Q7p801 burkholderi	801	36	46.8	612	2	Q5ALH2_CANAL	Q5alh2 candida alb
729	36	46.8	427	2	Q92HP5_RICCN	Q92hp5 burkholderi	802	36	46.8	612	2	Q5ALH2_CANAL	Q5alh2 candida alb
730	36	46.8	429	2	Q92HP5_RICCN	Q92hp5 burkholderi	803	36	46.8	612	2	Q5ALH2_CANAL	Q5alh2 candida alb
731	36	46.8	429	2	Q68WP9_RICTY	Q68wp9 burkholderi	804	36	46.8	612	2	Q5ALH2_CANAL	Q5alh2 candida alb
732	36	46.8	432	2	Q791X6_CITFR	Q791x6 burkholderi	805	36	46.8	612	2	Q5ALH2_CANAL	Q5alh2 candida alb
733	36	46.8	432	1	CG010_HUMAN	Q791x6 burkholderi	806	36	46.8	612	2	Q5ALH2_CANAL	Q5alh2 candida alb
734	36	46.8	445	2	Q4KMZ0_HUMAN	Q4kmz0 burkholderi	807	36	46.8	612	2	Q5ALH2_CANAL	Q5alh2 candida alb
735	36	46.8	445	2	Q5JMD3_ORISA	Q5jmd3 burkholderi	808	36	46.8	612	2	Q5ALH2_CANAL	Q5alh2 candida alb
736	36	46.8	448	2	Q83CC1_CONBU	Q83cc1 burkholderi	809	36	46.8	612	2	Q5ALH2_CANAL	Q5alh2 candida alb
737	36	46.8	450	2	Q8YOL5_9ANSP	Q8yol5 burkholderi	810	36	46.8	612	2	Q5ALH2_CANAL	Q5alh2 candida alb
738	36	46.8	455	1	PTSEC_KLEFN	Q8yol5 burkholderi	811	36	46.8	612	2	Q5ALH2_CANAL	Q5alh2 candida alb
739	36	46.8	456	1	Q8FNZ4_COREF	Q8fnz4 burkholderi	812	36	46.8	612	2	Q5ALH2_CANAL	Q5alh2 candida alb
740	36	46.8	457	2	Q52DM6_MAGGR	Q52dm6 burkholderi	813	36	46.8	612	2	Q5ALH2_CANAL	Q5alh2 candida alb
741	36	46.8	460	2	Q4P876_9UTMA	Q4p876 burkholderi	814	36	46.8	612	2	Q5ALH2_CANAL	Q5alh2 candida alb
742	36	46.8	460	2	Q61OQ4_BACAN	Q61oq4 burkholderi	815	36	46.8	612	2	Q5ALH2_CANAL	Q5alh2 candida alb
743	36	46.8	460	2	Q4K9Y0_PSEF5	Q4k9y0 burkholderi	816	36	46.8	612	2	Q5ALH2_CANAL	Q5alh2 candida alb
744	36	46.8	465	2	Q7XDP8_ORYSA	Q7xdp8 burkholderi	817	36	46.8	612	2	Q5ALH2_CANAL	Q5alh2 candida alb
745	36	46.8	469	2	Q7QEW1_9NOGA	Q7qew1 burkholderi	818	36	46.8	612	2	Q5ALH2_CANAL	Q5alh2 candida alb
746	36	46.8	469	2	Q6TK71_STRTT	Q6tk71 burkholderi	819	36	46.8	612	2	Q5ALH2_CANAL	Q5alh2 candida alb
747	36	46.8	470	2	Q9CP91_PASMU	Q9cp91 burkholderi	820	36	46.8	612	2	Q5ALH2_CANAL	Q5alh2 candida alb
748	36	46.8	471	2	Q4KMW4_HUMAN	Q4kmw4 burkholderi	821	36	46.8	612	2	Q5ALH2_CANAL	Q5alh2 candida alb
749	36	46.8	471	2	NUON_RHOCA	Q4kmw4 burkholderi	822	36	46.8	612	2	Q5ALH2_CANAL	Q5alh2 candida alb
750	36	46.8	478	1	Q7S2V5_NEUCR	Q7s2v5 burkholderi	823	36	46.8	612	2	Q5ALH2_CANAL	Q5alh2 candida alb
751	36	46.8	481	2	Q68J19_METCA	Q68j19 burkholderi	824	36	46.8	612	2	Q5ALH2_CANAL	Q5alh2 candida alb
752	36	46.8	484	2	Q8AAJ7_BACTN	Q8aa7 burkholderi	825	36	46.8	612	2	Q5ALH2_CANAL	Q5alh2 candida alb
753	36	46.8	489	2	Q7S4W5_NEUCR	Q7s4w5 burkholderi	826	36	46.8	612	2	Q5ALH2_CANAL	Q5alh2 candida alb
754	36	46.8	502	2	Q63LH2_BACLD	Q63lh2 burkholderi	827	36	46.8	612	2	Q5ALH2_CANAL	Q5alh2 candida alb
755	36	46.8	503	2	Q93W4_MASLA	Q93w4 burkholderi	828	36	46.8	612	2	Q5ALH2_CANAL	Q5alh2 candida alb
756	36	46.8	509	2	Q583L3_9TRYP	Q583l3 burkholderi	829	36	46.8	612	2	Q5ALH2_CANAL	Q5alh2 candida alb
757	36	46.8	510	2	Q4MT79_BACCE	Q4mt79 burkholderi	830	36	46.8	612	2	Q5ALH2_CANAL	Q5alh2 candida alb
758	36	46.8	515	2	Q48881_BACHK	Q48881 burkholderi	831	36	46.8	612	2	Q5ALH2_CANAL	Q5alh2 candida alb
759	36	46.8	523	2	Q6HKQ5_BRACH	Q6hkq5 burkholderi	832	36	46.8	612	2	Q5ALH2_CANAL	Q5alh2 candida alb
760	36	46.8	524	2	Q81FE6_BACCR	Q81fe6 burkholderi	833	36	46.8	612	2	Q5ALH2_CANAL	Q5alh2 candida alb
761	36	46.8	524	2	Q81FE6_BACCR	Q81fe6 burkholderi	834	36	46.8	612	2	Q5ALH2_CANAL	Q5alh2 candida alb

835	36	46.8	889	2	Q4JFF1_STRVR	Q4Jff1 streptomyce	908	36	46.8	2002	2	Q75IC9_ORYSA	Q75ic9 oryza sativ
836	36	46.8	897	2	Q5IW57_STRVR	Q5iw57 streptomyce	909	36	46.8	2002	2	Q8H7Y0_ORYSA	Q8h7y0 oryza sativ
837	36	46.8	894	2	Q7S7I3_NEUCR	Q7s7i3 neurospora	910	36	46.8	2010	2	Q6ATP4_ORYSA	Q6atp4 oryza sativ
838	36	45.8	898	2	Q74TN8_YERPE	Q74tn8 yersinia pe	911	36	46.8	2020	2	Q7XXC3_ORYSA	Q7xxc3 oryza sativ
839	36	46.8	898	2	Q8DK6_YERPE	Q8dk6 yersinia pe	912	36	46.8	2021	2	Q75HX8_ORYSA	Q75hx8 oryza sativ
840	36	46.8	898	2	Q8ZE56_YERPE	Q8ze56 yersinia pe	913	36	46.8	2023	2	Q7XL69_ORYSA	Q7xl69 oryza sativ
841	36	46.8	898	2	Q6EA85_YERPS	Q6ea85 yersinia ps	914	36	46.8	2025	2	Q7G4G2_ORYSA	Q7g4g2 oryza sativ
842	36	46.8	926	2	Q4JUH6_CORJK	Q4juh6 corynebacte	915	36	46.8	2026	2	Q7S4K5_ORYSA	Q7s4k5 oryza sativ
843	36	46.8	939	2	Q8PB16_ECOL6	Q8pb16 escherichia	916	36	46.8	2027	2	Q5VSK0_ORYSA	Q5vsk0 oryza sativ
844	36	46.8	945	1	XYLT1_PANTR	Q5qg57 pan troglod	917	36	46.8	2027	2	Q65WT8_ORYSA	Q65wt8 oryza sativ
845	36	46.8	945	2	Q8XOU9_NEUCR	Q8xou9 neurospora	918	36	45.8	2027	2	Q65X63_ORYSA	Q65x63 oryza sativ
846	36	46.8	955	2	Q6ZA28_BURMA	Q6za28 burkholderi	919	36	46.8	2027	2	Q6UW84_ORYSA	Q6uw84 oryza sativ
847	36	46.8	956	2	Q75N96_DAUCA	Q75n96 daucoms caro	920	36	46.8	2027	2	Q7F9Y4_ORYSA	Q7fy94 oryza sativ
848	36	46.8	956	2	Q75N99_DAUCA	Q75n99 daucoms caro	921	36	46.8	2027	2	Q7X7G0_ORYSA	Q7x7g0 oryza sativ
849	36	46.8	959	1	XYLT1_HUMAN	Q8y6338 homo sapien	922	36	46.8	2027	2	Q7XJU8_ORYSA	Q7xju8 oryza sativ
850	36	46.8	965	2	Q63NY9_BURPS	Q63ny9 burkholderi	923	36	46.8	2027	2	Q7XLL0_ORYSA	Q7xll0 oryza sativ
851	36	46.8	988	2	Q8QW4_AICCA	Q8qgw4 acinetobact	924	36	45.8	2027	2	Q7XQ50_ORYSA	Q7xq50 oryza sativ
852	36	46.8	1049	2	Q5VR20_ORYSA	Q5vr20 oryza sativ	925	36	46.8	2027	2	Q84T69_ORYSA	Q84t69 oryza sativ
853	36	46.8	1120	1	KEFA_ECOLI	Q77338 escherichia	926	36	46.8	2027	2	Q8GT93_ORYSA	Q8gt93 oryza sativ
854	36	46.8	1120	2	Q83SE8_SHIFL	Q83se8 shigella fl	927	36	46.8	2027	2	Q8H7K1_ORYSA	Q8h7k1 oryza sativ
855	36	46.8	1120	2	Q8XD54_ECO57	Q8xd54 escherichia	928	36	46.8	2027	2	Q94LM2_ORYSA	Q94lm2 oryza sativ
856	36	46.8	1138	2	Q5BAJ4_EWENI	Q5baj4 aspergillus	929	36	46.8	2027	2	Q75G96_ORYSA	Q75g96 oryza sativ
857	36	46.8	1142	2	Q8DKA_SYNEL	Q8dka7 synecococc	930	36	45.8	2027	2	Q53L26_ORYSA	Q53l26 oryza sativ
858	36	46.8	1164	2	Q8PX58_METMA	Q8px58 methanosarc	931	36	46.8	2027	2	Q53NC4_ORYSA	Q53nc4 oryza sativ
859	36	46.8	1173	2	Q4IMT5_GIBZE	Q4imt5 gibberella	932	36	46.8	2028	2	Q84R58_ORYSA	Q84r58 oryza sativ
860	36	46.8	1201	2	Q5BH35_EWENI	Q5bh35 aspergillus	933	36	46.8	2030	2	Q7XPH1_ORYSA	Q7xph1 oryza sativ
861	36	46.8	1210	2	Q7XH63_ORYSA	Q7xh63 oryza sativ	934	36	46.8	2030	2	Q7XT09_ORYSA	Q7xt09 oryza sativ
862	36	46.8	1210	2	Q8VWJ8_ORYSA	Q8vwj8 oryza sativ	935	36	46.8	2030	2	Q7XWB5_ORYSA	Q7xwb5 oryza sativ
863	36	46.8	1230	2	Q5WML4_ORYSA	Q5wml4 oryza sativ	936	36	46.8	2154	2	Q9ZVC8_ARATH	Q9zvc8 arabidopsis
864	36	46.8	1297	2	Q7XS51_ORYSA	Q7xs51 oryza sativ	937	36	46.8	3295	2	Q74RU8_YERPE	Q74ru8 yersinia pe
865	36	46.8	1333	2	Q65WY0_ORYSA	Q65wy0 oryza sativ	938	36	46.8	3295	2	Q8ZIA8_YERPE	Q8zia8 yersinia ps
866	36	46.8	1374	2	Q6CLT0_KLULA	Q6clt0 kluveromyc	939	36	46.8	3378	2	Q665Q6_YERPS	Q665q6 amycolatops
867	36	46.8	1431	2	Q6ATT1_ORYSA	Q6att1 oryza sativ	940	36	46.8	3413	2	Q54593_AMTMD	Q54593 caenorhabdi
868	36	46.8	1449	2	Q9VQZ1_DROME	Q9vqz1 drosophila	941	36	46.8	4568	1	DVHC_CAEEL	Q8xs39 ralstonia s
869	36	46.8	1459	2	Q6FKG9_CANGA	Q6fk99 candida gla	942	36	46.8	5953	2	Q8XS39_RALSO	Q6jhn6 saccharopol
870	36	46.8	1461	2	Q4QC44_LEITMA	Q4qc44 leishmania	943	36	46.8	7488	2	Q6JHN6_9PSEU	Q9tl136 bacterioph
871	36	46.8	1480	2	Q4HWU7_GIBZE	Q4hwu7 gibberella	944	35.5	46.1	45	2	Q9TL136_9CAUD	Q9tl136 bacterioph
872	36	46.8	1480	2	Q7XW05_ORYSA	Q7xw05 oryza sativ	945	35.5	46.1	104	2	Q4SF26_TETNG	Q4sf26 tetraodon n
873	36	46.8	1522	2	O15069_HUMAN	O15069 homo sapien	946	35.5	46.1	264	2	Q8YHH8_BRUME	Q8yhh8 bruceella me
874	36	46.8	1527	2	Q8LMB9_ORYSA	Q8lmb9 oryza sativ	947	35.5	46.1	276	2	Q4NPC2_9DELT	Q4npc2 anaeromyxob
875	36	46.8	1720	2	Q7XQ6C_ORYSA	Q7xq6c oryza sativ	948	35.5	46.1	280	2	Q57CX5_BRUAB	Q57cx5 bruceella ab
876	36	46.8	1737	2	Q7XNK5_ORYSA	Q7xnk5 oryza sativ	949	35.5	46.1	280	2	Q8G0D4_BRUSU	Q8g0d4 bruceella su
877	36	46.8	1764	2	Q5TKH3_ORYSA	Q5tkh3 oryza sativ	950	35.5	46.1	298	2	Q4XL78_ASPFU	Q4xl78 aspergillus x
878	36	46.8	1789	2	Q53N40_ORYSA	Q53n40 oryza sativ	951	35.5	46.1	319	2	Q6AFW7_LEIXX	Q6afw7 leifsonia x
879	36	46.8	1807	2	Q7XE08_ORYSA	Q7xe08 oryza sativ	952	35.5	46.1	319	2	Q4NHP5_9MICC	Q4nhp5 arthrobacte
880	36	46.8	1814	2	Q5JQX4_ORYSA	Q5jqx4 oryza sativ	953	35.5	46.1	402	1	Y1794_MYCLE	Q9cbm9 mycobacteri
881	36	46.8	1827	2	Q7XR55_ORYSA	Q7xr55 oryza sativ	954	35.5	46.1	407	1	Y2316_MYCBO	P63502 mycobacteri
882	36	46.8	1831	2	Q7X8X0_ORYSA	Q7x8x0 oryza sativ	955	35.5	46.1	407	1	Y2316_MYCBO	P63503 mycobacteri
883	36	46.8	1862	2	Q7XWP7_ORYSA	Q7xwp7 oryza sativ	956	35.5	46.1	455	2	Q4LR91_GIBZE	Q4lr91 gibberella
884	36	46.8	1869	2	Q6OD74_ORYSA	Q6od74 oryza sativ	957	35.5	46.1	493	2	Q9FYG3_ARATH	Q9fyg3 arabidopsis
885	36	46.8	1881	2	Q7XSU0_ORYSA	Q7xsu0 oryza sativ	958	35.5	46.1	539	1	G6P1_CAUCR	Q9abk5 caulobacter
886	36	46.8	1884	2	Q7XTV5_ORYSA	Q7xtv5 oryza sativ	959	35.5	46.1	628	1	GIDA_BACSU	P25812 bacillus su
887	36	46.8	1902	2	Q53LQ6_ORYSA	Q53lq6 oryza sativ	960	35.5	46.1	628	1	G65CN2_BACLD	Q65cn2 bacillus li
888	36	46.8	1909	2	Q7XPN1_ORYSA	Q7xpn1 oryza sativ	961	35.5	46.1	656	2	Q9K8Q8_BACHD	Q9k8q8 bacillus ha
889	36	46.8	1914	2	Q53J46_ORYSA	Q53j46 oryza sativ	962	35.5	46.1	667	2	Q8SLZ9_OCEIH	Q8slz9 oceanobacil
890	36	46.8	1914	2	Q53M75_ORYSA	Q53m75 oryza sativ	963	35.5	46.1	676	2	O26520_METHB	Q26520 methanobact
891	36	46.8	1923	2	Q6OEI3_ORYSA	Q6oei3 oryza sativ	964	35.5	46.1	679	2	Q9I474_PSEAE	Q9i474 pseudomonas
892	36	46.8	1932	2	Q707I3_ORYSA	Q707i3 oryza sativ	965	35.5	46.1	693	1	SUVH7_ARATH	Q9c5p1 arabidopsis
893	36	46.8	1941	2	Q4P4M1_USTMA	Q4p4m1 ustilago ma	966	35.5	46.1	884	2	Q7VNV9_HAEDU	Q7vnv9 haemophilus
894	36	46.8	1943	2	Q614W2_ORYSA	Q614w2 oryza sativ	967	35.5	46.1	947	2	Q8VGS8_BRAJA	Q8vgs8 bradyrhizob
895	36	46.8	1952	2	Q7XPA8_ORYSA	Q7xpa8 oryza sativ	968	35.5	46.1	985	2	Q5I121_MAGGR	Q5i121 magnaporthe
896	36	46.8	1969	2	Q7XW75_ORYSA	Q7xw75 oryza sativ	969	35.5	46.1	1662	2	Q525F1_MAGGR	Q525f1 magnaporthe
897	36	46.8	1974	2	Q688L3_ORYSA	Q688l3 oryza sativ	970	35	45.5	39	2	Q6IE99_MACMU	Q6ie99 macaca mula
898	36	46.8	1980	2	Q6FP3A3_ORYSA	Q6fp3a3 oryza sativ	971	35	45.5	50	1	YCX7_OENHO	Q9mtm9 oenothera h
899	36	46.8	1987	2	Q7Y1G3_ORYSA	Q7y1g3 oryza sativ	972	35	45.5	80	2	O96468_PLAFA	Q96468 plasmodonas
900	36	46.8	1988	2	Q7X8Q5_ORYSA	Q7x8q5 oryza sativ	973	35	45.5	81	2	Q4KD04_PSEF5	Q4kd04 plasmodium
901	36	46.8	1989	2	Q6ATB5_ORYSA	Q6atb5 oryza sativ	974	35	45.5	84	2	Q4YAG6_PLABE	Q4yag6 epicrates i
902	36	46.8	1989	2	Q7FP9P9_ORYSA	Q7fp9p9 oryza sativ	975	35	45.5	93	2	Q7GFP6_9SAUR	Q7gfp6 epirachia x
903	36	46.8	1991	2	Q65X31_ORYSA	Q65x31 oryza sativ	976	35	45.5	96	2	Q6AGT8_LEIXX	Q6agt8 leifsonia x
904	36	46.8	1992	2	Q6AU86_ORYSA	Q6au86 oryza sativ	977	35	45.5	96	2	Q6TEC8_BRARE	Q6tec8 brachydanio
905	36	46.8	1993	2	Q7XXU4_ORYSA	Q7xxu4 oryza sativ	978	35	45.5	102	2	Q95955_THACO	Q95955 thamnophis
906	36	46.8	1997	2	Q8WZ27_ORYSA	Q8wz27 oryza sativ	979	35	45.5	105	2	Q5FRL5_GLIOX	Q5frl5 gluconobact
907	36	46.8	2001	2	Q7XW28_ORYSA	Q7xw28 oryza sativ	980	35	45.5	109	2	Q5ZB56_ORYSA	Q5zb56 oryza sativ

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981 35 45.5 114 2 Q5U9W1 CARCR
982 35 45.5 115 2 Q48070 9SAUR
983 35 45.5 117 2 Q70K92 9ACTO
984 35 45.5 117 2 Q7GFP7 9SAUR
985 35 45.5 118 2 Q5U9W2 CHEMY
986 35 45.5 119 2 Q8W9L1 HAPGR
987 35 45.5 119 2 Q8W9K8 HAPGR
988 35 45.5 119 2 Q8W9K1 HAPGR
989 35 45.5 119 2 Q8W9L0 HAPGR
990 35 45.5 119 2 Q8W9K6 HAPGR
991 35 45.5 119 2 Q9MEK0 PROTA
992 35 45.5 119 2 Q8W9K9 HAPGR
993 35 45.5 119 2 Q8W9J7 HAPSI
994 35 45.5 119 2 Q8W9K4 HAPGR
995 35 45.5 119 2 Q8W9L8 EULMP
996 35 45.5 119 2 Q8W9K0 HAPGR
997 35 45.5 119 2 Q8W8U6 HAPGR
998 35 45.5 119 2 Q8W8U8 HAPGR
999 35 45.5 119 2 Q8W8U7 HAPGR
1000 35 45.5 119 2 Q8W8U9 HAPGR
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ALIGNMENTS

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RESULT 1
ESXA_MYCBO STANDARD; PRT; 94 AA.
AC F0A565; 084901; Q57165;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE 6 kDa early secretory antigenic target (ESAT-6).
GN Name=esxA; Synonyms=esat6; OrderedLocusNames=Mb3905;
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium;
OC Mycobacterium tuberculosis complex.
OX NCBI_TaxID=1765;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96200095; PubMed=8631702;
RA Mahairas G.G., Sabo P.J., Hickey M.J., Singh D.C., Stover C.K.;
RT "Molecular analysis of genetic differences between Mycobacterium bovis
  BCG and virulent M. bovis.";
RL J. Bacteriol. 178:1274-1282(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=AF2122/97; PubMed=12788972; DOI=10.1073/pnas.1130426100;
RX MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;
RA Garnier T., Eigimeier K., Camus J.-C., Medina N., Mansoor H.,
  Pryor M., Duthoy S., Grondin S., Jacroix C., Monsemp C., Simon S.,
  Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
  Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
RT "The complete genome sequence of Mycobacterium bovis.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
CC -!- FUNCTION: Not known. Elicits high level of IFN-gamma from memory
  effector cells during the first phase of a protective immune
  response.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the ESAT-6 (esx) family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; U34848; AAC44033.1; -; Genomic DNA.
CC EMBL; BX248347; CAD96091.1; -; Genomic DNA.
CC Fungi; Complete proteome.
CC INIT_MBI 0
CC SEQUENCE 94 AA; 9773 MW; 19245B0BC478BC84 CRC64;
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Query Match 100.0%; Score 77; DB 1; Length 94;
Best Local Similarity 100.0%; Pred. No. 6.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAASAIQ 15
DB 5 WNFAGIEAASAIQ 19

RESULT 2
ESXA_MYCTU STANDARD; PRT; 94 AA.
ID POA564; 084901; Q57165;
AC 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE 6 kDa early secretory antigenic target (ESAT-6).
GN Name=esxA; Synonyms=esat6; OrderedLocusNames=RV3875, MT3989;
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium;
OC Mycobacterium tuberculosis complex.
OX NCBI_TaxID=1773;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=H378V;
RX MEDLINE=95204931; PubMed=7897219;
RA Andersen P., Andersen A.B., Sorensen A.L., Nagai S.;
RT "Recall of long-lived immunity to Mycobacterium tuberculosis infection
  in mice.";
RL J. Immunol. 154:3359-3372(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE, PROTEIN SEQUENCE OF 1-10, AND CHARACTERIZATION.
RC STRAIN=Brdmann;
RX MEDLINE=95247251; PubMed=7729876;
RA Soerensen A.L., Nagai S., Houen G., Anderson P., Anderson A.B.;
RT "Purification and characterization of a low-molecular-mass T-cell
  antigen secreted by Mycobacterium tuberculosis.";
RL Infect. Immun. 63:1710-1717(1995).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Singh B., Siddiqui Z., Singh S., Sharma P.;
RT "ESAT-6 gene of a clinical isolate of Mycobacterium tuberculosis from
  India.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=H378V;
RX MEDLINE=98295987; PubMed=9634230; DOI=10.1038/311159;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,
  Harris D.E., Gordon S.V., Eigimeier K., Gas S., Barry C.E. III,
  Tekaita F., Badoock K., Basham D., Brown D., Chillingworth T.,
  Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,
  Holroyd S., Hornby T., Jagels K., Krogh A., McLean J., Moule S.,
  Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,
  Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
  Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
  complete genome sequence.";
RL Nature 393:537-544(1998).
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CDC 1551 / Oshkosh;
RX MEDLINE=22206494; PubMed=12218036;
RX DOI=10.1126/JB.184.19.5479-5490.2002;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
  Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,
  Hickey E.K., Kolony J.F., Nelson W.C., Unayam L.A., Ermolaeva M.D.,
  Salzberg S.L., Delcher A., Uitterback T.R., Weidman J.F., Khouri H.M.,
  Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,
  Fraser C.M.;
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RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
 RL laboratory strains.";
 RL J. Bacteriol. 184:5479-5490(2002).
 RN [6]

RP NUCLEOTIDE SEQUENCE OF 1-70.

RC STRAIN=H37RV;
 RX MEDLINE=99061212; PubMed=9846755;
 RA Berthet P.-X., Ragunathan P.B., Rosenkrands I., Andersen P.,
 RA Gicquel B.;
 RT "A Mycobacterium tuberculosis operon encoding ESAT-6 and a novel low-
 RT molecular-mass culture filtrate protein (CFP-10).";
 RL Microbiology 144:3195-3203(1998).
 CC -I- FUNCTION: Not known. Elicits high level of IFN-gamma from memory
 CC effector cells during the first phase of a protective immune
 CC response.

CC -I- SUBCELLULAR LOCATION: Secreted.

CC -I- SIMILARITY: Belongs to the ESAT-6 (esx) family.

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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

CC EMBL; X79562; CAA56099.1; -; Genomic DNA.
 DR EMBL; AF420491; AAL16996.1; -; Genomic DNA.
 DR EMBL; BX842584; CAF55648.1; -; Genomic DNA.
 DR EMBL; AE000516; AAK48357.1; -; Genomic DNA.
 DR EMBL; AF004671; AAC83446.1; -; Genomic DNA.
 DR FJ; A70803; A70803.
 DR TIGR; MT3989; -.

DR Tuberculin; Rv3875; -.

KW Antigen; Complete proteome; Direct protein sequencing.

FT INIT_MET 0 0

SQ SEQUENCE 94 AA; 9773 MW; 19245B0EC478BC84 CRC64;

Query Match 100.0%; Score 77; DB 1; Length 94;
 Best Local Similarity 100.0%; Pred. No. 6.3e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAIQG 15
 |||||
 DB 5 WNFAGIEAAASAIQG 19

RESULT 3

Q540D8 MYCTU
 ID Q540D8 MYCTU PRELIMINARY; PRT; 95 AA.
 AC Q540D8;
 DT 13-SEP-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
 DE Secreted low molecular-mass T-cell antigen ESAT6.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium;
 OC Mycobacterium tuberculosis complex.
 OX NCBI_TaxID=1773;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Lee C.F.;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY207398; AAG62007.1; -; Genomic DNA.
 SQ SEQUENCE 95 AA; 9904 MW; 79BD529E3D8F519 CRC64;

Query Match 100.0%; Score 77; DB 2; Length 95;
 Best Local Similarity 100.0%; Pred. No. 6.4e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAIQG 15
 |||||
 DB 6 WNFAGIEAAASAIQG 20

RESULT 4

Q5G541 MYCUL
 ID Q5G541 MYCUL PRELIMINARY; PRT; 56 AA.
 AC Q5G541;
 DT 10-MAY-2005 (TREMBlrel. 30, Created)
 DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
 DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
 DE ESAT-6 (Fragment).
 OS Mycobacterium ulcerans.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1809;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=98-912, and 7922;
 RA Mve-Obiang A., Lee R.E., Umstot E.S., Trott K.A., Grammer T.C.,
 RA Parker J.M., Ranger B.S., Small P.C.;
 RT "A newly discovered mycobacterial pathogen isolated from lethal
 RT infections in laboratory colonies of xenopus species produces a novel
 RT form of the M. ulcerans macrolide toxin, mycolactone.";
 RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY854677; AAW68024.1; -; Genomic DNA.
 DR EMBL; AY854675; AAW68022.1; -; Genomic DNA.
 FT NON_TER 1 1
 FT SEQUENCE 56 AA; 5787 MW; 4FB7FEBB455D1CEE CRC64;

Query Match 83.1%; Score 64; DB 2; Length 56;
 Best Local Similarity 80.0%; Pred. No. 0.0059;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAIQG 15
 |||||
 DB 5 WNFAGIEAAASAIQG 19

RESULT 5

Q5G545 MYCUL
 ID Q5G545 MYCUL PRELIMINARY; PRT; 56 AA.
 AC Q5G545;
 DT 10-MAY-2005 (TREMBlrel. 30, Created)
 DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
 DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
 DE ESAT-6 (Fragment).
 OS Mycobacterium ulcerans.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1809;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=5143;
 RA Mve-Obiang A., Lee R.E., Umstot E.S., Trott K.A., Grammer T.C.,
 RA Parker J.M., Ranger B.S., Small P.C.;
 RT "A newly discovered mycobacterial pathogen isolated from lethal
 RT infections in laboratory colonies of xenopus species produces a novel
 RT form of the M. ulcerans macrolide toxin, mycolactone.";
 RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY854673; AAW68020.1; -; Genomic DNA.
 FT NON_TER 1 1
 FT SEQUENCE 56 AA; 5788 MW; 4FB7FEB145FD1CBE CRC64;

Query Match 83.1%; Score 64; DB 2; Length 56;
 Best Local Similarity 80.0%; Pred. No. 0.0059;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAIQG 15
 |||||
 DB 5 WNFAGIEAAASAIQG 19

RESULT 6

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QVQH8_9MYCO PRELIMINARY; PRT; 72 AA.
ID QVQH8_9MYCO PRELIMINARY; PRT; 72 AA.
AC QVQH8_9MYCO PRELIMINARY; PRT; 72 AA.
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DE Small secreted antigenic protein Esat6 (Fragment).
OS Mycobacterium liflandii.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OK NCBI_TaxID=261524;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=XT-128;
RX PubMed=15908356; DOI=10.1128/IAI.73.6.3307-3312.2005;
RA Mve-Obiang A., Lee R.E., Umstot E.S., Trott K.A., Grammer T.C.,
RA Parker J.M., Ranger B.S., Grainger R., Mahrous E.A., Small P.L.;
RT "A Newly Discovered Mycobacterial Pathogen Isolated from Laboratory
RT Colonies of Xenopus Species with Lethal Infections Produces a Novel
RT Form of Mycolactone, the Mycobacterium ulcerans Macrolide Toxin.";
RL Infect. Immun. 73:3307-3312(2005)
DR EMBL: AY736851; AAX20068.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 72
SQ SEQUENCE 72 AA; 7527 MW; BBE8911F7654352D CRC64;
Query Match 83.1%; Score 64; DB 2; Length 72;
Best Local Similarity 80.0%; Pred. No. 0.0075;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 WNFAGTAAASAIQ 15
|||||:::|
Db 4 WNFAGTAAASSIGG 18

RESULT 7
Q4KSH1_LACLC
ID Q4KSH1_LACLC PRELIMINARY; PRT; 714 AA.
AC Q4KSH1_LACLC PRELIMINARY; PRT; 714 AA.
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DE GlnP.
GN Name=glnP;
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OK NCBI_TaxID=1359;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MGI363;
RA Larsen R., Kloosterman T.G., Kok J., Kuipers O.P.;
RT "GlnR-mediated gene regulation in Lactococcus lactis subsp. cremoris
RT MGI363.";
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY881998; AAX82492.1; -; Genomic DNA.
SQ SEQUENCE 714 AA; 78527 MW; 04953CD8539343C9 CRC64;
Query Match 61.0%; Score 47; DB 2; Length 714;
Best Local Similarity 50.0%; Pred. No. 46;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 WNFAGTAAASAIQ 14
|||||:::|
Db 303 WNFAGTAAAVDSVQ 316

RESULT 8
Q9CESS_LACLA
ID Q9CESS_LACLA PRELIMINARY; PRT; 714 AA.
AC Q9CESS_LACLA PRELIMINARY; PRT; 714 AA.
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-MAR-2004 (TREMBlrel. 26, Last annotation update)

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DE Glutamine ABC transporter permease and substrate binding protein
DE PROTEIN.
GN Name=glnP; OrderedLocusNames=LL1759;
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OK NCBI_TaxID=1360;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=LL1403;
RX MEDLINE=21235186; PubMed=11337471; DOI=10.1101/gr.GR-1697R;
RA Bolotin A., Wincker P., Mauger S., Jallion O., Malarne K.,
RA Weissenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis ssp. lactis IL1403.";
RL Genome Res. 11:731-753(2001).
DR EMBL: AB006406; AAK05857.1; -; Genomic_DNA.
DR HSP; P10344; 1WDN.
DR PIR; G86844; G86844.
DR GO; GO:0019866; C:inner membrane; IEA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000515; BPD transp.
DR InterPro; IPR010065; HEOfc_ABC_3TM.
DR InterPro; IPR001311; SBP/glu receptor.
DR InterPro; IPR001636; SBP_bac_3.
DR Pfam; PF00528; BPD_transp_1; 1.
DR Pfam; PF00497; SBP_bac_3; 2.
DR SMART; SM00062; PBPb; 2.
DR TIGRFAME; TIGR01726; HEOfc_perm_3TM; 1.
DR PROSITE; PS00928; ABC_TM1; 1.
DR PROSITE; PS01039; SBP_BACTERIAL_3; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 714 AA; 78377 MW; 4EBE8E5453A968EB CRC64;
Query Match 61.0%; Score 47; DB 2; Length 714;
Best Local Similarity 50.0%; Pred. No. 46;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 WNFAGTAAASAIQ 14
|||||:::|
Db 303 WNFAGTAAAVDSVQ 316

RESULT 9
QBH746_PHYCI PRELIMINARY; PRT; 377 AA.
ID QBH746_PHYCI PRELIMINARY; PRT; 377 AA.
AC QBH746_PHYCI PRELIMINARY; PRT; 377 AA.
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DE 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Polygalacturonase.
GN Name=Pgg;
OS Phytophthora cinnamomi.
OC Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
OC Phytophthora.
OK NCBI_TaxID=4785;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=2221401; PubMed=12236597;
RA Goetsesson A., Marshall J.S., Jones D.A., Hardham A.R.;
RT "Characterization and evolutionary analysis of a large
RT polygalacturonase gene family in the oomycete plant pathogen
RT Phytophthora cinnamomi.";
RL Mol. Plant Microbe Interact. 15:907-921(2002).
DR EMBL: AF398948; AAN05468.1; -; Genomic_DNA.
DR HSP; P36213; 1NHC.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016798; C:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0004650; E:polygalacturonase activity; IEA.
DR GO; GO:0005975; E:carbohydrate metabolism; IEA.
DR InterPro; IPR000743; Glyco_Hydro_28.

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DR InterPro; IPR006626; PbH1.
DR InterPro; IPR010916; TONB_Box N.
DR Pfam; PF00295; Glyco_hydro_28; 1.
DR SMART; SM00710; PbH1; 6.
DR PROSITE; PS00502; POLYGALACTURONASE; 1.
DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
DR Cell wall; Glycosidase; Hydrolase.
SQ SEQUENCE 377 AA; 39236 MW; 10BA93D812B3D8DC CRC64;

Query Match 59.7%; Score 46; DB 2; Length 377;
Best Local Similarity 66.7%; Pred. No. 37;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WNFAGIEAASA 12
| | : | | : | |
Db 353 WTFSGIEVSASA 364

RESULT 10
Q8H749_PHYCI
ID Q8H749 PHYCI PRELIMINARY; PRT; 454 AA.
AC Q8H749;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Polyalacturonase.
GN Name=Pg10;
OS Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
OC Phytophthora.
OC Phytophthora.
NCBI_TaxID=4785;
RN [1]
NUCLEOTIDE SEQUENCE.
RP MEDLINE=222121401; PubMed=12236597;
RX Gaetesson A., Marshall J.S., Jones D.A., Hardham A.R.;
RT "Characterization and evolutionary analysis of a large
RT polyalacturonase gene family in the oomycete plant pathogen
RT Phytophthora cinnamomi.";
RL Mol. Plant Microbe Interact. 15:907-921(2002).
RR EMBL; AF398945; AAN05465.1; -; Genomic_DNA.
DR HSP; 074213; 1fB4.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0004650; F:polysaccharonase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR000743; Glyco_hydro_28.
DR InterPro; IPR006626; PbH1.
DR Pfam; PF00295; Glyco_hydro_28; 1.
DR SMART; SM00710; PbH1; 5.
DR PROSITE; PS00502; POLYGALACTURONASE; 1.
DR Cell wall; Glycosidase; Hydrolase.
KW Cell wall; Glycosidase.
SQ SEQUENCE 454 AA; 47542 MW; 961E56001AD2C0BB CRC64;

Query Match 59.7%; Score 46; DB 2; Length 454;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WNFAGIEAASA 12
| | : | | : | |
Db 430 WTFSGIEVSASA 441

RESULT 11
Q5Z1P8_NOCPA
ID Q5Z1P8 NOCPA PRELIMINARY; PRT; 2348 AA.
AC Q5Z1P8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=nfa7980;
OS Nocardia farcinica.
OC Bacteria; Actinobacteriae; Actinobacteridae; Actinomycetales;
OC

Corynebacterinae; Nocardiaceae; Nocardia.
NCBI_TaxID=37329;
[1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=IFM 10152;
RX PubMed=15466710; DOI=10.1073/pnas.0406410101;
RA Ishikawa J., Yamaehita A., Mikami Y., Hoshino Y., Kurita H., Hotta K.,
RA Siba T., Hattori M.;
RT "The complete genomic sequence of Nocardia farcinica IFM 10152.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14925-14930(2004).
RR EMBL; AP006618; BAD55643.1; -; Genomic_DNA.
DR InterPro; IPR001734; Na/solut_sympot.
DR InterPro; IPR000719; Prot_kinase.
DR PROSITE; PS00457; NA_SOLUT_SYMP_2; UNKNOWN_1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 2348 AA; 245055 MW; 9A5FAB706A7BE97D CRC64;

Query Match 59.7%; Score 46; DB 2; Length 2348;
Best Local Similarity 53.3%; Pred. No. 2.1e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 WNFAGIEAASAIQG 15
| | : | | : | |
Db 228 WNAVGLNALSISAVAG 242

RESULT 12
Q4WZC2_ASPPU
ID Q4WZC2 ASPPU PRELIMINARY; PRT; 495 AA.
AC Q4WZC2;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Aldehyde dehydrogenase, putative.
GN OSFNAMES=Afu2g17460;
DE Aspergillus fumigatus Af293.
OS Aspergillus fumigatus Af293.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=330879;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=AF293;
RA Nierman W., Pain A., Anderson M.J., Wortman J., Kim H.Stanley.,
RA Arroyo J., Bertram M., Abe K., Archer D.B., Bernhejo C., Bennett J.,
RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,
RA Farman M., Fedorova N., Fedorova N., Feldblum T.V., Fischer R.,
RA Fosker N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
RA Goldman G.H., Goni K., Griffith-Jones S., Gwilliam R., Haas B.,
RA Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulakarni R.,
RA Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,
RA Majors W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
RA Mouyna I., Mulligan S., Murphy L., O'Neil S., Paulsen I.,
RA Penalba M.A., Pertea M., Price C., Pritchard B.L., Quail M.A.,
RA Rabinowitz E., Rawlins N., Rajandream M.-A., Reichard U.,
RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
RA Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,
RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
RA Takeuchi M., Tekala F., Turner G., Vazquez de Aldana C.R., Weidman J.,
RA White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,
RA Machida M., Hall N., Barrell B., Denning D.W.;
RT "Genomic sequence of the pathogenic and allergenic filamentous fungus
RT Aspergillus fumigatus";
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC preliminary data.
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
DR EMBL; AAHF01000001; EAL94043.1; -; Genomic DNA.
DR DR SEQUENCE 495 AA; 54267 MW; A9DC5283882D6DB2 CRC64;

Query Match 58.4%; Score 45; DB 2; Length 495;
Best Local Similarity 57.1%; Pred. No. 71

```
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 WNFAGTAAASAIQ 14
DB 5 WDYASTAAASLIQ 18

RESULT 13
Q2AVB0 NITRU
ID Q82AVB0 NITEU PRELIMINARY; PRT; 715 AA.
AC Q82VBO;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Glycyl-tRNA synthetase, beta subunit (EC 6.1.1.14).
GN Name=GlyS; OrderedLocusNames=NEI186;
OS Nitrosomonas europaea.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadaceae; Nitrosomonas.
OX NCBI_TaxID=915;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 19718 / IFO 14298;
RX MEDLINE=22596410; PubMed=12700255;
RA Chain P., Lamerdin J.E., Klitz M.G., Regala W., Lao V., Land M.L.,
RA Hauser L., Hooper A.B., Klitz M.G., Norton J., Sayavedra-Soto L.A.,
RA Acierio B.M., Hommes N.G., Whittaker M.M., Art D.J.,
RA "Complete genome sequence of the ammonia-oxidizing bacterium and
RT obligate chemolithoautotroph Nitrosomonas europaea.";
RL J. Bacteriol. 185:2759-2773 (2003).
CC -!- CATALYTIC ACTIVITY: ATP + glycine + tRNA(Gly) = AMP + diphosphate
CC + glycyl-tRNA(Gly).
CC -!- SUBUNIT: Tetramer of two alpha and two beta chains (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
DR EMBL; BX321860; CAD85097.1; -; Genomic DNA.
DR GO; GO:0004814; P:arginine-tRNA ligase activity; IEA.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0004820; P:glycine-tRNA ligase activity; IEA.
DR GO; GO:0016974; P:ligase activity; IEA.
DR GO; GO:0006420; P:arginyl-tRNA aminoacylation; IEA.
DR GO; GO:0006420; P:arginyl-tRNA aminoacylation; IEA.
DR InterPro; IPR008909; DALR anticod bd.
DR InterPro; IPR006194; tRNA-synt_2f.
DR Pfam; PF05746; tRNA-synt_1d_C; 1.
DR Pfam; PF02092; tRNA-synt_2f; 1.
DR PRINTS; PR01045; TRNASYNTHGB.
DR TIGRfam; TIGR00211; GlyS.1.
DR PROSITE; PS00861; AA_tRNA_LIGASE_II_GLYAB; 1.
KW Aminoacyl-tRNA synthetase; Complete proteome; Ligase.
SQ SEQUENCE 715 AA; 78442 MW; 8C6E74D095053B5E CRC64;

Query Match 58.4%; Score 45; DB 2; Length 715;
Best Local Similarity 64.3%; Pred. No. 1e+02;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WNFAGTAAASAIQ 14
DB 235 WIREGLAAASAVQ 248

RESULT 14
Q57DJ6 BRUAB
ID Q57DJ6 BRUAB PRELIMINARY; PRT; 61 AA.
AC Q57DJ6;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=Brubab1_0924;
OS Brucella abortus.
```

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OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=9-941 / Biovar 1;
RX PubMed=15805518; DOI=10.1128/JB.187.8.2715-2726.2005;
RA Halling S.M., Peterson-Burch B.D., Bricker B.J., Zuerner R.L.,
RA Qiang Z., Li L.-L., Kapur V., Alt D.P., Olsen S.C.;
RT "Completion of the genome sequence of Brucella abortus and comparison
RT to the highly similar genomes of Brucella melitensis and Brucella
RT suis.";
RL J. Bacteriol. 187:2715-2726 (2005).
DR EMBL; AS017223; AAX74288.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 61 AA; 6498 MW; 8FA93ABA827B2C0B CRC64;

Query Match 57.1%; Score 44; DB 2; Length 61;
Best Local Similarity 76.9%; Pred. No. 15;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 FAGIEAASAIQ 15
DB 34 FAGIKAAASARDG 46

RESULT 15
Q8G115 BRUSU
ID Q8G115 BRUSU PRELIMINARY; PRT; 61 AA.
AC Q8G115;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BR0913;
OS Brucella suis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=1330 / Biovar 1;
RX MEDLINE=22247741; PubMed=12271122; DOI=10.1073/pnas.192319099;
RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
RA Read T.D., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
RA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J.A.,
RA Van Aken S.E., Riedmuller S., Tettelin H., Gill S.R., White O.,
RA Salzberg S.L., Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M.,
RA Fraser C.M.;
RT "The Brucella suis genome reveals fundamental similarities between
RT animal and plant pathogens and symbionts.";
RL Proc. Natl Acad Sci U.S.A. 99:13148-13153 (2002).
DR EMBL; AS014291; AAN29841.1; -; Genomic DNA.
DR TIGR; BR0913; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 61 AA; 6498 MW; 8FA93ABA827B2C0B CRC64;

Query Match 57.1%; Score 44; DB 2; Length 61;
Best Local Similarity 76.9%; Pred. No. 15;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 FAGIEAASAIQ 15
DB 34 FAGIKAAASARDG 46

RESULT 16
Q9RFF6 RHOSH
ID Q9RFF6 RHOSH PRELIMINARY; PRT; 225 AA.
AC Q9RFF6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ured.
OS Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Rhodobacter.
OX NCBI_TaxID=1063;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1;
RX MEDLINE=20115911; PubMed=10648776; DOI=10.1093/nar/28.4.862;
RA Choudhary M., Kaplan S.;
RT "DNA sequence analysis of the photosynthesis region of Rhodobacter
sphaeroides 2.4.1.";
RL Nucleic Acids Res. 28:862-867(2000).
DR EMBL; AF195122; AAF24251.1; -; Genomic_DNA.
DR PIR; T50707;
DR GO; GO:0016151; F:nickel ion binding; IEA.
DR GO; GO:0006807; P:nitrogen compound metabolism; IEA.
DR InterPro; IPR002669; Ured.
DR Pfam; PF01774; Ured; 1.
DR PIRSF; PIRSF016083; Ureas acces Ured; 1.
SQ SEQUENCE 225 AA; 23417 MW; 59EC44A05802C29F CRC64;

Query Match 57.1%; Score 44; DB 2; Length 225;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 AGTEMAASAIQ 15
Db 178 AGVEAASAFDG 189

RESULT 17
Q86G78 LEIDO
ID Q86G78_LEIDO PRELIMINARY; PRT; 517 AA.
AC Q86G78;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Amino acid permease AAP10LD.
OS Leishmania donovani.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5661;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC PubMed=15522240; DOI=10.1016/j.bbrc.2004.09.212;
RA Akerman M., Shaked-Wishan P., Mazareb S., Volpin H., Zilberstein D.;
RT "Novel motifs in amino acid permease genes from Leishmania.";
RL Biochem. Biophys. Res. Commun. 325:353-366(2004).
DR EMBL; AY247005; AAC88095.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/rel_permease1.
DR InterPro; IPR004841; Permease_region.
DR Pfam; PF00324; AA_permease_1.
KW Transmembrane; Transport.
SQ SEQUENCE 517 AA; 56179 MW; A52B2B321DF4A9F2 CRC64;

Query Match 57.1%; Score 44; DB 2; Length 517;
Best Local Similarity 42.9%; Pred. No. 1.1e+02;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 WNFAGIEAASAIQ 14
Db 221 WNFSGFDSAGNVIE 234

RESULT 18
Q4FW28 LEIMA
ID Q4FW28_LEIMA PRELIMINARY; PRT; 517 AA.

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AC Q4FW28;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Amino acid permease, putative (EC 3.6.3.-).
OX ORFNames=LMJ1372;
OS Leishmania major.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Friedlin;
RX PubMed=16020728; DOI=10.1126/science.1112680;
RA Ivens A.C., Peacock C.S., Worthey E.A., Murphy L., Aggarwal G.,
Berriman M., Sisk E., Rajandream M.A., Adlem E., Aert R., Anupama A.,
Apostolou Z., Attipoe P., Bason N., Bauser C., Beck A., Beverley S.M.,
Blanchettin G., Borzym K., Bothe G., Bruschi C.V., Collins M.,
Cadag E., Ciaroni L., Clayton C., Coulson R.M., Cronin A., Cruz A.K.,
Davies R.M., De Gaudenzi J., Dobson D.E., Duesterhoeft A.,
Fazelina G., Fosker N., Frasch A.C., Fraser A., Fuchs M., Gabel C.,
Goble A., Goffeau A., Harris D., Hertz-Fowler C., Hilbert H., Horn D.,
Huang Y., Klages S., Knights A., Kube M., Larke N., Litvin L.,
Lord A., Louie T., Marra M., Masuy D., Matthews K., Michaeli S.,
Mottam J.C., Muller-Auer S., Munden H., Nelson S., Norbertczak H.,
Oliver K., O'Neil S., Pentony M., Pohl T.M., Price C., Purnelle B.,
Quail M.A., Rabinowitsch E., Reinhardt R., Rieger M., Rinta J.,
Robben J., Robertson L., Ruiz J.C., Rutter S., Saunders D.,
Shin H., Sivam D., Squares R., Squares S., Seyler A., Sharp S.,
Volckaert G., Wambutt R., Warren T., Wedler H., Woodward J., Zhou S.,
Zimmermann W., Smith D.F., Blackwell J.M., Stuart K.D., Barrell B.,
Myler P.J.;
RT "The Genome of the Kinetoplastid Parasite, Leishmania major.";
RL Science 309:436-442(2005).
DR EMBL; CP000081; AAZ14665.1; -; Genomic_DNA.
KW Hydrolase.
SQ SEQUENCE 517 AA; 56097 MW; 2816B3C96B750F5D CRC64;

Query Match 57.1%; Score 44; DB 2; Length 517;
Best Local Similarity 42.9%; Pred. No. 1.1e+02;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 WNFAGIEAASAIQ 14
Db 221 WNFSGFDSAGNVIE 234

RESULT 19
Q6KHL9 MYCWO
ID Q6KHL9_MYCWO PRELIMINARY; PRT; 1460 AA.
AC Q6KHL9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE P65 lipoprotein-like protein.
OS OrderedLocustNames=MMOB4250;
OC Mycoplasma mobile.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2118;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=163K / ATCC 43663;
RX PubMed=15289470; DOI=10.1101/gr.2674004;
RA Jaffe J.D., Stange-Thomann N., Smith C., DeCaprio D., Fisher S.,
Butler J., Calvo S., Elkins T., Fitzgerald M.G., Hafez N.,
Kodira C.D., Major J., Wang S., Wilkinson J., Nicol R., Nussbaum C.,
Birren B., Berg H.C., Church G.M.;
RT "The complete genome and proteome of Mycoplasma mobile.";
RL Genome Res. 14:1447-1461(2004).
DR EMBL; AE017338; AAT27911.1; -; Genomic DNA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR InterPro; IPR001087; Lipase_GDSL.
KW Complete proteome; Lipoprotein.

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KW Complete proteome.
SQ SEQUENCE 508 AA; 57252 MW; B267BACBF6283711 CRC64;

Query Match 55.8%; Score 43; DB 2; Length 508;
Best Local Similarity 71.1%; Pred. No. 1.6e+02;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 NFAGIEAASAIQ 15
|||:|||||
DB 398 NFHTIEASAIAG 411

RESULT 23
Q5V3L9 HALMA
ID Q5V3L9 HALMA PRELIMINARY; PRT; 540 AA.
AC Q5V3L9;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Iron ABC transporter permease protein.
GN Names-sfub; OrderedLocNames-rinAC0907;
OS Haloarcula marismortui (Halo bacterium marismortui).
OC Archaea; Euryarchaeota; Halobacteriia; Halobacteriales;
OC Halobacteriaceae; Haloarcula.
OX NCBI_TaxID=2238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 43049;
RX PubMed=15520287; DOI=10.1101/gr.2700304;
RA Baliga N.S., Bonneau R., Facciotti M.T., Pan M., Glusman G.,
RA Deutsch E.W., Shannon P., Chiu Y., Weng R.S., Gan R.R., Hung P.,
RA Date S.V., Marcotte E., Hood L., Ng W.V.;
RT "Genome sequence of Haloarcula marismortui: a halophilic archaeon from
RT the Dead Sea.";
RL Genome Res. 14:2221-2234(2004).
CC -1- FUNCTION: Part of a binding-protein-dependent transport system.
CC Probably responsible for the translocation of the substrate across
CC the membrane (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the binding-protein-dependent transport
CC system permease family.
CC EMBL; AY596297; AAV45883.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000515; BPD transp.
DR Pfam; PF00528; BPD transp.1; 2.
DR PROSITE; PS50928; ABC_TM1; 2.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 540 AA; 57701 MW; B097B697216CDSDF CRC64;

Query Match 55.8%; Score 43; DB 2; Length 540;
Best Local Similarity 61.5%; Pred. No. 1.7e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WNFAGIEAASAI 13
|||:|||||
DB 344 WNSVGLAASAI 356

RESULT 24
Q5B2P0 EMENI
ID Q5B2P0 EMENI PRELIMINARY; PRT; 717 AA.
AC Q5B2P0;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=AN5190.2;
OS Aspergillus nidulans FGSC A4.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.

OX NCBI_TaxID=227321;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FGSC A4;
RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
RA Boukhgaiter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., Dearellano K.,
RA Diaz J.S., Dodge S., Doolley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,
RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schupback R., Seaman S., Severy P., Smirnov S.,
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talanas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
RT "Genome Sequence of Aspergillus nidulans.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AACD0100089; RAA62371.1; -; Genomic DNA.
KW Hypothetical protein.
SQ SEQUENCE 717 AA; 80113 MW; 2218A1BADB46E550 CRC64;

Query Match 55.8%; Score 43; DB 2; Length 717;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 NFAGIEAASAIQ 15
|||:|||||
DB 627 HFQIEAASMLQG 640

RESULT 25
Q870X8_NEUCR
ID Q870X8_NEUCR PRELIMINARY; PRT; 833 AA.
AC Q870X8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein 103E1.200.
GN Names=103E1.200;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Mannhaupt G.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA German Neurospora genome project;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX294028; CAD71130.1; -; Genomic DNA.
DR InterPro; IPR007111; NACHT_NTPase.
DR PROSITE; PS50837; NACHT; 1.
KW Hypothetical protein.
SQ SEQUENCE 833 AA; 93582 MW; 82BDD6118E2865A0 CRC64;

Query Match 55.8%; Score 43; DB 2; Length 833;

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KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 141 AA; 15920 MW; 9CD6F69C6C0C5BB CRC64;

Query Match 55.2%; Score 42.5; DB 2; Length 141;
Best Local Similarity 40.9%; Pred. No. 58;
Matches 9; Conservative 2; Mismatches 4; Indels 7; Gaps 1;

QY 1 WNPAGIEAASAIQ 15
DB 239 WNIQIQASNSIQ 253

RESULT 26
QSP997_ANAMM PRELIMINARY; PRT; 953 AA.
AC QSP997; 2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=AM1352;
OS Anaplasma marginale (strain St. Maries).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Anaplasmataceae; Anaplasma.
OX NCBI_TaxID=234826;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15618402; DOI=10.1073/pnas.0406656102;
RA Brayton K.A., Kapmeyer L.S., Herndon D.R., Dark M.J., Tibbals D.L.,
RA Palmer G.H., McGuire T.C., Knowles D.P., Jr.;
RT "Complete genome sequencing of Anaplasma marginale reveals that the
RT surface is skewed to two superfamilies of outer membrane proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 102:844-849(2005).
RL EMBL; CP000030; AAV87133.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 953 AA; 103400 MW; 59DD09F42C43D480 CRC64;

Query Match 55.8%; Score 43; DB 2; Length 953;
Best Local Similarity 57.1%; Pred. No. 2.8e+02;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 NFAGIEAASAIQ 15
DB 71 NFAGNPSAASVQ 84

RESULT 27
Q9HYR3_PSEAE PRELIMINARY; PRT; 141 AA.
AC Q9HYR3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=PA3332;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Huftnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Coulter L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H. Jr., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen";
RL Nature 406:959-964(2000).
RL EMBL; AB004755; AAG06720.1; -; Genomic_DNA.
DR FIK; H83229; H83229.
DR GO; GO:0017000; Antibiotic biosynthesis; IEA.
DR InterPro; IPR004964; PhzA_PhzB.
DR ProDom; PD011053; PhzA_PhzB; 1.
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KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 141 AA; 15920 MW; 9CD6F69C6C0C5BB CRC64;

Query Match 55.2%; Score 42.5; DB 2; Length 141;
Best Local Similarity 40.9%; Pred. No. 58;
Matches 9; Conservative 2; Mismatches 4; Indels 7; Gaps 1;

QY 1 WNPAGIEAASAIQ 15
DB 119 WNPFLHLEALGVERRAAKIVQ 140

RESULT 28
YI312_BIFLO
ID YI312_BIFLO STANDARD; PRT; 146 AA.
AC Q8G4R4;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Hypothetical UPF0168 protein BL1312.
GN OrderedLocusNames=BL1312;
OS Bifidobacterium longum.
OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
OC Bifidobacteriaceae; Bifidobacterium.
OX NCBI_TaxID=216816;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=NCC 2705;
RX MEDLINE=22294977; PubMed=12381787; DOI=10.1073/pnas.212527599;
RA Scheil M.A., Karimanzou M., Snel B., Vilanova D., Berger B.,
RA Pessi G., Wahlen M.-C., Desiere F., Bork P., Belley M.,
RA Pridmore R.B., Arigoni F.,
RT "The genome sequence of Bifidobacterium longum reflects its adaptation
RT to the human gastrointestinal tract.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
CC -1- SIMILARITY: Belongs to the UPF0168 family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; AB014295; AAN25112.1; ALT_INIT; Genomic_DNA.
DR HAMAP; MF 00440; -; 1.
DR InterPro; IPR005144; ATP-cone.
DR InterPro; IPR003796; DUF193.
DR Pfam; PF03477; ATP-cone; 1.
DR TIGRFAMs; TIGR00244; DUF193; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 146 AA; 16456 MW; 993F4A34C324D9DE CRC64;

Query Match 54.5%; Score 42; DB 1; Length 146;
Best Local Similarity 64.3%; Pred. No. 72;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 NFAGIEAASAIQ 15
DB 130 NFAGLEDPQSAID 143

RESULT 29
Q9Z839_CHLFP
ID Q9Z839_CHLFP PRELIMINARY; PRT; 369 AA.
AC Q9Z839; Q7A1NS; Q7DEX4;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Fe-S oxidoreductase (Hypothetical protein CP0240).
GN OrderedLocusNames=CP0240; CPY0513; CPY0513;
OS Chlamydia pneumoniae (Chlamydia pneumoniae).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83558;
```

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[1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=CWL029;
RX MEDLINE=99206606; PubMed=10192388; DOI=10.1038/7716;
RA Kalman S., Mitchell W.P., Marathe R., Lammel C.J., Fan J., Hyman R.W.,
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL Nat. Genet. 21:385-389(1999).
[2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=JL38;
RX MEDLINE=20330349; PubMed=10871362; DOI=10.1093/nar/28.12.2311;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT from Japan and CWL029 from USA";
RL Nucleic Acids Res. 28:2311-2314 (2000).
[3]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935; DOI=10.1093/nar/28.6.1397;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J.D., Utterback T.R., Berry K.J.,
RA Bass S., Linher K.D., Weidman J.F., Khouri H.M., Craven B., Bowman C.,
RA Dodson R.J., Gwinn M.L., Nelson W.C., DeBoy R.T., Kolonay J.F.,
RA McClarty G., Salzberg S.L., Eisen J.A., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
DR EMBL; AE001636; AAD18653.1; -; Genomic DNA.
DR EMBL; BA000008; BAA98719.1; -; Genomic DNA.
DR EMBL; AE002184; AAF38105.1; -; Genomic DNA.
DR PIR; E86554; E86554.
DR PIR; G72069; G72069.
DR TIGR; CP0240; -.
DR GO; GO:0003824; F: catalytic activity; IEA.
DR GO; GO:0005506; F: iron ion binding; IEA.
DR InterPro; IPR005244; Cons hypoth423.
DR InterPro; IPR006638; Elp3/MiAB/NiFB.
DR InterPro; IPR007197; Radical SAM.
DR Pfam; PF04055; Radical_SAM; 1.
DR SMART; SM00729; Elp3; 1.
DR TIGRFAMs; TIGR00423; Cons hypoth423; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 369 AA; 41556 MW; 05AC33C15479B192 CRC64;
Query Match 54.5%; Score 42; DB 2; Length 369;
Best Local Similarity 77.8%; Pred. No. 1.7e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WNFAGIEAA 9
DB 305 WNYLGIEAA 313

RESULT 30
Q7VPZ4_CHLPN
ID Q7VPZ4_CHLPN PRELIMINARY; PRT; 384 AA.
AC Q7VPZ4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=CpB0534;
OS Chlamydia pneumoniae (Chlamydiales: Chlamydiaceae; Chlamydia).
OC Bacteria; Chlamydiae; Chlamydiaceae; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83558;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=TW-183;
RA Geng M.M., Schumacher A., Muehldorfer I., Bensch K.W., Schaefer K.P.,
RA Schneider S., Pohl T., Essig A., Marre R., Melchers K.;
RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with
[1]
other Chlamydia strains based on whole genome sequence analysis.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017158; AAP98463.1; -; Genomic DNA.
DR GO; GO:0003824; F: catalytic activity; IEA.
DR GO; GO:0005506; F: iron ion binding; IEA.
DR InterPro; IPR005244; Cons hypoth423.
DR InterPro; IPR006638; Elp3/MiAB/NiFB.
DR InterPro; IPR007197; Radical SAM.
DR Pfam; PF04055; Radical_SAM; 1.
DR SMART; SM00729; Elp3; 1.
DR TIGRFAMs; TIGR00423; Cons hypoth423; 1.
KW Hypothetical protein.
SQ SEQUENCE 384 AA; 43370 MW; 30AF539371084119 CRC64;
Query Match 54.5%; Score 42; DB 2; Length 384;
Best Local Similarity 77.8%; Pred. No. 1.8e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WNFAGIEAA 9
DB 320 WNYLGIEAA 328

RESULT 31
Q518C5_ENTHI
ID Q518C5_ENTHI PRELIMINARY; PRT; 476 AA.
AC Q518C5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Amino acid transporter, putative.
DE ORFNames=49.t00031;
OS Entamoeba histolytica HM-1:IMSS.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=294381;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HM-1:IMSS;
RX PubMed=15729342; DOI=10.1038/nature03291;
RA Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
RA Anedee P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,
RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,
RA Hofer M., Bruchhaus I., Willhoest U., Bhattacharya A.,
RA Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,
RA Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,
RA Quail M.A., Rabinowitsch E., Norbertczak H., Price C., Wang Z.,
RA Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S., Lohia A.,
RA Foster P.G., Sichertitz-Ponten I., Weber C., Singh U., Mukherjee C.,
RA El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,
RA Fraser C.M., Hall N.;
RT "The genome of the protist parasite Entamoeba histolytica.";
RL Nature 433:865-868(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAFB0100201; EAL49197.1; -; Genomic DNA.
DR InterPro; IPR002293; AA/rel_permease1.
DR InterPro; IPR004841; Permease region.
DR InterPro; IPR009014; TransketO_C-like.
DR Pfam; PF0324; AA_permease; 1.
KW Transmembrane; Transport.
SQ SEQUENCE 476 AA; 53486 MW; BE56967CD3C2C64D CRC64;
Query Match 54.5%; Score 42; DB 2; Length 476;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 WNFAGIEAAATIQ 14
DB 202 WNLGVENAAVIE 215

RESULT 32
```


RA Park S.-H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,
RA Prescott A.M., Presecan E., Pujic P., Purnelle B., Rappoport G.,
RA Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,
RA Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
RA Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P.,
RA Shin B.-S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
RA Takemaru K., Takeuchi M., Tanakoshi A., Tanaka T., Terptrak P.,
RA Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,
RA Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H.,
RA Weitzenecker T., Winters P., Wipat A., Yamamoto H., Yamane K.,
RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.-F., Zumbstein E.,
RA Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*,"
RL Nature 390:249-256 (1997).
RN [4]
RP NUCLEOTIDE SEQUENCE OF 1-38.
RC STRAIN=168 / Marburg;
RX MEDLINE=93268086; PubMed=8388528;
RN Schneider R., Hantke K.;
RT "Iron-hydroxamate uptake systems in *Bacillus subtilis*: identification of a lipoprotein as part of a binding protein-dependent transport system,"
RL Mol. Microbiol. 8:111-121 (1993).
RN [4]
CC -1- FUNCTION: This is one of the proteins involved in the high-affinity transport of Fe(3+)-ferrichrome into the cell.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: Belongs to the binding-protein-dependent transport system permease family. FeCD subfamily.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC -----
CC ENBL; X93092; CAA63643.1; -; Genomic DNA.
CC ENBL; AJ223978; CAA11720.1; -; Genomic DNA.
CC ENBL; Z99121; CAB15337.1; -; Genomic DNA.
CC ENBL; M87283; -; NOT_ANNOTATED_CDS; Genomic DNA.
CC PIR; A69622; A69622.
CC HSP; P06609; IL7V.
CC Subtilisin; BG11389; fhuB.
CC InterPro; IPR000522; FeCD.
CC Pfam; PF01032; FeCD; 1.
CC Complete proteome; Iron; Iron transport; Transmembrane; Transport.
CC TRANSMEM 58 78 Potential.
CC TRANSMEM 115 135 Potential.
CC TRANSMEM 154 174 Potential.
CC TRANSMEM 176 196 Potential.
CC TRANSMEM 202 222 Potential.
CC TRANSMEM 243 263 Potential.
CC TRANSMEM 296 316 Potential.
CC TRANSMEM 330 350 Potential.
CC TRANSMEM 357 377 Potential.
CC SEQUENCE 384 AA; 40720 MW; 7E4D75CAB36AB8FB CRC64;
KW Complete proteome; Iron; Iron transport; Transmembrane; Transport.
FT TRANSMEM 58 78 Potential.
FT TRANSMEM 115 135 Potential.
FT TRANSMEM 154 174 Potential.
FT TRANSMEM 176 196 Potential.
FT TRANSMEM 202 222 Potential.
FT TRANSMEM 243 263 Potential.
FT TRANSMEM 296 316 Potential.
FT TRANSMEM 330 350 Potential.
FT TRANSMEM 357 377 Potential.
SQ SEQUENCE 384 AA; 40720 MW; 7E4D75CAB36AB8FB CRC64;
Query Match 53.2%; Score 41; DB 1; Length 384;
Best Local Similarity 46.7%; Pred. No. 2.6e+02;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 1 WNFAGIEAASATG 15
DB 174 WSPAGAGLGASTVWG 188
RESULT 35
DGTLL BRAJA STANDARD; PRT; 402 AA.
AC Q89KZ0;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Deoxyguanosinetriphosphate triphosphohydrolase-like protein.
GN OrderedLocusNames=bl14758;
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=USDA 110;
RX MEDLINE=22484998; PubMed=12597275;
RN Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiyama T.,
RA Sasanoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimpō S., Teurouka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium *Bradyrhizobium japonicum* USDA110,"
RL DNA Res. 9:189-197 (2002).
CC -1- SIMILARITY: Belongs to the dGTPase family. Type 2 subfamily.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC -----
CC ENBL; BA000040; BAC50023.1; -; Genomic DNA.
CC HAMAP; MF 01212; -; 1.
CC InterPro; IPR006261; dGTP_triP_hydro.
CC InterPro; IPR006674; HD_hydro.
CC InterPro; IPR003607; Met_phos_hydro.
CC Pfam; PF01966; HD; 1.
CC SMART; SM00471; HDc; 1.
CC TIGRFAMs; TIGR01353; dGTP_triPase; 1.
CC Complete proteome; Hydrolase; Hypothetical protein.
KW Complete proteome; Hydrolase; Hypothetical protein.
SQ SEQUENCE 402 AA; 44975 MW; 670D43D2D357F4D2 CRC64;
Query Match 53.2%; Score 41; DB 1; Length 402;
Best Local Similarity 53.8%; Pred. No. 2.7e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 WNFAGIEAASAI 13
DB 198 WSPASLEAQVAAI 210
RESULT 36
Q6NSW5 RHOPA PRELIMINARY; PRT; 404 AA.
AC Q6NSW5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE DGTTP triphosphohydrolase.
GN OrderedLocusNames=RPA2855;
OS Rhodopseudomonas palustris.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Rhodopseudomonas.
OX NCBI_TaxID=1076;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CGA009 / ATCC BAA-98;
RX PubMed=14704707; DOI=10.1038/nbt923;
RN Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,
RA Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
RA Gibson J.L., Hanson T.E., Bobst C., Torres Y., Torres J.L., Peres C.,
RA Harrison F.H., Gibson J., Harwood C.S.;
RT "Complete genome sequence of the metabolically versatile photosynthetic bacterium *Rhodopseudomonas palustris*,"
RL Nat. Biotechnol. 22:55-61 (2004).
RL ENBL; BX572602; CAE28296.1; -; Genomic DNA.
DR GO; GO:0008832; F:dGTPase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.

```

DR GO:0046039; P:GTP metabolism; IEA.
DR InterPro: IPR000923; BlueCu.1.
DR InterPro: IPR006261; dgtp_trip_hydro.
DR InterPro: IPR006674; HD_hydro_hydro.
DR InterPro: IPR003607; Met_phos_hydro.
DR Pfam: PF01966; HD; 1.
DR SMART: SM00471; HDc; 1.
DR TIGRFAMs: TIGR01353; dgtp_tripase; 1.
DR PROSITE: PS00196; COPPER_BLUE; UNKNOWN_1.
KW Complete proteome; Hydrolase.
SQ SEQUENCE 404 AA; 45370 MW; 8806F1D7528E2216 CRC64;

Query Match 53.2%; Score 41; DB 2; Length 404;
Best Local Similarity 53.8%; Pred. No. 2.8e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAI 13
   |:| |:| |:| |:|
DB 198 WSPASLEAQVAI 210

RESULT 37
ID Q9FAD1 MORJA PRELIMINARY; PRT; 440 AA.
AC Q9FAD1.
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE CagB.
GN Name=cagB;
OS Moritella japonica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Moritellaceae; Moritella.
OX NCBI_TaxID=89067;
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=D8K1;
RA Li L., Fujii S., Kato C., Koki H.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AB041735; BAB16717.1; -; Genomic DNA.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005279; P:amino acid-polyamine transporter activity; IEA.
DR GO: GO:0006865; P:amino acid transport; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR002293; AA/rel_permease1.
DR Pfam: PF00324; AA_permease_1.
KW Transmembrane; Transport.
SQ SEQUENCE 440 AA; 45577 MW; D8DE4CADF8958CD9 CRC64;

Query Match 53.2%; Score 41; DB 2; Length 440;
Best Local Similarity 60.0%; Pred. No. 3e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 WNFAGIEAAA 10
   |:| |:| |:| |:|
DB 199 WSVFVGESAA 208

RESULT 38
ID Q9AMK7 VIBVU PRELIMINARY; PRT; 443 AA.
AC Q9AMK7.
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Cadaverine/lysine antiporter.
GN Name=cadB;
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=672;

DR GO:0046039; P:GTP metabolism; IEA.
DR InterPro: IPR000923; BlueCu.1.
DR InterPro: IPR006261; dgtp_trip_hydro.
DR InterPro: IPR006674; HD_hydro_hydro.
DR InterPro: IPR003607; Met_phos_hydro.
DR Pfam: PF01966; HD; 1.
DR SMART: SM00471; HDc; 1.
DR TIGRFAMs: TIGR01353; dgtp_tripase; 1.
DR PROSITE: PS00196; COPPER_BLUE; UNKNOWN_1.
KW Complete proteome; Hydrolase.
SQ SEQUENCE 404 AA; 45370 MW; 8806F1D7528E2216 CRC64;

Query Match 53.2%; Score 41; DB 2; Length 404;
Best Local Similarity 53.8%; Pred. No. 2.8e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAI 13
   |:| |:| |:| |:|
DB 198 WSPASLEAQVAI 210

RESULT 37
ID Q9FAD1 MORJA PRELIMINARY; PRT; 440 AA.
AC Q9FAD1.
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE CagB.
GN Name=cagB;
OS Moritella japonica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Moritellaceae; Moritella.
OX NCBI_TaxID=89067;
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=D8K1;
RA Li L., Fujii S., Kato C., Koki H.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AB041735; BAB16717.1; -; Genomic DNA.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005279; P:amino acid-polyamine transporter activity; IEA.
DR GO: GO:0006865; P:amino acid transport; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR002293; AA/rel_permease1.
DR Pfam: PF00324; AA_permease_1.
KW Transmembrane; Transport.
SQ SEQUENCE 440 AA; 45577 MW; D8DE4CADF8958CD9 CRC64;

Query Match 53.2%; Score 41; DB 2; Length 440;
Best Local Similarity 60.0%; Pred. No. 3e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 WNFAGIEAAA 10
   |:| |:| |:| |:|
DB 199 WSVFVGESAA 208

RESULT 38
ID Q9AMK7 VIBVU PRELIMINARY; PRT; 443 AA.
AC Q9AMK7.
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Cadaverine/lysine antiporter.
GN Name=cadB;
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=672;

DR GO:0046039; P:GTP metabolism; IEA.
DR InterPro: IPR000923; BlueCu.1.
DR InterPro: IPR006261; dgtp_trip_hydro.
DR InterPro: IPR006674; HD_hydro_hydro.
DR InterPro: IPR003607; Met_phos_hydro.
DR Pfam: PF01966; HD; 1.
DR SMART: SM00471; HDc; 1.
DR TIGRFAMs: TIGR01353; dgtp_tripase; 1.
DR PROSITE: PS00196; COPPER_BLUE; UNKNOWN_1.
KW Complete proteome; Hydrolase.
SQ SEQUENCE 404 AA; 45370 MW; 8806F1D7528E2216 CRC64;

Query Match 53.2%; Score 41; DB 2; Length 443;
Best Local Similarity 60.0%; Pred. No. 3e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 WNFAGIEAAA 10
   |:| |:| |:| |:|
DB 199 WSVFVGESAA 208

RESULT 39
ID Q9E343 VIBF1 PRELIMINARY; PRT; 444 AA.
AC Q9E343.
DT 10-MAY-2005 (T-EMBLrel. 30, Created)
DT 10-MAY-2005 (T-EMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (T-EMBLrel. 30, Last annotation update)
DE Cadaverine/lysine antiporter.
GN OrderedLocusNames=VF2058;
OS Vibrio fischeri (strain ATCC 700601 / ES114).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=312309;
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP PubMed=15703294; DOI=10.1073/pnas.040990102;
RA Ruby E.G., Urbanowski M., Campbell J., Dunn A., Paine M., Gunsalus R.,
RA Lestrich P., Lupp C., McCann J., Millikan D., Schaefer A., Stabb E.,
RA Stevens A., Visick K., Whistler C., Greenberg E.P.;
RT "Complete genome sequence of Vibrio fischeri: a symbiotic bacterium
   with pathogenic congeners."
RT Proc. Natl. Acad. Sci. U.S.A. 102:3004-3009(2005).
RL EMBL; CP000020; AAW86553.1; -; Genomic DNA.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005279; P:amino acid-polyamine transporter activity; IEA.
DR GO: GO:0006865; P:amino acid transport; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR002293; AA/rel_permease1.
DR Pfam: PF00324; AA_permease_1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 444 AA; 46393 MW; 3A3073C0E26ED4BA CRC64;

Query Match 53.2%; Score 41; DB 2; Length 444;
Best Local Similarity 60.0%; Pred. No. 3e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 WNFAGIEAAA 10
   |:| |:| |:| |:|
DB 199 WSVFVGESAA 208

RESULT 40
ID Q8DAX6 VIBVU PRELIMINARY; PRT; 445 AA.
AC Q8DAX6.

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DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cadaverine/lysine antiporter.
GN OrderedLocusNames=VV12059;
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=672;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CMCP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA Choy H.E.;
RT "Complete genome sequence of Vibrio vulnificus CMCP6.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR ENBL; AE016803; AA010448.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/rel_permease1.
DR InterPro; IPR004841; Permease region.
DR Pfam; PF00324; AA_permease; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 445 AA; 46856 MW; 358CA9B01FC7CFA9 CRC64;

Query Match 53.2%; Score 41; DB 2; Length 445;
Best Local Similarity 60.0%; Pred. No. 3e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 WNFAGIEAAA 10
|:| |:|
Db 199 WSPFVGESAA 208

RESULT 41
Q9KV76 VIBCH
ID Q9KV76 VIBCH PRELIMINARY; PRT; 445 AA.
AC Q9KV76;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cadaverine/lysine antiporter CadB, putative.
GN OrderedLocusNames=VC0280;
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=El Tor N1691 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301; DOI=10.1038/35020000;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.L.,
RA Ermolaeva M.D., Vamathevan J.J., Bass S., Qin H., Dragoi I.,
RA Sellers P., McDonald L.A., Utterback T.R., Fleischmann R.D.,
RA Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R.,
RA Mekalanos J.J., Venter J.C., Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae";
RL Nature 406:477-483(2000).
DR ENBL; AE004116; AAF93455.1; -; Genomic DNA.
DR PIR; D82342; D82342.
DR TIGR; VC0280; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/rel_permease1.

DR InterPro; IPR004841; Permease region.
DR Pfam; PF00324; AA_permease; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 445 AA; 46908 MW; 3A64F21B9680684C CRC64;

Query Match 53.2%; Score 41; DB 2; Length 445;
Best Local Similarity 60.0%; Pred. No. 3e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 WNFAGIEAAA 10
|:| |:|
Db 199 WSPFVGESAA 208

RESULT 42
Q75VK9 VIBPA
ID Q75VK9 VIBPA PRELIMINARY; PRT; 447 AA.
AC Q75VK9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Lysine:cadaverine antiporter.
GN Name=cadB;
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=V02-64;
RA Tanaka Y., Kimura B., Watanabe T., Iwase K., Fujii T.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR ENBL; AB124819; BAD12082.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/rel_permease1.
DR InterPro; IPR004841; Permease region.
DR Pfam; PF00324; AA_permease; 1.
KW Transmembrane; Transport.
SQ SEQUENCE 447 AA; 47082 MW; 1A4E14027C225903 CRC64;

Query Match 53.2%; Score 41; DB 2; Length 447;
Best Local Similarity 60.0%; Pred. No. 3e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 WNFAGIEAAA 10
|:| |:|
Db 199 WSPFVGESAA 208

RESULT 43
Q87KT5 VIBPA
ID Q87KT5 VIBPA PRELIMINARY; PRT; 447 AA.
AC Q87KT5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Putative cadaverine/lysine antiporter CadB (lysine:cadaverine
DE antiporter).
GN Name=cadB; OrderedLocusNames=VP2891;
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=RIMD 2210633 / Serotype O3:k6;
RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,

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RA Yaenaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RL distinct from that of V. cholerae.";
RN Lancet 361:743-749 (2003).
[2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=Vp +11;
RA Kimura B., Tanaka Y., Iwase K., Fujii T.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BA000031; BAC61154.1; -; Genomic DNA.
DR EMBL; AB089504; BAC77061.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; P:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/rel permease1.
DR InterPro; IPR004841; Permease_region.
DR Pfam; PF00324; AA_permease_1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 447 AA; 47070 MW; 359CE2DB780866F0 CRC64;

Query Match 53.2%; Score 41; DB 2; Length 447;
Best Local Similarity 60.0%; Pred. No. 3e+02; 1; Indels 0; Gaps 0;
Matches 6; Conservative 3; Mismatches 1;

QY 1 WNFAGIEAAA 10
DB 199 WSPVGVESAA 208

RESULT 44
Q7MIY1 VIBVY PRELIMINARY; PRT; 452 AA.
AC Q7MIY1;
DT 01-MAR-2004 (T-EMBLrel. 26, Created)
DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Cadaverine/lysine antiporter.
DE OrderedLocuNames=VW2382;
GN Vibrio vulnificus (strain VJ016).
OS Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=196600;
[1]
RN NUCLEOTIDE SEQUENCE.
RX PubMed=14656965; DOI=10.1101/gr.1295503;
RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
RA Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,
RA Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;
RT "Comparative genome analysis of Vibrio vulnificus, a marine
RL pathogen.";
RL Genome Res. 13:2577-2587 (2003).
DR EMBL; BA000037; BAC95146.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; P:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/rel permease1.
DR InterPro; IPR004841; Permease_region.
DR Pfam; PF00324; AA_permease_1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 452 AA; 47628 MW; 5552E3796HC2E7A CRC64;

Query Match 53.2%; Score 41; DB 2; Length 452;
Best Local Similarity 60.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 WNFAGIEAAA 10
DB 206 WSPVGVESAA 215

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RESULT 45
Q82D65 STRAW PRELIMINARY; PRT; 463 AA.
AC Q82D65;
DT 01-JUN-2003 (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Putative nitrate extrusion protein.
GN Name=nark; OrderedLocuNames=SAV5119;
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=NA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22608306; PubMed=12692562; DOI=10.1038/nbt820;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531 (2003).
[2]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=NA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horioka H., Nakazawa H., Osone T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220 (2001).
DR EMBL; BA000030; BAC72831.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0015103; P:inorganic anion transporter activity; IEA.
DR GO; GO:0015698; P:inorganic anion transport; IEA.
DR InterPro; IPR011701; MFS_1.
DR InterPro; IPR004737; NO3_transporter.
DR Pfam; PF07690; MFS_1; 1.
DR TIGRFAMs; TIGR00886; 2A0108; 1.
KW Complete proteome.
SQ SEQUENCE 463 AA; 48642 MW; BB5636A5899DBDB8 CRC64;

Query Match 53.2%; Score 41; DB 2; Length 463;
Best Local Similarity 53.8%; Pred. No. 3.1e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 WNFAGIEAASAI 13
DB 311 WNPVGMGAATGVI 323

RESULT 46
Q562K7 LACRE PRELIMINARY; PRT; 465 AA.
AC Q562K7;
DT 10-MAY-2005 (T-EMBLrel. 30, Created)
DT 10-MAY-2005 (T-EMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (T-EMBLrel. 30, Last annotation update)
DE Putative arginine/ornithine antiporter.
GN ORFNames=1:0531;
OS Lactobacillus reuteri.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1598;
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 55730;
RA Roos S., Jonsson H.;
RT "The draft genome sequence of Lactobacillus reuteri ATCC 55730.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AY970978; AAX82597.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; P:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
KW Transmembrane; Transport.
SQ SEQUENCE 465 AA; 50586 MW; BE8785DA40634561 CRC64;

Query Match 53.2%; Score 41; DB 2; Length 465;
Best Local Similarity 72.2%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAI 11
DB 209 WCFVGIEAAVS 219

RESULT 47
Q62AX2 BURMA
ID Q62AX2 BURMA PRELIMINARY; PRT; 494 AA.
AC Q62AX2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Phosphate transporter family protein.
GN OrderedLocusNames=BMAA1572;
OS Burkholderia mallei (Pseudomonas mallei).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=13373;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=ATCC 23344;
RX PubMed=15377793; DOI=10.1073/pnas.040306101;
RA Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
RA Feldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M.,
RA Daugherty S.C., Davidse T.D., DeBoy R.T., Dimitrov G., Dodson R.J.,
RA Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F.,
RA Madupu R., Mohammud Y., Nelson W.C., Radune D., Romero C.M.,
RA Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y.,
RA Zafar N., Zhou L., Fraser C.M.;
RT "Structural flexibility in the Burkholderia mallei genome.";
Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).
DR EMBL; CP000011; AAU45811.1; -; Genomic DNA.
DR TIGR; BMAA1572; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005315; F:inorganic phosphate transporter activity; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR001204; Phos_transporter.
DR PANTHER; PTHR11101; Phos_Transporter; 1.
DR Pfam; PF01384; PHO4; 1.
KW Complete proteome.
SQ SEQUENCE 494 AA; 51838 MW; 51BE9BEC4A5AAB5 CRC64;

Query Match 53.2%; Score 41; DB 2; Length 494;
Best Local Similarity 46.2%; Pred. No. 3.3e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAI 13
DB 67 WNFVGWASTGAV 79

RESULT 48
Q63K00 BURPS
ID Q63K00 BURPS PRELIMINARY; PRT; 528 AA.
AC Q63K00;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Probable phosphate transporter.
GN OrderedLocusNames=BPS81566;

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OS Burkholderia pseudomallei (Pseudomonas pseudomallei).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; pseudomallei group.
OX NCBI_TaxID=28450;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=K96243;
RX PubMed=15377794; DOI=10.1073/pnas.04033020101;
RA Holden M.T.G., Titball R.W., Peacock S.J., Cerdano-Tarraga A.-M.,
RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.L.,
RA Bentley S.D., Sebahia M., Thomson N.R., Bason N., Beacham I.R.,
RA Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
RA Chillingworth T., Cronin A., Crossett B., Davis P., Deshazer D.,
RA Fellwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA Rabinowitsch E., Rutherford K., Sanders M., Simmonds M.,
RA Songvilai S., Stevens K., Tumapa S., Vesaratchaveit M.,
RA Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
RT "Genomic plasticity of the causative agent of melioidosis,
RT Burkholderia pseudomallei.";
Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
DR EMBL; BX571966; CAH39039.1; -; Genomic DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005315; F:inorganic phosphate transporter activity; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR001204; Phos_transporter.
DR PANTHER; PTHR11101; Phos_transporter; 1.
DR Pfam; PF01384; PHO4; 1.
KW Complete proteome.
SQ SEQUENCE 528 AA; 55203 MW; 4ADDD89F4BAF084 CRC64;

Query Match 53.2%; Score 41; DB 2; Length 528;
Best Local Similarity 46.2%; Pred. No. 3.5e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAI 13
DB 101 WNFVGWASTGAV 113

RESULT 49
Q9CGX6 LACIA
ID Q9CGX6 LACIA PRELIMINARY; PRT; 540 AA.
AC Q9CGX6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE ABC transporter permease protein.
GN NamesyJJD; OrderedLocusNames=L40966;
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=IL1403;
RX MEDLINE=21235186; PubMed=11337471; DOI=10.1101/gr-1697R;
RA Bolotin A., Wincker P., Manger S., Jaillon O., Malarne K.,
RA Weisenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis ssp. lactis IL1403.";
RL Genome Res. 11:731-753(2001).
DR EMBL; AE006331; AAK05064.1; -; Genomic DNA.
DR PIR; F86745; F86745.
KW Complete proteome.
SQ SEQUENCE 540 AA; 60283 MW; E896CF783987560E CRC64;

Query Match 53.2%; Score 41; DB 2; Length 540;
Best Local Similarity 69.2%; Pred. No. 3.6e+02;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 FAGIEAAASAIQ 15
DB 339 FVGNETAASAIRG 351

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RESULT 50
QSW116_BACSK PRELIMINARY; PRT; 751 AA.
AC QSW116;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DE Beta-glucosidase (EC 3.2.1.21).
GN OrderedLocusNames=ABC1454;
OS Bacillus clausii (strain KSM-K16).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=66692;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=KSM-K16;
RA Takai Y., Kageyama Y., Shimamura S., Suzuki H., Nishi S., Hatada Y.,
RA Kawai S., Ito S., Horikoshi K.;
RT "The complete genome sequence of the alkaliphilic Bacillus clausii
RT KSM-K16.";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP006627; BAD3989.1; -; Genomic DNA.
DR GO; GO:0008422; F:beta-glucosidase activity; IEA.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0030245; P:cellulose catabolism; IEA.
DR GO; GO:0000272; P:polysaccharide catabolism; IEA.
DR InterPro; IPR002772; Glyco_hydro_3C.
DR InterPro; IPR001764; Glyco_hydro_3N.
DR Pfam; PF00933; Glyco_hydro_3; 1.
DR Pfam; PF01915; Glyco_hydro_3_C; 1.
DR PRINTS; PR00133; GLHYDRIASE3.
DR PROSITE; PS00775; GLYCOSYL HYDROL F3; 1.
KW Complete proteome; Glycosidase; Hydrolase.
SQ SEQUENCE 751 AA; 83450 MW; C62B2203E5CD1CE5 CRC64;

Query Match 53.2%; Score 41; DB 2; Length 751;
Best Local Similarity 72.7%; Pred. No. 4.9e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WNFAGIERAAS 11
Db 109 WNFESIEYRAAS 119

Search completed: May 4, 2006, 15:17:03
Job time : 201 secs

GenCore version 5.1.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 15:18:01 ; Search time 33 Seconds
(without alignments)
37.580 Million cell updates/sec

Title: US-09-830-839-6

Perfect score: 77

Sequence: 1 WNFAGTAAASAIQ 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	77	100.0	51	2	US-08-818-112-104
2	77	100.0	51	2	US-08-818-111-99
3	77	100.0	51	2	US-09-056-556-104
4	77	100.0	51	2	US-09-072-596-99
5	77	100.0	51	2	US-09-072-967-104
6	77	100.0	51	2	US-10-193-002-99
7	77	100.0	51	2	US-10-084-843-104
8	77	100.0	95	1	US-08-465-640-2
9	77	100.0	403	2	US-09-050-739-173
10	77	100.0	404	2	US-09-050-739-172
11	42.5	55.2	556	2	US-09-252-991A-17793
12	42	54.5	116	2	US-09-302-540-13488
13	42	54.5	409	2	US-09-198-452A-554
14	42	54.5	413	2	US-09-438-185A-515
15	41	53.2	149	2	US-09-634-238-265
16	41	53.2	282	2	US-09-724-623-113
17	40	51.9	2293	2	US-09-368-590-2
18	40	51.9	2600	2	US-09-949-016-7309
19	39	50.6	221	2	US-09-904-615-155
20	39	50.6	221	2	US-10-054-988-155
21	39	50.6	413	2	US-09-252-991A-29788
22	39	50.6	1138	2	US-09-489-039A-13574
23	38	49.4	185	2	US-09-489-039A-11336
24	38	49.4	349	2	US-09-489-039A-13578
25	38	49.4	365	2	US-09-252-991A-30166
26	38	49.4	366	2	US-09-830-807-35
27	38	49.4	418	2	US-09-202-893B-4

28	49.4	435	2	US-09-252-991A-23220	Sequence 23220, A
29	48.1	153	2	US-09-909-474D-9	Sequence 9, Appl
30	48.1	209	2	US-09-252-991A-24013	Sequence 24013, A
31	48.1	360	2	US-09-509-902A-9	Sequence 9, Appl
32	48.1	360	2	US-10-024-828-9	Sequence 9, Appl
33	48.1	360	2	US-09-909-474D-11	Sequence 11, Appl
34	48.1	360	2	US-09-902-540-15461	Sequence 15461, A
35	48.1	475	2	US-09-252-991A-20838	Sequence 20838, A
36	48.1	551	2	US-09-026-400A-4	Sequence 4, Appl
37	48.1	898	2	US-09-902-540-11561	Sequence 11561, A
38	48.1	947	2	US-09-252-991A-21335	Sequence 21335, A
39	48.1	981	2	US-09-902-540-9848	Sequence 9848, Ap
40	48.1	1138	2	US-09-252-991A-25952	Sequence 25952, A
41	48.1	1223	2	US-09-538-092-777	Sequence 777, App
42	46.8	294	2	US-09-489-039A-10933	Sequence 10933, A
43	46.8	323	2	US-09-489-039A-13907	Sequence 13907, A
44	46.8	328	2	US-09-489-039A-10986	Sequence 10986, A
45	46.8	368	2	US-09-489-039A-13753	Sequence 13753, A
46	46.8	389	2	US-09-489-039A-8540	Sequence 8540, Ap
47	46.8	429	2	US-09-134-000C-3817	Sequence 3817, Ap
48	46.8	483	2	US-09-489-039A-13018	Sequence 13018, A
49	46.8	578	2	US-09-949-016-9799	Sequence 9799, Ap
50	46.8	582	2	US-09-477-962-94	Sequence 94, Appl
51	46.8	630	2	US-09-248-796A-25512	Sequence 25512, A
52	46.8	759	2	US-09-902-540-18161	Sequence 16161, A
53	46.8	1534	2	US-09-543-681A-5182	Sequence 5182, Ap
54	46.8	3413	2	US-10-042-665A-8	Sequence 8, Appl
55	46.1	467	2	US-09-252-991A-29729	Sequence 29729, A
56	45.5	29	1	US-08-482-142-11	Sequence 11, Appl
57	45.5	29	1	US-08-482-142-74	Sequence 74, Appl
58	45.5	29	1	US-08-478-572-11	Sequence 11, Appl
59	45.5	29	1	US-08-478-572-74	Sequence 74, Appl
60	45.5	29	2	US-08-484-296-11	Sequence 11, Appl
61	45.5	29	2	US-08-484-296-74	Sequence 74, Appl
62	45.5	29	4	PCT-US95-04481-3	Sequence 3, Appl
63	45.5	47	2	US-09-902-540-15443	Sequence 15443, A
64	45.5	80	2	US-09-513-999C-4148	Sequence 4148, Ap
65	45.5	94	2	US-09-513-999C-4135	Sequence 4135, Ap
66	45.5	94	2	US-09-513-999C-4146	Sequence 4146, Ap
67	45.5	97	2	US-09-513-999C-4149	Sequence 4149, Ap
68	45.5	99	2	US-09-513-999C-4127	Sequence 4127, Ap
69	45.5	99	2	US-09-513-999C-4136	Sequence 4136, Ap
70	45.5	99	2	US-09-513-999C-4147	Sequence 4147, Ap
71	45.5	102	2	US-09-513-999C-4128	Sequence 4128, Ap
72	45.5	103	2	US-09-513-999C-4152	Sequence 4152, Ap
73	45.5	103	2	US-09-513-999C-4142	Sequence 4142, Ap
74	45.5	104	2	US-09-513-999C-4137	Sequence 4137, Ap
75	45.5	106	2	US-09-513-999C-7803	Sequence 7803, Ap
76	45.5	107	2	US-09-513-999C-7804	Sequence 7804, Ap
77	45.5	107	2	US-09-513-999C-7805	Sequence 7805, Ap
78	45.5	115	2	US-09-513-999C-4132	Sequence 4132, Ap
79	45.5	116	2	US-09-513-999C-4131	Sequence 4131, Ap
80	45.5	117	2	US-09-042-353-232	Sequence 232, App
81	45.5	117	2	US-08-758-417A-80	Sequence 80, Appl
82	45.5	121	2	US-09-513-999C-4130	Sequence 4130, Ap
83	45.5	121	2	US-09-513-999C-4140	Sequence 4140, Ap
84	45.5	121	2	US-09-513-999C-4144	Sequence 4144, Ap
85	45.5	126	2	US-09-513-999C-4134	Sequence 4134, Ap
86	45.5	126	2	US-09-513-999C-4138	Sequence 4138, Ap
87	45.5	126	2	US-09-513-999C-4150	Sequence 4150, Ap
88	45.5	129	2	US-09-513-999C-4133	Sequence 4133, Ap
89	45.5	129	2	US-09-513-999C-4139	Sequence 4139, Ap
90	45.5	129	2	US-09-513-999C-4151	Sequence 4151, Ap
91	45.5	133	2	US-09-471-276-885	Sequence 885, App
92	45.5	142	2	US-09-270-767-39080	Sequence 39080, A
93	45.5	142	2	US-09-270-767-54297	Sequence 54297, A
94	45.5	142	2	US-09-513-999C-4141	Sequence 4141, Ap
95	45.5	142	2	US-09-513-999C-4145	Sequence 4145, Ap
96	45.5	142	2	US-09-471-276-872	Sequence 872, App
97	45.5	143	2	US-09-513-999C-4129	Sequence 4129, Ap
98	45.5	159	2	US-09-347-803-18	Sequence 18, Appl
99	45.5	222	1	US-07-945-288-11	Sequence 11, Appl
100	45.5	222	1	US-08-462-831-11	Sequence 11, Appl

101	35	45.5	222	1	US-08-461-809-11	Sequence 11, Appl	174	34	44.2	67	1	US-08-208-887A-37	Sequence 37, Appl
102	35	45.5	222	1	US-08-461-441-11	Sequence 11, Appl	175	34	44.2	67	1	US-08-539-005-37	Sequence 37, Appl
103	35	45.5	222	4	PCT-US93-08518-11	Sequence 11, Appl	176	34	44.2	67	2	US-09-280-598-57	Sequence 57, Appl
104	35	45.5	245	1	US-07-945-888-2	Sequence 2, Appl	177	34	44.2	89	2	US-09-583-110-4570	Sequence 4570, Ap
105	35	45.5	245	1	US-08-462-831-2	Sequence 2, Appl	178	34	44.2	92	2	US-09-489-039A-7604	Sequence 7604, Ap
106	35	45.5	245	1	US-08-461-809-2	Sequence 2, Appl	179	34	44.2	121	2	US-09-252-991A-22007	Sequence 22007, A
107	35	45.5	245	1	US-08-461-441-2	Sequence 2, Appl	180	34	44.2	133	2	US-09-732-210-539	Sequence 539, App
108	35	45.5	245	1	US-08-482-142-2	Sequence 2, Appl	181	34	44.2	148	2	US-08-818-111-65	Sequence 64, Appl
109	35	45.5	245	1	US-08-482-142-2	Sequence 2, Appl	182	34	44.2	148	2	US-09-056-536-64	Sequence 65, Appl
110	35	45.5	245	2	US-08-460-040-2	Sequence 2, Appl	183	34	44.2	148	2	US-09-072-967-64	Sequence 64, Appl
111	35	45.5	245	2	US-08-484-296-2	Sequence 2, Appl	184	34	44.2	148	2	US-10-193-002-65	Sequence 65, Appl
112	35	45.5	245	4	PCT-US93-08518-2	Sequence 180, App	185	34	44.2	148	2	US-10-084-843-64	Sequence 64, Appl
113	35	45.5	281	2	US-09-302-626B-180	Sequence 58, Appl	186	34	44.2	162	2	US-09-050-739-6	Sequence 35, Appl
114	35	45.5	319	2	US-09-302-626B-58	Sequence 14554, A	187	34	44.2	170	1	US-08-477-451-35	Sequence 11620, A
115	35	45.5	320	1	US-07-945-288-10	Sequence 10, Appl	189	34	44.2	188	2	US-09-107-433-3365	Sequence 13977, A
116	35	45.5	320	1	US-08-462-831-10	Sequence 10, Appl	190	34	44.2	202	2	US-09-489-039A-13977	Sequence 12, Appl
117	35	45.5	320	1	US-08-461-809-10	Sequence 10, Appl	191	34	44.2	225	2	US-10-010-160-12	Sequence 6, Appl
118	35	45.5	320	1	US-08-461-441-10	Sequence 10, Appl	192	34	44.2	237	2	US-09-522-714-6	Sequence 17083, A
119	35	45.5	320	4	PCT-US93-08518-10	Sequence 6, Appl	193	34	44.2	251	2	US-09-252-991A-17083	Sequence 3, Appl
120	35	45.5	320	1	US-08-462-831-6	Sequence 6, Appl	194	34	44.2	297	2	US-08-660-645A-3	Sequence 3, Appl
121	35	45.5	321	1	US-08-461-809-6	Sequence 6, Appl	195	34	44.2	303	2	US-09-298-718-3	Sequence 3, Appl
122	35	45.5	321	1	US-08-482-142-6	Sequence 6, Appl	196	34	44.2	303	2	US-09-546-969-3	Sequence 3, Appl
123	35	45.5	321	1	US-08-482-142-6	Sequence 6, Appl	197	34	44.2	303	2	US-08-980-832-3	Sequence 3, Appl
124	35	45.5	321	1	US-08-478-572-6	Sequence 6, Appl	198	34	44.2	303	2	US-09-328-352-8214	Sequence 8214, Ap
125	35	45.5	321	1	US-08-484-296-6	Sequence 6, Appl	199	34	44.2	303	2	US-09-547-267-3	Sequence 3, Appl
126	35	45.5	321	4	PCT-US93-08518-6	Sequence 17672, A	200	34	44.2	303	2	US-09-920-923B-3	Sequence 3, Appl
127	35	45.5	321	4	US-09-252-991A-17672	Sequence 178, App	201	34	44.2	303	2	US-09-252-991A-17617	Sequence 14280, A
128	35	45.5	353	2	US-09-302-626B-178	Sequence 6344, Ap	202	34	44.2	314	2	US-09-902-540-14280	Sequence 20511, A
129	35	45.5	353	2	US-09-543-681A-6344	Sequence 19674, A	203	34	44.2	344	2	US-09-232-991A-20511	Sequence 692, App
130	35	45.5	384	2	US-09-252-991A-19674	Sequence 7574, Ap	204	34	44.2	344	2	US-09-830-230A-692	Sequence 9639, Ap
131	35	45.5	394	2	US-09-489-039A-7574	Sequence 5536, Ap	205	34	44.2	344	2	US-09-252-991A-28255	Sequence 28255, A
132	35	45.5	405	2	US-09-134-001C-5536	Sequence 30013, A	206	34	44.2	331	2	US-09-830-230A-691	Sequence 691, App
133	35	45.5	423	2	US-09-252-991A-30013	Sequence 1642, Ap	207	34	44.2	337	2	US-08-382-505-2	Sequence 16462, A
134	35	45.5	454	2	US-09-605-703B-1642	Sequence 10, Appl	208	34	44.2	359	2	US-10-104-047-2482	Sequence 2482, Ap
135	35	45.5	473	2	US-08-378-939-10	Sequence 31662, A	209	34	44.2	385	1	US-09-902-540-14180	Sequence 14180, A
136	35	45.5	476	1	US-09-252-991A-31662	Sequence 21509, A	210	34	44.2	417	2	US-09-604-231-2	Sequence 2, Appl
137	35	45.5	481	2	US-09-252-991A-21509	Sequence 8062, Ap	211	34	44.2	466	2	US-09-107-532A-6868	Sequence 6868, Ap
138	35	45.5	495	2	US-09-949-016-8062	Sequence 183, App	212	34	44.2	478	2	US-09-252-991A-25447	Sequence 25447, A
139	35	45.5	504	2	US-08-926-842B-19	Sequence 30945, A	213	34	44.2	481	2	US-09-252-991A-17979	Sequence 17979, A
140	35	45.5	569	2	US-09-302-626B-19	Sequence 16877, A	214	34	44.2	492	2	US-09-107-532A-6945	Sequence 6945, Ap
141	35	45.5	628	2	US-09-252-991A-30945	Sequence 4174, Ap	215	34	44.2	505	2	US-08-993-260-1	Sequence 1, Appl
142	35	45.5	744	2	US-09-252-991A-16877	Sequence 4, Appl	216	34	44.2	511	2	US-09-991-677-4	Sequence 6, Appl
143	35	45.5	749	2	US-10-041-007-33	Sequence 33, Appl	217	34	44.2	514	2	US-09-564-808-6	Sequence 6, Appl
144	35	45.5	847	2	US-08-627-873-7	Sequence 2, Appl	218	34	44.2	520	2	US-09-091-432-2	Sequence 2, Appl
145	35	45.5	873	2	US-08-853-310-2	Sequence 7, Appl	219	34	44.2	520	2	US-09-387-663-2	Sequence 2, Appl
146	35	45.5	903	1	US-09-270-767-43656	Sequence 43656, A	220	34	44.2	520	2	US-09-564-808-2	Sequence 4, Appl
147	35	45.5	915	2	US-08-627-873-7	Sequence 7, Appl	221	34	44.2	520	2	US-09-214-139B-4	Sequence 405, App
148	35	45.5	1056	1	US-08-347-878-5	Sequence 84, Appl	222	34	44.2	529	2	US-09-615-192A-405	Sequence 7330, Ap
149	35	45.5	1265	2	US-08-980-326-2	Sequence 84, Appl	223	34	44.2	531	2	US-09-489-039A-7330	Sequence 13044, A
150	35	45.5	1265	2	US-08-469-260A-84	Sequence 84, Appl	224	34	44.2	531	2	Sequence 1084, Ap	
151	35	45.5	1265	2	US-08-488-446-84	Sequence 84, Appl	225	34	44.2	537	2	Sequence 25, Appl	
152	35	45.5	1265	2	US-08-424-550B-84	Sequence 62, Appl	226	34	44.2	616	2	Sequence 32, Appl	
153	35	45.5	1265	2	US-09-302-626B-62	Sequence 84, Appl	227	34	44.2	616	2	Sequence 38, Appl	
154	35	45.5	1265	2	US-08-687-956A-23	Sequence 23, Appl	228	34	44.2	646	2	Sequence 43, Appl	
155	35	45.5	1566	1	US-09-302-626B-179	Sequence 179, App	229	34	44.2	646	2	Sequence 47, Appl	
156	35	45.5	1574	2	US-09-302-626B-179	Sequence 12643, A	230	34	44.2	646	2	Sequence 25, Appl	
157	35	45.5	1858	2	US-09-302-626B-60	Sequence 60, Appl	231	34	44.2	646	2	Sequence 32, Appl	
158	35	45.5	3079	4	PCT-US94-00198-4	Sequence 4, Appl	232	34	44.2	646	2	Sequence 38, Appl	
159	35	45.5	3079	2	US-08-005-232-492	Sequence 492, App	233	34	44.2	646	2	Sequence 43, Appl	
160	35	45.5	3079	2	US-08-252-991A-22676	Sequence 22676, A	234	34	44.2	646	2	Sequence 25, Appl	
161	35	45.5	650	2	US-10-104-047-3636	Sequence 3636, Ap	235	34	44.2	646	2	Sequence 32, Appl	
162	35	45.5	650	2	US-08-119-361-12	Sequence 12, Appl	236	34	44.2	646	2	Sequence 47, Appl	
163	35	45.5	14	1	US-08-336-308A-12	Sequence 12, Appl	237	34	44.2	646	2	Sequence 25, Appl	
164	35	45.5	14	2	US-09-490-931-12	Sequence 12, Appl	238	34	44.2	646	2	Sequence 38, Appl	
165	35	45.5	14	2	US-08-849-634B-8	Sequence 8, Appl	239	34	44.2	646	2	Sequence 47, Appl	
166	35	45.5	14	2	US-09-513-999C-4143	Sequence 4143, Ap	240	34	44.2	646	2	Sequence 32, Appl	
167	35	45.5	58	2	US-08-167-035-37	Sequence 37, Appl	241	34	44.2	646	2	Sequence 43, Appl	
168	35	45.5	67	1			242	34	44.2	646	2	Sequence 25, Appl	
169	35	45.5	67	1			243	34	44.2	646	2	Sequence 32, Appl	
170	35	45.5	67	1			244	34	44.2	646	2	Sequence 47, Appl	
171	35	45.5	67	1			245	34	44.2	646	2	Sequence 25, Appl	
172	35	45.5	67	1			246	34	44.2	646	2	Sequence 38, Appl	
173	35	45.5	67	1			246	34	44.2	646	2	Sequence 43, Appl	

247	34	44.2	646	2	US-09-232-195-25	Sequence 25, Appl	320	33	42.9	474	1	US-08-907-706-6	Sequence 6, Appli
248	34	44.2	646	2	US-09-232-195-32	Sequence 32, Appl	321	33	42.9	485	2	US-09-198-452A-1105	Sequence 1105, Ap
249	34	44.2	646	2	US-09-232-195-38	Sequence 38, Appl	322	33	42.9	486	2	US-10-142-231-92	Sequence 92, Appl
250	34	44.2	646	2	US-09-232-195-43	Sequence 43, Appl	323	33	42.9	490	2	US-09-438-185A-1032	Sequence 1032, Ap
251	34	44.2	646	2	US-09-232-195-47	Sequence 47, Appl	324	33	42.9	493	2	US-09-252-991A-25746	Sequence 25746, A
252	34	44.2	661	2	US-10-019-284B-2	Sequence 2, Appli	325	33	42.9	496	2	US-09-134-001C-3001	Sequence 3001, Ap
253	34	44.2	716	2	US-09-107-532A-5208	Sequence 5208, Ap	326	33	42.9	499	2	US-09-252-991A-23328	Sequence 23328, A
254	34	44.2	895	2	US-09-489-039A-7893	Sequence 7893, Ap	327	33	42.9	503	2	US-09-252-991A-23643	Sequence 23643, A
255	34	44.2	904	2	US-09-543-681A-4485	Sequence 4485, Ap	328	33	42.9	506	2	US-09-252-991A-18165	Sequence 18165, A
256	34	44.2	927	2	US-09-328-352-7922	Sequence 7922, Ap	329	33	42.9	556	2	US-09-902-540-12461	Sequence 12461, A
257	34	44.2	981	2	US-09-252-991A-16798	Sequence 16798, A	330	33	42.9	560	2	US-09-489-039A-12127	Sequence 12127, A
258	34	44.2	1024	2	US-09-562-737-42	Sequence 42, Appl	331	33	42.9	564	2	US-09-543-681A-5271	Sequence 5271, Ap
259	34	44.2	1732	1	US-08-477-451-14	Sequence 14, Appl	332	33	42.9	566	2	US-10-104-047-2407	Sequence 2407, Ap
260	33.5	43.5	409	2	US-09-587-066-2	Sequence 2, Appli	333	33	42.9	571	2	US-09-999-833A-132	Sequence 132, App
261	33	42.9	63	2	US-09-042-012-9	Sequence 9, Appli	334	33	42.9	571	2	US-10-020-445A-132	Sequence 132, App
262	33	42.9	63	2	US-09-042-012-11	Sequence 11, Appl	335	33	42.9	573	2	US-09-134-000C-6366	Sequence 6366, Ap
263	33	42.9	63	2	US-09-457-324-9	Sequence 9, Appli	336	33	42.9	582	2	US-09-270-767-45532	Sequence 45532, A
264	33	42.9	63	2	US-09-457-324-11	Sequence 11, Appl	337	33	42.9	594	2	US-09-134-000C-5007	Sequence 5007, Ap
265	33	42.9	64	2	US-09-042-012-7	Sequence 7, Appli	338	33	42.9	629	2	US-09-248-796A-19256	Sequence 19256, A
266	33	42.9	64	2	US-09-305-086-1	Sequence 1, Appli	339	33	42.9	633	2	US-09-252-991A-26576	Sequence 26576, A
267	33	42.9	64	2	US-09-457-324-7	Sequence 7, Appli	340	33	42.9	636	2	US-08-737-752A-2	Sequence 2, Appli
268	33	42.9	64	2	US-09-923-317-1	Sequence 1, Appli	341	33	42.9	636	2	US-09-807-063-5	Sequence 5, Appli
269	33	42.9	97	2	US-09-270-767-61917	Sequence 61917, A	342	33	42.9	636	2	US-09-843-007A-2	Sequence 2, Appli
270	33	42.9	98	2	US-09-902-540-10092	Sequence 10092, A	343	33	42.9	643	2	US-09-949-016-10023	Sequence 10023, A
271	33	42.9	118	2	US-09-830-807-41	Sequence 41, Appl	344	33	42.9	658	1	US-08-409-995-5	Sequence 5, Appli
272	33	42.9	121	2	US-09-902-540-10943	Sequence 10943, A	345	33	42.9	658	2	US-08-685-467-5	Sequence 5, Appli
273	33	42.9	129	2	US-09-902-540-10504	Sequence 10504, A	346	33	42.9	658	2	US-08-913-943-5	Sequence 5, Appli
274	33	42.9	169	2	US-09-489-039A-9006	Sequence 9006, Ap	347	33	42.9	658	2	US-09-684-707-5	Sequence 5, Appli
275	33	42.9	174	2	US-09-489-039A-10976	Sequence 10976, A	348	33	42.9	666	2	US-09-252-991A-19748	Sequence 19748, A
276	33	42.9	176	1	US-08-449-922-1	Sequence 1, Appli	349	33	42.9	725	2	US-10-118-328-5	Sequence 5, Appli
277	33	42.9	178	2	US-09-107-532A-6775	Sequence 6775, Ap	350	33	42.9	734	2	US-09-252-991A-33036	Sequence 33036, A
278	33	42.9	188	1	US-08-726-306A-57	Sequence 57, Appl	351	33	42.9	753	2	US-09-270-767-46781	Sequence 46781, A
279	33	42.9	232	2	US-09-605-703B-1472	Sequence 1472, Ap	352	33	42.9	768	1	US-08-408-519-2	Sequence 2, Appli
280	33	42.9	232	2	US-09-270-767-59452	Sequence 59452, A	353	33	42.9	782	2	PCT-US95-03552-2	Sequence 2, Appli
281	33	42.9	232	2	US-09-270-767-61265	Sequence 61265, A	354	33	42.9	865	2	US-09-949-016-11571	Sequence 11571, A
282	33	42.9	247	2	US-09-270-767-46348	Sequence 46348, A	355	33	42.9	865	2	US-09-252-991A-19339	Sequence 19339, A
283	33	42.9	257	2	US-09-540-236-3506	Sequence 3506, Ap	356	33	42.9	869	2	US-10-104-047-2532	Sequence 2532, Ap
284	33	42.9	268	2	US-09-710-279-1830	Sequence 1830, Ap	357	33	42.9	901	2	US-09-710-279-342	Sequence 342, App
285	33	42.9	273	2	US-09-134-001C-3917	Sequence 3917, Ap	358	33	42.9	914	2	US-09-134-001C-5208	Sequence 5208, Ap
286	33	42.9	273	2	US-09-902-540-13834	Sequence 13834, A	359	33	42.9	1098	1	US-08-409-995-2	Sequence 2, Appli
287	33	42.9	291	2	US-09-758-759-184	Sequence 184, App	360	33	42.9	1098	2	US-08-685-467-2	Sequence 2, Appli
288	33	42.9	302	2	US-08-311-731A-331	Sequence 331, App	361	33	42.9	1098	2	US-09-377-155-32	Sequence 32, Appl
289	33	42.9	312	2	US-09-252-991A-29965	Sequence 29965, A	362	33	42.9	1098	2	US-08-913-942-2	Sequence 2, Appli
290	33	42.9	312	2	US-09-134-000C-6207	Sequence 6207, Ap	363	33	42.9	1098	2	US-09-669-974-32	Sequence 32, Appl
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292	33	42.9	315	1	US-08-257-392-1	Sequence 1, Appli	365	33	42.9	1098	2	US-09-797-862-32	Sequence 32, Appl
293	33	42.9	315	2	US-08-770-035-1	Sequence 1, Appli	366	33	42.9	1098	2	US-09-684-707-2	Sequence 2, Appli
294	33	42.9	338	2	US-09-580-929-4	Sequence 4, Appli	367	33	42.9	1146	2	US-09-270-767-45747	Sequence 45747, A
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298	33	42.9	348	4	US-09-489-039A-10674	Sequence 2, Appli	371	33	42.9	1220	2	US-09-902-540-13967	Sequence 13967, A
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305	33	42.9	381	2	US-09-107-433-3123	Sequence 3123, Ap	378	33	42.9	4968	2	US-09-424-783-5	Sequence 4927, Ap
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311	33	42.9	418	2	US-09-543-681A-7634	Sequence 7634, Ap	384	32.5	42.2	442	2	US-09-828-062-7	Sequence 20060, A
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313	33	42.9	448	2	US-09-328-352-5694	Sequence 5694, Ap	386	32.5	42.2	1284	2	US-09-170-496D-294	Sequence 59, Appl
314	33	42.9	453	2	US-09-583-110-3842	Sequence 3842, Ap	387	32.5	42.2	1284	2	US-09-364-425B-59	Sequence 77, Appl
315	33	42.9	459	2	US-09-328-352-4648	Sequence 4648, Ap	388	32	41.6	10	2	US-09-001-984C-77	Sequence 77, Appl
316	33	42.9	461	2	US-09-107-433-3722	Sequence 3722, Ap	389	32	41.6	10	2	US-09-396-347F-77	Sequence 920, App
317	33	42.9	463	2	US-09-252-991A-26534	Sequence 26534, A	390	32	41.6	46	2	US-09-471-276-920	Sequence 4973, Ap
318	33	42.9	466	2	US-09-605-703B-2816	Sequence 2816, Ap	391	32	41.6	61	2	US-09-513-999C-4973	Sequence 8945, Ap
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397	32	41.6	127	2	US-08-467-023-189	Sequence 189, App	470
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469	32	41.6	422	2	US-09-368-431-18	Sequence 18, Appl	542
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497	32	41.6	511	2	US-09-438-185A-475	Sequence 475, App	570
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523	32	41.6	699	2	US-09-808-701A-34	Sequence 34, Appl	596
524	32	41.6	709	2	US-10-118-328-4	Sequence 4, Appli	597
525	32	41.6	710	2	US-09-287-849-16	Sequence 16, Appl	598
526	32	41.6	710	2	US-10-118-328-2	Sequence 2, Appli	599
527	32	41.6	715	2	US-09-808-701A-33	Sequence 33, Appl	600
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535	32	41.6	913	2	US-09-107-532A-4267	Sequence 4267, Ap	608
536	32	41.6	919	2	US-09-543-681A-7187	Sequence 7187, Ap	609
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545	32	41.6	1940	1	US-08-644-271-30	Sequence 30, Appl	618	31	40.3	223	2	US-08-778-717-4	Sequence 4, Appli
546	32	41.6	1940	2	US-09-077-955-34	Sequence 34, Appl	619	31	40.3	229	2	US-09-252-991A-27823	Sequence 27823, A
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551	32	41.6	2618	2	US-09-413-814-28	Sequence 28, Appl	624	31	40.3	243	2	US-09-978-248A-9	Sequence 9, Appli
552	31.5	40.9	93	2	US-09-543-681A-6152	Sequence 6152, Ap	625	31	40.3	251	2	US-09-252-991A-20606	Sequence 20606, A
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563	31	40.3	20	2	US-08-476-501-38	Sequence 38, Appl	636	31	40.3	278	2	US-09-252-991A-16859	Sequence 16859, A
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565	31	40.3	25	1	US-08-700-846-10	Sequence 10, Appl	638	31	40.3	280	2	US-09-583-110-3709	Sequence 3709, Ap
566	31	40.3	26	1	US-08-634-060-26	Sequence 26, Appl	639	31	40.3	282	1	US-08-324-301-15	Sequence 15, Appl
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864	31	40.3	893	2	US-09-489-039A-14127	Sequence 14127, A	937	30.5	39.6	1374	2	US-09-771-161A-267	Sequence 267, App
865	31	40.3	913	2	US-09-252-991A-22127	Sequence 22127, A	938	30.5	39.6	1375	2	US-09-171-410-1	Sequence 1, Appli
866	31	40.3	917	2	US-09-902-540-15387	Sequence 15387, A	939	30.5	39.6	2629	1	US-08-751-189-4	Sequence 4, Appli
867	31	40.3	926	2	US-09-489-039A-13928	Sequence 13928, A	940	30.5	39.6	2629	1	US-09-060-836-4	Sequence 4, Appli
868	31	40.3	935	2	US-09-134-000C-6493	Sequence 6493, Ap	941	30.5	39.6	2629	2	US-09-184-445-4	Sequence 4, Appli
869	31	40.3	951	2	US-09-252-991A-23338	Sequence 23338, A	942	30.5	39.6	2639	2	US-09-080-983-3	Sequence 3, Appli
870	31	40.3	968	1	US-08-426-236-2	Sequence 2, Appli	943	30.5	39.6	2639	2	US-09-613-486-3	Sequence 3, Appli
871	31	40.3	971	1	US-08-724-354D-22	Sequence 22, Appl	944	30	39.0	39	6	5187077-25	Patent No. 5187077
872	31	40.3	971	2	US-09-720-984A-22	Sequence 22, Appl	945	30	39.0	69	2	US-09-328-352-5556	Sequence 5556, Ap
873	31	40.3	971	2	US-09-177-431-8	Sequence 8, Appli	946	30	39.0	70	2	US-09-270-767-58773	Sequence 58773, A
874	31	40.3	977	2	US-09-134-000C-5653	Sequence 5653, Ap	947	30	39.0	78	2	US-09-270-767-43496	Sequence 43496, A
875	31	40.3	982	2	US-09-252-991A-27095	Sequence 27095, A	948	30	39.0	81	2	US-10-290-579A-241	Sequence 241, App
876	31	40.3	993	2	US-09-538-092-1100	Sequence 1100, Ap	949	30	39.0	82	2	US-09-228-986-85	Sequence 85, Appl
877	31	40.3	993	2	US-09-949-002-332	Sequence 332, App	950	30	39.0	82	2	US-10-101-464A-85	Sequence 85, Appl
878	31	40.3	1000	2	US-09-949-002-484	Sequence 484, App	951	30	39.0	87	2	US-09-270-767-37992	Sequence 37992, A
879	31	40.3	1004	2	US-09-949-016-9925	Sequence 9925, Ap	952	30	39.0	87	2	US-09-270-767-53209	Sequence 53209, A
880	31	40.3	1027	2	US-09-710-279-3106	Sequence 3106, Ap	953	30	39.0	97	2	US-09-270-767-42326	Sequence 42326, A
881	31	40.3	1040	2	US-09-328-352-7238	Sequence 7238, Ap	954	30	39.0	100	2	US-09-621-976-5460	Sequence 5460, Ap
882	31	40.3	1094	2	US-09-268-347-32	Sequence 32, Appl	955	30	39.0	100	2	US-09-513-999C-5026	Sequence 5026, Ap
883	31	40.3	1179	2	US-09-949-016-7088	Sequence 7088, Ap	956	30	39.0	101	2	US-09-543-681A-4289	Sequence 4289, Ap
884	31	40.3	1234	1	US-08-317-310A-15	Sequence 15, Appl	957	30	39.0	101	2	US-09-492-709A-333	Sequence 333, App
885	31	40.3	1234	4	PCT-US95-13041-15	Sequence 15, Appl	958	30	39.0	103	2	US-09-543-681A-7839	Sequence 7839, Ap
886	31	40.3	1242	2	US-09-508-691-1	Sequence 1, Appli	959	30	39.0	114	2	US-09-489-039A-8747	Sequence 8747, Ap
887	31	40.3	1242	2	US-09-903-248-5	Sequence 5, Appli	960	30	39.0	116	2	US-09-489-039A-9295	Sequence 9295, Ap
888	31	40.3	1242	2	US-09-903-199-5	Sequence 5, Appli	961	30	39.0	123	2	US-09-270-767-34741	Sequence 34741, A
889	31	40.3	1242	2	US-09-903-216-5	Sequence 5, Appli	962	30	39.0	123	2	US-09-270-767-49558	Sequence 49558, A
890	31	40.3	1242	2	US-09-903-063-5	Sequence 5, Appli	963	30	39.0	129	2	US-09-270-767-31736	Sequence 31736, A
891	31	40.3	1242	2	US-09-859-604-5	Sequence 5, Appli	964	30	39.0	137	2	US-10-268-883-8	Sequence 8, Appli
892	31	40.3	1243	1	US-08-557-139-2	Sequence 2, Appli	965	30	39.0	138	2	US-10-268-883-2	Sequence 2, Appli
893	31	40.3	1243	2	US-09-376-330-15	Sequence 15, Appl	966	30	39.0	140	2	US-08-569-147-76	Sequence 76, Appl
894	31	40.3	1564	2	US-09-976-594-309	Sequence 309, App	967	30	39.0	141	2	US-09-583-110-5284	Sequence 5284, Ap
895	31	40.3	1650	2	US-09-252-991A-21798	Sequence 21798, A	968	30	39.0	147	1	US-08-217-918-4	Sequence 4, Appli
896	31	40.3	1765	2	US-09-270-767-45587	Sequence 45587, A	969	30	39.0	151	2	US-09-521-511C-9	Sequence 9, Appli
897	31	40.3	1844	2	US-08-851-567B-53	Sequence 53, Appl	970	30	39.0	157	2	US-09-489-039A-11147	Sequence 11147, A
898	31	40.3	2291	1	US-08-286-819A-29	Sequence 29, Appl	971	30	39.0	161	2	US-09-902-540-14869	Sequence 14869, A
899	31	40.3	2291	2	US-08-980-357-29	Sequence 29, Appl	972	30	39.0	166	2	US-09-252-991A-28518	Sequence 28518, A
900	31	40.3	2291	2	US-09-357-375-29	Sequence 29, Appl	973	30	39.0	166	2	US-09-328-352-5696	Sequence 5696, Ap
901	31	40.3	2504	2	US-08-851-567B-12	Sequence 12, Appl	974	30	39.0	166	2	US-09-797-464A-5	Sequence 5, Appli
902	31	40.3	2504	2	US-09-817-514A-8	Sequence 8, Appli	975	30	39.0	166	2	US-09-902-540-16507	Sequence 16507, A
903	31	40.3	4302	2	US-08-658-136-5	Sequence 5, Appli	976	30	39.0	174	2	US-09-797-464A-9	Sequence 9, Appli

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991 30 39.0 199 2 US-09-270-767-43423
992 30 39.0 201 2 US-09-543-681A-6084
993 30 39.0 201 2 US-09-107-433-2998
994 30 39.0 208 1 US-07-661-610C-5
995 30 39.0 209 2 US-09-685-166A-897
996 30 39.0 209 2 US-09-759-143-897
997 30 39.0 209 2 US-10-012-896-897
998 30 39.0 212 2 US-09-252-991A-17649
999 30 39.0 212 2 US-09-905-666A-55
1000 30 39.0 212 2 US-09-905-666A-57

ALIGNMENTS

RESULT 1
US-08-818-112-104
; Sequence 104, Application US/08818112
; Patent No. 6290969
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Houghton, Raymond
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Twardzik, Daniel R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/818,112
; FILING DATE: 13-MAR-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.411C6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-818-112-104

Query Match 100.0%; Score 77; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAIQG 15
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DB 6 WNFAGIEAAASAIQG 20
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RESULT 2

US-08-818-111-99
; Sequence 99, Application US/08818111
; Patent No. 6338852
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Houghton, Raymond
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Twardzik, Daniel R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
; TUBERCULOSIS
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/818,111
; FILING DATE: 13-MAR-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.417C6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-818-111-99

Query Match 100.0%; Score 77; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAIQG 15
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DB 6 WNFAGIEAAASAIQG 20
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RESULT 3

US-09-056-556-104
; Sequence 104, Application US/09056556
; Patent No. 6350456
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.

/ TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND
/ NUMBER OF SEQUENCES: 241
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: SEED and BERRY LLP
/ STREET: 6300 Columbia Center, 701 Fifth Avenue
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: USA
/ ZIP: 98104-7092
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/056,556
/ FILING DATE: 07-APR-1998
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Maki, David J.
/ REGISTRATION NUMBER: 31,392
/ REFERENCE/DOCKET NUMBER: 210121.457
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 104:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 51 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-09-056-556-104

Query Match 100.0%; Score 77; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNPAGIEAAASAIQG 15
Db 6 WNPAGIEAAASAIQG 20

RESULT 4
US-09-072-596-99
/ Sequence 99, Application US/09072596
/ Patent No. 6458366
/ GENERAL INFORMATION:
/ APPLICANT: Reed, Steven G.
/ APPLICANT: Skeiky, Yasir A.W.
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Campos-Neto, Antonia
/ APPLICANT: Houghton, Raymond
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Twardzik, Daniel R.
/ APPLICANT: Lodes, Michael J.
/ APPLICANT: Hendrickson, Ronald C.
/ TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
/ NUMBER OF SEQUENCES: 350
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: SEED and BERRY LLP
/ STREET: 6300 Columbia Center, 701 Fifth Avenue
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: USA
/ ZIP: 98104-7092
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/072,596
/ FILING DATE: 05-MAY-1998

/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Maki, David J.
/ REGISTRATION NUMBER: 31,392
/ REFERENCE/DOCKET NUMBER: 210121.417C9
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 99:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 51 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-09-072-596-99

Query Match 100.0%; Score 77; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNPAGIEAAASAIQG 15
Db 6 WNPAGIEAAASAIQG 20

RESULT 5
US-09-072-967-104
/ Sequence 104, Application US/09072967
/ Patent No. 6592877
/ GENERAL INFORMATION:
/ APPLICANT: Reed, Steven G.
/ APPLICANT: Skeiky, Yasir A.W.
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Campos-Neto, Antonio
/ APPLICANT: Houghton, Raymond
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Twardzik, Daniel R.
/ APPLICANT: Lodes, Michael J.
/ APPLICANT: Hendrickson, Ronald C.
/ TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
/ NUMBER OF SEQUENCES: 355
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: SEED and BERRY LLP
/ STREET: 6300 Columbia Center, 701 Fifth Avenue
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: USA
/ ZIP: 98104-7092
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/072,967
/ FILING DATE: 05-MAY-1998
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Maki, David J.
/ REGISTRATION NUMBER: 31,392
/ REFERENCE/DOCKET NUMBER: 210121.411C9
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 104:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 51 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-09-072-967-104

Query Match 100.0%; Score 77; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.7e-06; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY 1 WNPAGIEAASAIQG 15
Db 6 WNPAGIEAASAIQG 20

RESULT 6

US-10-193-002-99
; Sequence 99, Application US/10193002
; Patent No. 6949246

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, David C.
Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
TUBERCULOSIS
NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-Jul-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 99:

US-10-193-002-99

Query Match 100.0%; Score 77; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.7e-06; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY 1 WNPAGIEAASAIQG 15
Db 6 WNPAGIEAASAIQG 20

RESULT 7

US-10-084-843-104
; Sequence 104, Application US/10084843

Patent No. 6962710
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, David C.
Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 104:

US-10-084-843-104

Query Match 100.0%; Score 77; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.7e-06; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY 1 WNPAGIEAASAIQG 15
Db 6 WNPAGIEAASAIQG 20

RESULT 8

US-08-465-640-2
; Sequence 2, Application US/08465640
; Patent No. 5955077

GENERAL INFORMATION:

APPLICANT: ANDERSEN, Peter
APPLICANT: ANDERSEN, Ase Bengaard
APPLICANT: HASLOV, Kaare
APPLICANT: SORENSEN, Anne Lund
TITLE OF INVENTION: TUBERCULOSIS VACCINE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington

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1 FILE REFERENCE: 670001-2002.1
2 CURRENT APPLICATION NUMBER: US/09/050.739
3 CURRENT FILING DATE: 1998-03-30
4 EARLIER APPLICATION NUMBER: 0376/97
5 EARLIER FILING DATE: 1997-04-02
6 EARLIER APPLICATION NUMBER: 1277/97
7 EARLIER FILING DATE: 1997-11-10
8 EARLIER APPLICATION NUMBER: 60/044.624
9 EARLIER FILING DATE: 1997-04-18
10 EARLIER APPLICATION NUMBER: 60/070.488
11 EARLIER FILING DATE: 1998-01-05

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; EARLIER FILING DATE: 1997-04-18
 ; EARLIER APPLICATION NUMBER: 60/070,488
 ; EARLIER FILING DATE: 1998-01-05

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 172
; LENGTH: 404

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Query Match	100.0%	Score 77;	DB 2;	Length 404;
Best Local Similarity	100.0%;	Pred. No. 1.9e-05;		
Matches 15;	Conservative 0;	Mismatches 0;	Indels	

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Db      315 WNFAGIENASATQG 329
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RESULT 11
US-09-252-991A-17793
; Sequence 17793, Application US/09252991A
; Patent NO. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMIN
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNO
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17793
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

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US-09-252-991A-17793
; Sequence 17793, Application US/09252991A

```

/ GENERAL INFORMATION:
/ APPLICANT: Marc J. Rubenfield et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RE
/ TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUT
/ FILE REFERENCE: 107196.136
/ CURRENT APPLICATION NUMBER: US/09/252,991A
/ CURRENT FILING DATE: 1999-02-18
/ PRIOR APPLICATION NUMBER: US 60/074,788
/ PRIOR FILING DATE: 1998-02-18
/ PRIOR APPLICATION NUMBER: US 60/094,190
/ PRIOR FILING DATE: 1998-07-27
/ NUMBER OF SEQ ID NOS: 33142
/ SEQ ID NO 17793
/ LENGTH: 556
/ TYPE: PRT
/ ORGANISM: Pseudomonas aeruginosa

```

```
US-09-252-991A-17793
Query Match      55.2%; Score 42.5; DB 2; Length 556;
Best Local Similarity 40.9%; Pred. No. 32;
Matches 9; Conservative 2; Mismatches 4; Indels 7; Gaps 1;

QY 1 WN-----FAGIEAASAIQ 15
    |||:||||:|
Db 534 WNPRLHLEALGVEAAKIVQ 555

RESULT 12
US-09-902-540-13488
; Sequence 13488, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 13488
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-13488

Query Match      54.5%; Score 42; DB 2; Length 116;
Best Local Similarity 50.0%; Pred. No. 6.3;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 WNFAGIEAASAIQ 14
    |||:||||:|
Db 37 WNTGLEALEAAVQ 50

RESULT 13
US-09-198-452A-554
; Sequence 554, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 554
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-554

Query Match      54.5%; Score 42; DB 2; Length 409;
Best Local Similarity 77.8%; Pred. No. 28;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WNFAGIEAA 9
    |||:||||:|
Db 345 WNYLGIEAA 353

RESULT 14
US-09-438-185A-515
; Sequence 515, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kalman, Sue
; APPLICANT: Davis, Ronald
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 515
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: CPn0513
US-09-438-185A-515

Query Match      54.5%; Score 42; DB 2; Length 413;
Best Local Similarity 77.8%; Pred. No. 28;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WNFAGIEAA 9
    |||:||||:|
Db 349 WNYLGIEAA 357

RESULT 15
US-09-634-238-265
; Sequence 265, Application US/09634238
; Patent No. 6544772
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Havukkala, Ilkka J.
; APPLICANT: Bloksberg, Leonard, N.
; APPLICANT: Lubbers, Mark W.
; APPLICANT: Dekker, James
; APPLICANT: Christenson, Anna C.
; APPLICANT: Holland, Ross
; APPLICANT: O'Toole, Paul W.
; APPLICANT: Reid, Julian R.
; APPLICANT: Coolbear, Timothy
; TITLE OF INVENTION: Polynucleotides, materials incorporating them and methods for using them.
; TITLE OF INVENTION: them and methods for using them.
; FILE REFERENCE: 11000.1043U1
; CURRENT APPLICATION NUMBER: US/09/634,238
; CURRENT FILING DATE: 2000-08-08
; NUMBER OF SEQ ID NOS: 422
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 265
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Lactobacillus rhamnosus
US-09-634-238-265

Query Match      53.2%; Score 41; DB 2; Length 149;
Best Local Similarity 57.1%; Pred. No. 13;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 NFAGIEAASAIQ 15
    |||:||||:|
Db 67 NIAGVEAAQGLFG 80

RESULT 16
US-09-724-623-113
```

; Sequence 113, Application US/09724623
; Patent No. 6476209
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Lubbers, Mark W
; APPLICANT: Dekker, James
; TITLE OF INVENTION: Polynucleotides, materials incorporating
; TITLE OF INVENTION: them, and methods for using them.
; FILE REFERENCE: 1048U1
; CURRENT APPLICATION NUMBER: US/09/724,623
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Lactobacillus rhamnosus
US-09-724-623-113

Query Match 53.2%; Score 41; DB 2; Length 282;
Best Local Similarity 57.1%; Pred. No. 27;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 NFAGIEAAASAIQ 15
| : : : : :
Db 191 NIAGVEAAQGLFG 204

RESULT 17
US-09-368-590-2
; Sequence 2, Application US/09368590
; Patent No. 6187563
; GENERAL INFORMATION:
; APPLICANT: Solimena, Michele
; TITLE OF INVENTION: INTERACTING POLYPEPTIDES FOR
; TITLE OF INVENTION: AUTOANTIGENS OF AUTOIMMUNE DISEASES
; FILE REFERENCE: 101918-200 (OCR-941)
; CURRENT APPLICATION NUMBER: US/09/368,590
; CURRENT FILING DATE: 1999-08-04
; EARLIER APPLICATION NUMBER: 60/095,657
; EARLIER FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 2293
; TYPE: PRT
; ORGANISM: Human
US-09-368-590-2

Query Match 51.9%; Score 40; DB 2; Length 2293;
Best Local Similarity 42.9%; Pred. No. 4.6e+02;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAIQ 14
| : : : : :
Db 720 WRLSGLEAAALQALE 733

RESULT 18
US-09-949-016-7309
; Sequence 7309, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7309
; LENGTH: 2600
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7309

Query Match 51.9%; Score 40; DB 2; Length 2600;
Best Local Similarity 42.9%; Pred. No. 5.4e+02;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAIQ 14
| : : : : :
Db 1058 WRLSGLEAAALQALE 1071

RESULT 19
US-09-904-615-155
; Sequence 155, Application US/09904615
; Patent No. 6566325
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 49 Human Secreted Proteins
; FILE REFERENCE: P2032P1
; CURRENT APPLICATION NUMBER: US/09/904,615
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/511,554
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/097,917
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: 60/098,634
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 155
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-615-155

Query Match 50.6%; Score 39; DB 2; Length 221;
Best Local Similarity 57.1%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAIQ 14
| : : : : :
Db 132 WNLGDEAAALQALE 145

RESULT 20
US-10-054-988-155
; Sequence 155, Application US/10054988
; Patent No. 6953667
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 49 Human Secreted Proteins
; FILE REFERENCE: P2032P1
; CURRENT APPLICATION NUMBER: US/10/054,988
; CURRENT FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: 09/904,615
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/511,554
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/097,917
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: 60/098,634
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 155

```

; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
Us-10-054-988-155

Query Match      50.6%; Score 39; DB 2; Length 221;
Best Local Similarity 57.1%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      1 WNFAGIEAAASAIQ 14
Db      132 WNLGDEAAAEALQ 145

RESULT 21
US-09-252-991A-29788
; Sequence 29788, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29788
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29788

Query Match      50.6%; Score 39; DB 2; Length 413;
Best Local Similarity 66.7%; Pred. No. 94;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      4 AGIEAAASAIQ 15
Db      202 AGIESAAEVLG 213

RESULT 22
US-09-489-039A-13574
; Sequence 13574, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13574
; LENGTH: 1138
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13574

Query Match      50.6%; Score 39; DB 2; Length 1138;
Best Local Similarity 42.9%; Pred. No. 3.1e+02;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy      1 WNFAGIEAAASAIQ 14
Db      843 WHYNGTEAGASVVR 856

RESULT 23
US-09-489-039A-111336
; Sequence 11336, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11336
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-111336

Query Match      49.4%; Score 38; DB 2; Length 185;
Best Local Similarity 46.7%; Pred. No. 55;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy      1 WNFAGIEAAASAIQ 15
Db      122 WNTVYLERAAHALRG 136

RESULT 24
US-09-489-039A-13578
; Sequence 13578, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13578
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13578

Query Match      49.4%; Score 38; DB 2; Length 349;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 WNFAGIEAAA 10
Db      243 WAFVGVESAA 252

RESULT 25
US-09-252-991A-30166
; Sequence 30166, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
```

; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30166
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30166

Query Match 49.4%; Score 38; DB 2; Length 365;
Best Local Similarity 46.2%; Pred. No. 1.2e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 WNFAGIEAAASAI 13
|:|:|:|:
Db 286 WSARGVEVGASV 298

RESULT 26
US-09-830-807-35
; Sequence 35, Application US/09830807
; Patent No. 6846667
; GENERAL INFORMATION:
; APPLICANT: Crooke, Helen R.
; APPLICANT: Clarke, Enda E.
; APPLICANT: Everest, Paul H.
; APPLICANT: Dougan, Gordon
; APPLICANT: Holden, David W.
; APPLICANT: Shea, Jacqueline E.
; APPLICANT: Feldman, Robert G.
; TITLE OF INVENTION: VIRULENCE GENES AND PROTEINS, AND THEIR USE
; FILE REFERENCE: GJE-65
; CURRENT APPLICATION NUMBER: US/09/830,807
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-830-807-35

Query Match 49.4%; Score 38; DB 2; Length 366;
Best Local Similarity 63.6%; Pred. No. 1.2e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GIEAASAIQ 15
|:|:|:|:
Db 6 GIOAATAAQ 16

RESULT 27
US-09-202-893B-4
; Sequence 4, Application US/09202893B
; Patent No. 6319692
; GENERAL INFORMATION:
; APPLICANT: KADOTA, Mariko
; APPLICANT: KIWAKI, Mayumi
; APPLICANT: SAWAKI, Saeko
; APPLICANT: SHIRASAWA, Yukiko
; APPLICANT: SONE, Harue
; APPLICANT: SAKO, Tomoyuki
; TITLE OF INVENTION: METHODS FOR TRANSFERRING GENE INTO CHROMOSOME
; FILE REFERENCE: 980794/HG
; CURRENT APPLICATION NUMBER: US/09/202,893B
; CURRENT FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/JP97/02187
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: JP 8/184266
; PRIOR FILING DATE: 1996-06-26
; PRIOR APPLICATION NUMBER: JP 8/257764
; PRIOR FILING DATE: 1996-09-06
; NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 4

; LENGTH: 418
; TYPE: PRT
; ORGANISM: Lactobacillus casei
US-09-202-893B-4

Query Match 49.4%; Score 38; DB 2; Length 418;
Best Local Similarity 61.5%; Pred. No. 1.4e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 FAGIEAAASAIQ 15
|:|:|:|:
Db 31 FARIKAAKVKQ 43

RESULT 28
US-09-252-991A-23220
; Sequence 23220, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23220
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23220

Query Match 49.4%; Score 38; DB 2; Length 435;
Best Local Similarity 63.6%; Pred. No. 1.5e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WNFAGIEAAAS 11
|:|:|:|:
Db 298 WSTAGIDATAS 308

RESULT 29
US-09-909-474D-9
; Sequence 9, Application US/090909474D
; Patent No. 6881542
; GENERAL INFORMATION:
; APPLICANT: Boylan, John
; APPLICANT: Bowers, Alex
; TITLE OF INVENTION: No. 6881542el Serine Threonine Kinase Member, h2520-59
; FILE REFERENCE: 01017/36524A
; CURRENT APPLICATION NUMBER: US/09/909,474D
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,204
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (136)
; OTHER INFORMATION: Xaa = unknown or other
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (138)
; OTHER INFORMATION: Xaa = unknown or other
; FEATURE:

```
; NAME/KEY: misc feature
; LOCATION: (141)
; OTHER INFORMATION: Xaa = unknown or other
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (142)
; OTHER INFORMATION: Xaa = unknown or other
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (143)
; OTHER INFORMATION: Xaa = unknown or other
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (152)
; OTHER INFORMATION: Xaa = unknown or other
;
US-09-909-474D-9
```

```
Query Match 48.1%; Score 37; DB 2; Length 153;
Best Local Similarity 50.0%; Pred. No. 66;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 WNFAGIEAAASA 12
   |::|||::|:|
Db 35 WSWAGIPSSAAA 46
```

RESULT 30

```
US-09-252-991A-24013
; Sequence 24013; Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24013
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
;
US-09-252-991A-24013
```

```
Query Match 48.1%; Score 37; DB 2; Length 209;
Best Local Similarity 53.3%; Pred. No. 95;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 1 WNFAGIEAAASAIAQC 15
   |||||::|:|
Db 115 WVFARSAARSALAE 129
```

RESULT 31

```
US-09-509-902A-9
; Sequence 9; Application US/09509902A
; Patent No. 6387676
; GENERAL INFORMATION:
; APPLICANT: Virca, Duke
; APPLICANT: Bird, Timothy A.
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: Human cDNAs Encoding Polypeptides Having Kinase Functions
; FILE REFERENCE: 2877-US
; CURRENT APPLICATION NUMBER: US/09/509,902A
; CURRENT FILING DATE: 1999-08-03
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
```

```
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-509-902A-9
```

```
Query Match 48.1%; Score 37; DB 2; Length 360;
Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 WNFAGIEAAASA 12
   |::|||::|:|
Db 4 WSWAGIPSSAAA 15
```

RESULT 32

```
US-10-024-828-9
; Sequence 9; Application US/10024828
; Patent No. 6867013
; GENERAL INFORMATION:
; APPLICANT: Virca, Duke
; APPLICANT: Bird, Timothy A.
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Marken, John S.
; TITLE OF INVENTION: Human cDNAs Encoding Polypeptides Having Kinase
; FILE REFERENCE: 2877-US
; CURRENT APPLICATION NUMBER: US/10/024,828
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US/09/509,902A
; PRIOR FILING DATE: 1999-08-03
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-10-024-828-9
```

```
Query Match 48.1%; Score 37; DB 2; Length 360;
Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
```

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QY 1 WNFAGIEAAASA 12
   |::|||::|:|
Db 4 WSWAGIPSSAAA 15
```

RESULT 33

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US-09-909-474D-11
; Sequence 11; Application US/09909474D
; Patent No. 6861542
; GENERAL INFORMATION:
; APPLICANT: Boylan, John
; APPLICANT: Bowers, Alex
; TITLE OF INVENTION: No. 6861542el Serine Threonine Kinase Member, h2520-59
; FILE REFERENCE: 01017/36524A
; CURRENT APPLICATION NUMBER: US/09/909,474D
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,204
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-909-474D-11
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Query Match 48.1%; Score 37; DB 2; Length 360;
Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 WNFAGIEAAASA 12
```

```
|: :: || | | : : } : |
WSWAGIPSSAA 15
```

4 WSWAGIPSSAAA 15

```

/ AFFILIATION: 18000001, 18000002
/ TITLE OF INVENTION: Nicotianamine Aminotransferase and Gene Therefor
/ FILE REFERENCE: 2185-0226P
/ CURRENT APPLICATION NUMBER: US/09/026,400A
/ CURRENT FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: 09-037499 JAPAN
/ PRIOR FILING DATE: 1997-02-21
/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 4
/ LENGTH: 551
/ TYPE: PRT
/ ORGANISM: Hordeum vulgare
/ US-09-026-400A-4

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Query Match	48.1%;	Score 37;	DB 2;	Length 551;
Best Local Similarity	46.7%;	Pred. No. 3e+02;		

Qy 1 WNFAGIEAAASAIQG 15
||| : |
Db 132 WNFAGAKDGVLAATG 146

RESULT 37

```

US-09-902-540-11561
; Sequence 11561, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11561
; LENGTH: 898
; TYPE: PRF
; ORGANISM: Myxococcus xanthus
US-09-902-540-11561

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Query Match 48.1%; Score 37; DB 2; Length 898;
Best Local Similarity 58.3%; Pred. No. 5.2e+02;
Matches 7: Conservative 2; Mismatches 3; Indels

QY 4 AGIEAAASAIQG 15
||:| ||:|
Db 244 AGLERIASVVOG 255

38 T.J. PEEBLES

```

US-09-252-991A-21335
; Sequence 21335, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21335
; LENGTH: 947

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db 4 WSWAGIPSSAAA 15

4 WSWAGIPSSAAA 15

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RESULT 34
US-09-902-540-15461
; Sequence 15461, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiesand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 15461
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-15461

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```
Query Match      48.1%; Score 37; DB 2; Length 472;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 7: Conservative 2; Mismatches 5; Indels 0; Gaps 0;
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Qy 1 WNFAGIEAAASAIQ 14
||| ||| ||| : :
db 362 WNKEGYEKHATAVO 375

RESULT 35

```

US-09-252-991A-20838
; Sequence 20838, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20838
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20838

```

Query Match 48.1%; Score 37; DB 2; Length 475;
Best Local Similarity 40.0%; Pred. No. 2.5e+02;
Matches 6: Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WNFAGIEAAASAIQG 15
|:|:|:|:
Db 267 WHPAGVEAGGEGVGG 281

RESULT 36

US-09-026-400A-4
; Sequence 4, Application US/09026400A
; Patent No. 6897300
; GENERAL INFORMATION:
; APPLICANT: MORI, Satoshi
; APPLICANT: NAKANISHI, Hiromi

; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21335

Query Match 48.1%; Score 37; DB 2; Length 947;
Best Local Similarity 40.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 WNPAGIEAAASAIQG 15
DB 657 WQAAGLTANGNALRG 671

RESULT 39

US-09-902-540-9848
; Sequence 9848, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 9848
; LENGTH: 981
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-9848

Query Match 48.1%; Score 37; DB 2; Length 981;
Best Local Similarity 53.8%; Pred. No. 5.8e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 WNPAGIEAAASAI 13
DB 787 WNSQGLEAAYRAL 799

RESULT 40

US-09-252-991A-25952
; Sequence 25952, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25952
; LENGTH: 1138
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25952

Query Match 48.1%; Score 37; DB 2; Length 1138;
Best Local Similarity 50.0%; Pred. No. 6.9e+02;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 4 AGIEAASAIQ 15
DB 209 AGVDAEAAVQG 220

RESULT 41

US-09-538-092-777
; Sequence 777, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glot, Ioig
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 777
; LENGTH: 1223
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (0)-(0)
; OTHER INFORMATION: Polypeptide Accession Number YPL110C
US-09-538-092-777

Query Match 48.1%; Score 37; DB 2; Length 1223;
Best Local Similarity 53.8%; Pred. No. 7.5e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 WNPAGIEAAASAI 13
DB 1152 WNLGIVSAAPI 1164

RESULT 42

US-09-489-039A-10933
; Sequence 10933, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10933
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10933

Query Match 45.8%; Score 36; DB 2; Length 294;
Best Local Similarity 45.2%; Pred. No. 2.1e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 WNPAGIEAAASAI 13
DB 219 WTFSTIDAAIDAV 231

RESULT 43

US-09-489-039A-13907
; Sequence 13907, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al

;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
;; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

;; FILE REFERENCE: 2709.2004001

;; CURRENT APPLICATION NUMBER: US/09/489,039A

;; CURRENT FILING DATE: 2000-01-27

;; PRIOR APPLICATION NUMBER: US 60/117,747

;; PRIOR FILING DATE: 1999-01-29

;; NUMBER OF SEQ ID NOS: 14342

;; SEQ ID NO 13907

;; LENGTH: 323

;; TYPE: PRT

;; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-13907

Query Match 46.8%; Score 36; DB 2; Length 323;

Best Local Similarity 53.8%; Pred. No. 2.4e+02;

Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 WNFAGIEAASAI 13

|||: |||

Db 218 WFFAGLSVAALVI 230

RESULT 44

US-09-489-039A-10986

;; Sequence 10986, Application US/09489039A

;; Patent No. 6610836

;; GENERAL INFORMATION:

;; APPLICANT: Gary Breton et. al

;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

;; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

;; FILE REFERENCE: 2709.2004001

;; CURRENT APPLICATION NUMBER: US/09/489,039A

;; CURRENT FILING DATE: 2000-01-27

;; PRIOR APPLICATION NUMBER: US 60/117,747

;; PRIOR FILING DATE: 1999-01-29

;; NUMBER OF SEQ ID NOS: 14342

;; SEQ ID NO 10986

;; LENGTH: 328

;; TYPE: PRT

;; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-10986

Query Match

Best Local Similarity 46.8%; Score 36; DB 2; Length 328;

Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 FAGIEAASAIQ 14

|||: |||

Db 291 FAGLISASAAQ 302

RESULT 45

US-09-489-039A-13753

;; Sequence 13753, Application US/09489039A

;; Patent No. 6610836

;; GENERAL INFORMATION:

;; APPLICANT: Gary Breton et. al

;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

;; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

;; FILE REFERENCE: 2709.2004001

;; CURRENT APPLICATION NUMBER: US/09/489,039A

;; CURRENT FILING DATE: 2000-01-27

;; PRIOR APPLICATION NUMBER: US 60/117,747

;; PRIOR FILING DATE: 1999-01-29

;; NUMBER OF SEQ ID NOS: 14342

;; SEQ ID NO 13753

;; LENGTH: 368

;; TYPE: PRT

;; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-13753

Query Match

Best Local Similarity 46.8%; Score 36; DB 2; Length 368;

Best Local Similarity 33.3%; Pred. No. 2.8e+02;

Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 WNFAGIEAASAIQ 15

|||: |||

Db 11 WQYSGINGASACPEG 25

RESULT 46

US-09-489-039A-8540

;; Sequence 8540, Application US/09489039A

;; Patent No. 6610836

;; GENERAL INFORMATION:

;; APPLICANT: Gary Breton et. al

;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

;; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

;; FILE REFERENCE: 2709.2004001

;; CURRENT APPLICATION NUMBER: US/09/489,039A

;; CURRENT FILING DATE: 2000-01-27

;; PRIOR APPLICATION NUMBER: US 60/117,747

;; PRIOR FILING DATE: 1999-01-29

;; NUMBER OF SEQ ID NOS: 14342

;; SEQ ID NO 8540

;; LENGTH: 389

;; TYPE: PRT

;; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-8540

Query Match

Best Local Similarity 46.8%; Score 36; DB 2; Length 389;

Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 NFAGIEAASAIQ 15

|||: |||

Db 97 HFAGVDFAGDAQ 110

RESULT 47

US-09-134-000C-3817

;; Sequence 3817, Application US/09134000C

;; Patent No. 6617156

;; GENERAL INFORMATION:

;; APPLICANT: Lynn Doucette-Stamm et al

;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

;; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

;; FILE REFERENCE: 032796-032

;; CURRENT APPLICATION NUMBER: US/09/134,000C

;; CURRENT FILING DATE: 1998-08-13

;; PRIOR APPLICATION NUMBER: US 60/055,778

;; PRIOR FILING DATE: 1997-08-15

;; NUMBER OF SEQ ID NOS: 6812

;; SOFTWARE: PatentIn version 3.1

;; SEQ ID NO 3817

;; LENGTH: 429

;; TYPE: PRT

;; ORGANISM: Enterococcus faecalis

US-09-134-000C-3817

Query Match

Best Local Similarity 46.8%; Score 36; DB 2; Length 429;

Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 NFAGIEAASAIQ 15

|||: |||

Db 215 NIAGVEAAKGLFG 228

RESULT 48

US-09-489-039A-13018

;; Sequence 13018, Application US/09489039A

;; Patent No. 6610836

;; GENERAL INFORMATION:

;; APPLICANT: Gary Breton et. al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13018
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13018

Query Match 46.8%; Score 36; DB 2; Length 483;
Best Local Similarity 57.1%; Pred. No. 3.8e+02;
Matches 8; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 NFAGIEAAASAIQG 15
||| ||| |||
Db 232 NPFGEVAMIGYQG 245

RESULT 49
US-09-949-016-9799
; Sequence 9799; Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9799
; LENGTH: 578
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9799

Query Match 46.8%; Score 36; DB 2; Length 578;
Best Local Similarity 60.0%; Pred. No. 4.7e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WNFAGIEAAA 10
|: ||: |||
Db 30 WDSAGVEVAA 39

RESULT 50
US-09-477-962-94
; Sequence 94; Application US/09477962
; Patent No. 6927286
; GENERAL INFORMATION:
; APPLICANT: SHEN, BEN
; APPLICANT: DU, LIANGCHENG
; APPLICANT: SANCHEZ, CESAR
; APPLICANT: CHEN, MEI
; APPLICANT: EDWARDS, DANIEL J.
; TITLE OF INVENTION: BLEOMYCIN GENE CLUSTER COMPONENTS AND THEIR USES
; FILE REFERENCE: 4077-895820US
; CURRENT APPLICATION NUMBER: US/09/477,962
; CURRENT FILING DATE: 2000-01-05
; PRIOR APPLICATION NUMBER: 60/115,435
; PRIOR FILING DATE: 1999-01-06

; PRIOR APPLICATION NUMBER: 60/118,848
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 94
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Streptomyces verticillius
; FEATURE:
; OTHER INFORMATION: ORF29
US-09-477-962-94

Query Match 46.8%; Score 36; DB 2; Length 582;
Best Local Similarity 46.2%; Pred. No. 4.7e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAI 13
|: ||: |||
Db 183 WTAAGLAAVAAV 195

Search completed: May 4, 2006, 15:19:25
Job time : 44 secs

GenCore version 5.1.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 15:33:46 ; Search time 124 Seconds
(without alignments)
50.544 Million cell updates/sec

Title: US-09-830-839-6

Perfect score: 77

Sequence: 1 WNFAGIERAASAIQ 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications_AA_Main:

1: /cgn2_6/prodata/1/pubpa/US07_PUBCOMB.pep.*
2: /cgn2_6/prodata/1/pubpa/US08_PUBCOMB.pep.*
3: /cgn2_6/prodata/1/pubpa/US09_PUBCOMB.pep.*
4: /cgn2_6/prodata/1/pubpa/US10_PUBCOMB.pep.*
5: /cgn2_6/prodata/1/pubpa/US10B_PUBCOMB.pep.*
6: /cgn2_6/prodata/1/pubpa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	77	100.0	15	4	US-10-079-167-80
2	77	100.0	15	4	US-10-345-000-2
3	77	100.0	15	5	US-10-520-084-2
4	77	100.0	20	3	US-09-813-333-60
5	77	100.0	20	4	US-10-044-703-60
6	77	100.0	20	4	US-10-239-103-60
7	77	100.0	51	3	US-09-886-349A-33
8	77	100.0	51	4	US-10-193-002-99
9	77	100.0	51	4	US-10-084-843-104
10	77	100.0	51	4	US-10-098-732A-33
11	77	100.0	51	6	US-11-028-898-104
12	77	100.0	51	6	US-11-082-005-99
13	77	100.0	95	3	US-09-805-427A-1
14	77	100.0	95	3	US-09-872-505-1
15	77	100.0	95	4	US-10-689-921-18
16	77	100.0	95	4	US-10-332-512A-12
17	77	100.0	95	5	US-10-520-084-36
18	77	100.0	95	5	US-10-510-021-65
19	77	100.0	403	3	US-09-791-171-173
20	77	100.0	403	3	US-09-805-427A-4
21	77	100.0	403	3	US-09-804-980-173
22	77	100.0	403	3	US-09-872-505-4
23	77	100.0	403	4	US-10-620-246-173
24	77	100.0	404	3	US-09-791-171-172
25	77	100.0	404	3	US-09-805-427A-3
26	77	100.0	404	3	US-09-804-980-172
27	77	100.0	404	3	US-09-872-505-3

28	77	100.0	404	4	US-10-620-246-172	Sequence 172, App
29	66	85.7	16	5	US-10-505-929-21	Sequence 21, Appl
30	66	85.7	20	3	US-09-813-333-61	Sequence 61, Appl
31	66	85.7	20	4	US-10-044-703-61	Sequence 61, Appl
32	66	85.7	20	4	US-10-239-103-61	Sequence 61, Appl
33	60	77.9	13	3	US-09-813-333-59	Sequence 59, Appl
34	60	77.9	13	4	US-10-044-703-59	Sequence 59, Appl
35	60	77.9	13	4	US-10-239-103-59	Sequence 59, Appl
36	54	70.1	15	4	US-10-079-167-79	Sequence 79, Appl
37	54	70.1	15	4	US-10-345-000-1	Sequence 1, Appl
38	54	70.1	15	5	US-10-520-084-1	Sequence 1, Appl
39	46	59.7	122	4	US-10-425-115-201779	Sequence 201779,
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548	35	45.5	212	5	US-10-809-689-116	Sequence 116, App	621	35	45.5	373	4	US-10-225-066A-134	Sequence 134, App
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561	35	45.5	222	4	US-10-001-245-26	Sequence 26, Appl	634	35	45.5	449	6	US-11-141-593-36	Sequence 36, Appl
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571	35	45.5	262	4	US-10-425-114-69329	Sequence 69329, A	644	35	45.5	482	5	US-10-756-149-4691	Sequence 4691, Ap
572	35	45.5	268	5	US-10-739-930-9952	Sequence 9952, Ap	645	35	45.5	486	4	US-10-153-668-432	Sequence 432, App
573	35	45.5	274	4	US-10-437-963-151838	Sequence 151838,	646	35	45.5	489	3	US-09-934-455-170	Sequence 170, App
574	35	45.5	276	6	US-11-051-785-16	Sequence 16, Appl	647	35	45.5	489	4	US-10-225-068-166	Sequence 166, App
575	35	45.5	276	6	US-11-141-593-16	Sequence 16, Appl	648	35	45.5	489	4	US-10-374-780A-220	Sequence 220, App
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857	34	44.2	505	4	US-10-052-586-450	Sequence 52, Appl	931	34	44.2	505	4	US-10-187-596-450	Sequence 450, App
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860	34	44.2	505	4	US-10-176-758-450	Sequence 450, App	934	34	44.2	505	4	US-10-187-886-450	Sequence 450, App
861	34	44.2	505	4	US-10-175-737-450	Sequence 450, App	935	34	44.2	505	4	US-10-187-886-450	Sequence 450, App
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864	34	44.2	505	4	US-10-176-749-450	Sequence 450, App	938	34	44.2	505	4	US-10-176-760-450	Sequence 450, App
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869	34	44.2	505	4	US-10-175-752-450	Sequence 450, App	943	34	44.2	505	4	US-10-180-551-450	Sequence 450, App
870	34	44.2	505	4	US-10-176-482-450	Sequence 450, App	944	34	44.2	505	4	US-10-180-998-450	Sequence 450, App
871	34	44.2	505	4	US-10-176-757-450	Sequence 450, App	945	34	44.2	505	4	US-10-180-999-450	Sequence 450, App
872	34	44.2	505	4	US-10-176-913-450	Sequence 450, App	946	34	44.2	505	4	US-10-183-013-450	Sequence 450, App
873	34	44.2	505	4	US-10-180-552-450	Sequence 450, App	947	34	44.2	505	4	US-10-184-612-450	Sequence 450, App
874	34	44.2	505	4	US-10-180-557-450	Sequence 450, App	948	34	44.2	505	4	US-10-184-616-450	Sequence 450, App
875	34	44.2	505	4	US-10-173-700-450	Sequence 450, App	949	34	44.2	505	4	US-10-184-617-450	Sequence 450, App
876	34	44.2	505	4	US-10-174-572-450	Sequence 450, App	950	34	44.2	505	4	US-10-184-622-450	Sequence 450, App
877	34	44.2	505	4	US-10-174-579-450	Sequence 450, App	951	34	44.2	505	4	US-10-184-628-450	Sequence 450, App
878	34	44.2	505	4	US-10-174-582-450	Sequence 450, App	952	34	44.2	505	4	US-10-184-629-450	Sequence 450, App
879	34	44.2	505	4	US-10-174-588-450	Sequence 450, App	953	34	44.2	505	4	US-10-184-630-450	Sequence 450, App
880	34	44.2	505	4	US-10-175-739-450	Sequence 450, App	954	34	44.2	505	4	US-10-184-631-450	Sequence 450, App
881	34	44.2	505	4	US-10-175-740-450	Sequence 450, App	955	34	44.2	505	4	US-10-184-632-450	Sequence 450, App
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883	34	44.2	505	4	US-10-176-488-450	Sequence 450, App	957	34	44.2	505	4	US-10-184-640-450	Sequence 450, App
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892	34	44.2	505	4	US-10-176-991-450	Sequence 450, App	966	34	44.2	505	4	US-10-187-603-450	Sequence 450, App
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896	34	44.2	505	4	US-10-173-695-450	Sequence 450, App	970	34	44.2	505	4	US-10-187-747-450	Sequence 450, App
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903	34	44.2	505	4	US-10-176-481-450	Sequence 450, App							

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981 34 44.2 505 4 US-10-194-361-450 Sequence 450, App
982 34 44.2 505 4 US-10-194-423-450 Sequence 450, App
983 34 44.2 505 4 US-10-195-897-450 Sequence 450, App
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985 34 44.2 505 4 US-10-195-902-450 Sequence 450, App
986 34 44.2 505 4 US-10-196-743-450 Sequence 450, App
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988 34 44.2 505 4 US-10-173-708-450 Sequence 450, App
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992 34 44.2 505 4 US-10-176-916-450 Sequence 450, App
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ALIGNMENTS

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RESULT 1
US-10-079-167-80
; Sequence 80, Application US/10079167
; Publication No. US20030138454A1
; GENERAL INFORMATION:
; APPLICANT: Hill, Adrian V.S.
; APPLICANT: McShane, Helen
; APPLICANT: Gilbert, Sarah C.
; APPLICANT: Reece, William
; APPLICANT: Schneider, Joerg
; TITLE OF INVENTION: Vaccination Method
; FILE REFERENCE: 2907 1000-001
; CURRENT APPLICATION NUMBER: US/10/079,167
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/454,204
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: PCT/GB98/01681
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: GB 97 11957.2
; PRIOR FILING DATE: 1997-06-09
; PRIOR APPLICATION NUMBER: PCT/GB01/04116
; PRIOR FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: GB 00 23203.3
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: T cell epitope in ESAT6
US-10-079-167-80
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Query Match 100.0%; Score 77; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 WNFAGIEAAASAIQG 15
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RESULT 2

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US-10-345-000-2
; Sequence 2, Application US/10345000
; Publication No. US20040018177A1
; GENERAL INFORMATION:
; APPLICANT: OXON PHARMACEUTICALS LIMITED
; TITLE OF INVENTION: VACCINATION METHOD
; FILE REFERENCE: 550-409
; CURRENT APPLICATION NUMBER: US/10/345,000
; CURRENT FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-345-000-2
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Query Match 100.0%; Score 77; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 WNFAGIEAAASAIQG 15
Db 1 WNFAGIEAAASAIQG 15
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RESULT 3

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US-10-520-084-2
; Sequence 2, Application US/10520084
; Publication No. US20050208594A1
; GENERAL INFORMATION:
; APPLICANT: Ajit LALVANI
; APPLICANT: Katie EWER
; APPLICANT: ISIS INNOVATION LIMITED
; TITLE OF INVENTION: DIAGNOSTICS METHOD
; FILE REFERENCE: 3772-22 / N.86130A JCI
; CURRENT APPLICATION NUMBER: US/10/520,084
; CURRENT FILING DATE: 2005-01-05
; PRIOR APPLICATION NUMBER: PCT/GB03/002936
; PRIOR FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: GB 0215710.5
; PRIOR FILING DATE: 2002-07-05
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-520-084-2
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Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 WNFAGIEAAASAIQG 15
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RESULT 4

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US-09-813-333-60
; Sequence 60, Application US/09813333
; Publication No. US20020119160A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004 US
; CURRENT APPLICATION NUMBER: US/09/813,333
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 60
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-813-333-60

Query Match      100.0%; Score 77; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAIQG 15
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Db 2 WNFAGIEAAASAIQG 16

RESULT 5
US-10-044-703-60
; Sequence 60, Application US/10044703
; Publication No. US20020192233A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004 US
; CURRENT APPLICATION NUMBER: US/10/044,703
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-044-703-60

Query Match      100.0%; Score 77; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAIQG 15
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Db 2 WNFAGIEAAASAIQG 16

RESULT 6
US-10-239-103-60
; Sequence 60, Application US/10239103
; Publication No. US20040057961A1
; GENERAL INFORMATION:
; APPLICANT: Brown University Research Foundation
; APPLICANT: DeGroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004-061
; CURRENT APPLICATION NUMBER: US/10/239,103
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 09/813,333
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-239-103-60

Query Match      100.0%; Score 77; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAIQG 15
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Db 2 WNFAGIEAAASAIQG 16

RESULT 7
US-09-886-349A-33
; Sequence 33, Application US/09886349A
; Publication No. US20040086523A1
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir
; APPLICANT: Reed, Steven
; APPLICANT: Alderson, Mark
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
; FILE REFERENCE: 014058-009070US
; CURRENT APPLICATION NUMBER: US/09/886,349A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 09/597,796
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US 60/265,737
; PRIOR FILING DATE: 2001-02-01
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: ESAT-6
US-09-886-349A-33

Query Match      100.0%; Score 77; DB 3; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAIQG 15
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Db 6 WNFAGIEAAASAIQG 20

RESULT 8
US-10-193-002-99
; Sequence 99, Application US/10193002
; Publication No. US20030135026A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Campos-Neto, Antonia
; APPLICANT: Houghton, Raymond
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Twardzik, Daniel R.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Hendrickson, Ronald C.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TUBERCULOSIS
; NUMBER OF SEQUENCES: 350
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/193,002
; FILING DATE: 10-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US/09/072,596
; FILING DATE: 05-MAY-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: MAKI, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.417C9
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 99:
US-10-193-002-99
;
; Query Match 100.0%; Score 77; DB 4; Length 51;
; Best Local Similarity 100.0%; Pred. No. 1.2e-05;
; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 1 WNFAGIEAASAIQG 15
DB 6 WNFAGIEAASAIQG 20
;
; RESULT 9
; US-10-084-843-104
; Sequence 104, Application US/10084843
; Publication No. US20030143243A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; SKEIKY, Yasir A.W.
; DILLON, Davin C.
; Campos-Neto, Antonio
; Houghton, Raymond
; Vedvick, Thomas S.
; Twardzik, Daniel R.
; Lodes, Michael J.
; Hendrickson, Ronald C.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
; NUMBER OF SEQUENCES: 355
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/084,843
; FILING DATE: 25-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/072,967
; FILING DATE: 05-MAY-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: MAKI, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.411C9
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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US-10-084-843-104
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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 104:
US-10-084-843-104
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; Query Match 100.0%; Score 77; DB 4; Length 51;
; Best Local Similarity 100.0%; Pred. No. 1.2e-05;
; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 WNFAGIEAASAIQG 15
DB 6 WNFAGIEAASAIQG 20
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; RESULT 10
; US-10-098-732A-33
; Sequence 33, Application US/10098732A
; Publication No. US20030175294A1
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir
; BRANNON, Mark
; APPLICANT: Guerdian, Jeffrey
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
; TITLE OF INVENTION: Tetrahymena Antigen
; FILE REFERENCE: 014058-012010US
; CURRENT APPLICATION NUMBER: US/10/098,732A
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US 60/275,837
; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: ESAT-6
; US-10-098-732A-33
;
; Query Match 100.0%; Score 77; DB 4; Length 51;
; Best Local Similarity 100.0%; Pred. No. 1.2e-05;
; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 1 WNFAGIEAASAIQG 15
DB 6 WNFAGIEAASAIQG 20
;
; RESULT 11
; US-11-028-898-104
; Sequence 104, Application US/11028898
; Publication No. US20050136069A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; SKEIKY, Yasir A.W.
; DILLON, Davin C.
; Campos-Neto, Antonio
; Houghton, Raymond
; Vedvick, Thomas S.
; Twardzik, Daniel R.
; Lodes, Michael J.
; Hendrickson, Ronald C.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
; NUMBER OF SEQUENCES: 355
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
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ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/11/028,898
FILING DATE: 03-Jan-2005
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/084,843
FILING DATE: 03-Jan-2005
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998

ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 104:
US-11-028-898-104

Query Match 100.0%; Score 77; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WNFAGIEAAASAIQG 15
| | | | | | | | | | | | | | | | | | | | |
Db 6 WNFAGIEAAASAIQG 20

RESULT 12

US-11-082-005-99
Sequence 99, Application US/11082005
Publication No. US20050181419A1

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
TUBERCULOSIS

NUMBER OF SEQUENCES: 350

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/11/082,005
FILING DATE: 15-Mar-2005
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-Jul-2002
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 99:
US-11-082-005-99

Query Match 100.0%; Score 77; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WNFAGIEAAASAIQG 15
| | | | | | | | | | | | | | | | | | | | |
Db 6 WNFAGIEAAASAIQG 20

RESULT 13

US-09-805-427A-1
Sequence 1, Application US/09805427A
Patent No. US20020176867A1

GENERAL INFORMATION:

APPLICANT: Statens Serum Institut
TITLE OF INVENTION: Hybrids of M. tuberculosis Antigens
FILE REFERENCE: 670001-2002.5
CURRENT APPLICATION NUMBER: US/09/805,427A
CURRENT FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 95
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis

US-09-805-427A-1

Query Match 100.0%; Score 77; DB 3; Length 95;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WNFAGIEAAASAIQG 15
| | | | | | | | | | | | | | | | | | | | |
Db 6 WNFAGIEAAASAIQG 20

RESULT 14

US-09-872-505-1

Sequence 1, Application US/09872505
Publication No. US20040013685A1

GENERAL INFORMATION:

APPLICANT: Statens Serum Institut
TITLE OF INVENTION: Nucleic Acid Fragments Derived From M. Tuberculosis
FILE REFERENCE: 670001-2002.6
CURRENT APPLICATION NUMBER: US/09/872,505
CURRENT FILING DATE: 2001-06-01
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 95
TYPE: PRT

ORGANISM: Mycobacterium tuberculosis

US-09-872-505-1

Query Match 100.0%; Score 77; DB 3; Length 95;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAIQG 15
|||||
DB 6 WNFAGIEAAASAIQG 20

RESULT 15

US-10-689-921-18
; Sequence 18, Application US/10689921
; Publication No. US20040146948A1
; GENERAL INFORMATION:
; APPLICANT: Britton, Warwick
; APPLICANT: Demangel, Caroline
; TITLE OF INVENTION: Compositions and Methods for Targeting
; TITLE OF INVENTION: Antigen-Presenting Cells With Antibody Single-Chain Variable
; TITLE OF INVENTION: Region Fragments
; FILE REFERENCE: 13311.1002U
; CURRENT APPLICATION NUMBER: US/10/689,921
; CURRENT FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-689-921-18

Query Match 100.0%; Score 77; DB 4; Length 95;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAIQG 15
|||||
DB 6 WNFAGIEAAASAIQG 20

RESULT 16

US-10-332-512A-12
; Sequence 12, Application US/10332512A
; Publication No. US20040180056A1
; GENERAL INFORMATION:
; APPLICANT: ORME, Ian M.
; APPLICANT: BELISLE, John T.
; TITLE OF INVENTION: MID-LIFE VACCINE AND METHODS FOR BOOSTING ANTI-MYCOBACTERIAL IMM
; FILE REFERENCE: 38861-186292
; CURRENT APPLICATION NUMBER: US/10/332,512A
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: PCT/US01/21717
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/217,646
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-332-512A-12

Query Match 100.0%; Score 77; DB 4; Length 95;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAIQG 15
|||||
DB 6 WNFAGIEAAASAIQG 20

RESULT 17

US-10-520-084-36
; Sequence 36, Application US/10520084
; Publication No. US20050208594A1
; GENERAL INFORMATION:
; APPLICANT: Ajit LALVANI
; APPLICANT: Katie EWER
; APPLICANT: ISIS INNOVATION LIMITED
; TITLE OF INVENTION: DIAGNOSTICS METHOD
; FILE REFERENCE: 3772-22 / N.86130A JCI
; CURRENT APPLICATION NUMBER: US/10/520,084
; CURRENT FILING DATE: 2005-01-05
; PRIOR APPLICATION NUMBER: PCT/GB03/002936
; PRIOR FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: GB 0215710.5
; PRIOR FILING DATE: 2002-07-05
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-520-084-36

Query Match 100.0%; Score 77; DB 5; Length 95;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAIQG 15
|||||
DB 6 WNFAGIEAAASAIQG 20

RESULT 18

US-10-510-021-65
; Sequence 65, Application US/10510021
; Publication No. US20050220811A1
; GENERAL INFORMATION:
; APPLICANT: Cole, Stewart
; APPLICANT: Fym, Alexander S
; APPLICANT: Brosch, Roland
; APPLICANT: Brodin, Priscille
; APPLICANT: Majlessi, Laleh
; APPLICANT: Demangel, Caroline
; APPLICANT: Leclerc, Claude
; TITLE OF INVENTION: Identification of virulence associated regions RD1 and
; TITLE OF INVENTION: RD5 leading to improve vaccine of M. bovis BCG and M.
; TITLE OF INVENTION: microti
; FILE REFERENCE: D20217
; CURRENT APPLICATION NUMBER: US/10/510,021
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: PCT/IB03/01789
; PRIOR FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: EP 02/290864
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 65
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: RV3875-Esat6 - 6 kDa early secretory antigenic
; OTHER INFORMATION: target Esat6 (Esat-6)
US-10-510-021-65

Query Match 100.0%; Score 77; DB 5; Length 95;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAIQG 15
|||||
DB 6 WNFAGIEAAASAIQG 20

RESULT 19
US-09-791-171-173
; Sequence 173, Application US/09791171
; Patent No. US20020094336A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSEN, Peter
; APPLICANT: NIELSEN, Rikke
; APPLICANT: OETTINGER, Thomas
; APPLICANT: RASMUSSEN, Peter Birk
; APPLICANT: ROSENKRANDS, Ida
; APPLICANT: WELDINGH, Karin
; APPLICANT: FLORIO, Walter
; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
; TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
; FILE REFERENCE: 670001-2002.1
; CURRENT APPLICATION NUMBER: US/09/791,171
; CURRENT FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 09/050,739
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 0376/97
; PRIOR FILING DATE: 1997-04-02
; PRIOR APPLICATION NUMBER: 1277/97
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/044,624
; PRIOR FILING DATE: 1997-04-18
; PRIOR APPLICATION NUMBER: 60/070,488
; PRIOR FILING DATE: 1998-01-05
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 173
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-791-171-173
Query Match 100.0%; Score 77; DB 3; Length 403;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WNFAGIEAAASAIQG 15
|||||
Db 27 WNFAGIEAAASAIQG 41

RESULT 20
US-09-805-427A-4
; Sequence 4, Application US/09805427A
; Patent No. US20020176867A1
; GENERAL INFORMATION:
; APPLICANT: Statens Serum Institut
; TITLE OF INVENTION: Hybrids of M. tuberculosis Antigens
; FILE REFERENCE: 670001-2002.5
; CURRENT APPLICATION NUMBER: US/09/805,427A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant Fusion protein ESAT-6-Ag85B
US-09-805-427A-4
Query Match 100.0%; Score 77; DB 3; Length 403;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WNFAGIEAAASAIQG 15
|||||
Db 27 WNFAGIEAAASAIQG 41

RESULT 21
US-09-804-980-173
; Sequence 173, Application US/09804980
; Publication No. US20030147897A1
; GENERAL INFORMATION:
; APPLICANT: Statens Serum Institut
; APPLICANT: ANDERSEN, Peter
; TITLE OF INVENTION: M. Tuberculosis Antigens
; FILE REFERENCE: 670001-2002.4
; CURRENT APPLICATION NUMBER: US/09/804,980
; CURRENT FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 257
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 173
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-804-980-173
Query Match 100.0%; Score 77; DB 3; Length 403;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WNFAGIEAAASAIQG 15
|||||
Db 27 WNFAGIEAAASAIQG 41

RESULT 22
US-09-872-505-4
; Sequence 4, Application US/09872505
; Publication No. US20040013685A1
; GENERAL INFORMATION:
; APPLICANT: Statens Serum Institut
; TITLE OF INVENTION: Nucleic Acid Fragments Derived From M. Tuberculosis
; FILE REFERENCE: 670001-2002.6
; CURRENT APPLICATION NUMBER: US/09/872,505
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant Fusion protein ESAT-6-Ag85B
US-09-872-505-4
Query Match 100.0%; Score 77; DB 3; Length 403;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WNFAGIEAAASAIQG 15
|||||
Db 27 WNFAGIEAAASAIQG 41

RESULT 23
US-10-620-246-173
; Sequence 173, Application US/10620246
; Publication No. US20040115211A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSEN, Peter
; APPLICANT: NIELSEN, Rikke
; APPLICANT: OETTINGER, Thomas
; APPLICANT: RASMUSSEN, Peter Birk
; APPLICANT: ROSENKRANDS, Ida
; APPLICANT: WELDINGH, Karin
; APPLICANT: FLORIO, Walter
; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
; TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
US-10-620-246-173
Query Match 100.0%; Score 77; DB 3; Length 403;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WNFAGIEAAASAIQG 15
|||||
Db 27 WNFAGIEAAASAIQG 41

FILE REFERENCE: 670001-2002.1A
; CURRENT APPLICATION NUMBER: US/10/620,246
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 09/050,739
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 0376/97
; PRIOR FILING DATE: 1997-04-02
; PRIOR APPLICATION NUMBER: 1277/97
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/044,624
; PRIOR FILING DATE: 1997-04-18
; PRIOR APPLICATION NUMBER: 60/070,488
; PRIOR FILING DATE: 1998-01-05
; PRIOR APPLICATION NUMBER: 10/138,473
; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 09/791,171
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 09/415,884
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: 60/116,673
; PRIOR FILING DATE: 1999-01-21
; PRIOR APPLICATION NUMBER: 1281/98
; PRIOR FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 173
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-620-246-173

Query Match 100.0%; Score 77; DB 4; Length 403;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAIQG 15
| | | | | | | | | | | | | | |
Db 27 WNFAGIEAAASAIQG 41

RESULT 24
US-09-791-171-172
; Sequence 172, Application US/09791171
; Patent No. US20020094336A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSEN, Peter
; APPLICANT: NIELSEN, Rikke
; APPLICANT: OETTINGER, Thomas
; APPLICANT: RASMUSSEN, Peter Birk
; APPLICANT: ROSENKRANDS, Ida
; APPLICANT: WELDINGH, Karin
; APPLICANT: FLORIO, Walter
; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
; FILE REFERENCE: 670001-2002.1
; CURRENT APPLICATION NUMBER: US/09/791,171
; CURRENT FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 09/050,739
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 0376/97
; PRIOR FILING DATE: 1997-04-02
; PRIOR APPLICATION NUMBER: 1277/97
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/044,624
; PRIOR FILING DATE: 1997-04-18
; PRIOR APPLICATION NUMBER: 60/070,488
; PRIOR FILING DATE: 1998-01-05
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 172
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis

US-09-791-171-172
Query Match 100.0%; Score 77; DB 3; Length 404;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAIQG 15
| | | | | | | | | | | | | | |
Db 315 WNFAGIEAAASAIQG 329

RESULT 25
US-09-805-427A-3
; Sequence 3, Application US/09805427A
; Patent No. US20020176867A1
; GENERAL INFORMATION:
; APPLICANT: Statens Serum Institut
; TITLE OF INVENTION: Hybrids of M. tuberculosis Antigens
; FILE REFERENCE: 670001-2002.5
; CURRENT APPLICATION NUMBER: US/09/805,427A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Recombinant Fusion protein Ag85B-ESAT-6
US-09-805-427A-3

Query Match 100.0%; Score 77; DB 3; Length 404;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAIQG 15
| | | | | | | | | | | | | | |
Db 315 WNFAGIEAAASAIQG 329

RESULT 26
US-09-804-980-172
; Sequence 172, Application US/09804980
; Publication No. US20030147897A1
; GENERAL INFORMATION:
; APPLICANT: Statens Serum Institut
; APPLICANT: Anderson, Peter
; TITLE OF INVENTION: M. Tuberculosis Antigens
; FILE REFERENCE: 670001-2002.4
; CURRENT APPLICATION NUMBER: US/09/804,980
; CURRENT FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 257
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 172
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-804-980-172

Query Match 100.0%; Score 77; DB 3; Length 404;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAIQG 15
| | | | | | | | | | | | | | |
Db 315 WNFAGIEAAASAIQG 329

RESULT 27
US-09-872-505-3
; Sequence 3, Application US/09872505
; Publication No. US20040013685A1
; GENERAL INFORMATION:

; APPLICANT: Statens Serum Institut
; TITLE OF INVENTION: Nucleic Acid Fragments Derived From M. Tuberculosis
; FILE REFERENCE: 670001-2002.6
; CURRENT APPLICATION NUMBER: US/09/872,505
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant Fusion protein Ag85B-ESAT-6
US-09-872-505-3

Query Match 100.0%; Score 77; DB 3; Length 404;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAIQ 15
Db 315 WNFAGIEAAASAIQ 329
|||||

RESULT 28
US-10-620-246-172
; Sequence 172, Application US/10620246
; Publication No. US20040115211A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSEN, Peter
; APPLICANT: NIELSEN, Rikke
; APPLICANT: OETTINGER, Thomas
; APPLICANT: RASMUSSEN, Peter Birk
; APPLICANT: ROSENKRANDS, Ida
; APPLICANT: WELDLINGH, Karin
; APPLICANT: FLORIO, Walter
; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
; FILE REFERENCE: 670001-2002.1A
; CURRENT APPLICATION NUMBER: US/10/620,246
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 09/050,739
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 0376/97
; PRIOR FILING DATE: 1997-04-02
; PRIOR APPLICATION NUMBER: 1277/97
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/044,624
; PRIOR FILING DATE: 1997-04-18
; PRIOR APPLICATION NUMBER: 60/070,488
; PRIOR FILING DATE: 1998-01-05
; PRIOR APPLICATION NUMBER: 10/138,473
; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 09/791,171
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 09/415,884
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: 60/116,673
; PRIOR FILING DATE: 1999-01-21
; PRIOR APPLICATION NUMBER: 1281/98
; PRIOR FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 172
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-620-246-172

Query Match 100.0%; Score 77; DB 4; Length 404;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAIQ 15
Db 315 WNFAGIEAAASAIQ 329
|||||

RESULT 29
US-10-505-929-21
; Sequence 21, Application US/10505929
; Publication No. US20050221381A1
; GENERAL INFORMATION:
; APPLICANT: KLADE, CHRISTOF
; APPLICANT: SCHALICH, JULIANE
; APPLICANT: VITVITSKA, ORESTA
; APPLICANT: AICHINGER, GERALD
; APPLICANT: OTAVA, ALEXANDER
; APPLICANT: MATTNER, FRANK
; TITLE OF INVENTION: METHOD FOR ISOLATING LIGANDS
; FILE REFERENCE: SONN:055US
; CURRENT APPLICATION NUMBER: US/10/505,929
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: PCT/EP03/02005
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: A 316/2002
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: A 1376/2002
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 584
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Cytomegalovirus
US-10-505-929-21

Query Match 85.7%; Score 66; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NFAGIEAAASAIQ 15
Db 1 NFAGIEAAASAIQ 14
|||||

RESULT 30
US-09-813-333-61
; Sequence 61, Application US/09813333
; Patent No. US20020119160A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004 US
; CURRENT APPLICATION NUMBER: US/09/813,333
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-813-333-61

Query Match 85.7%; Score 66; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00035;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NFAGIEAAASAIQ 15
Db 1 NFAGIEAAASAIQ 14
|||||

RESULT 31

```
US-10-044-703-61
; Sequence 61, Application US/10044703
; Publication No. US20020192233A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004 US
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-044-703-61
Query Match      85.7%; Score 66; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00035;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      2 NFAGIEAAASATQG 15
      |||||
Db      1 NFAGIEAAASATQG 14
      |||||
RESULT 32
US-10-239-103-61
; Sequence 61, Application US/10239103
; Publication No. US20040057961A1
; GENERAL INFORMATION:
; APPLICANT: Brown University Research Foundation
; APPLICANT: DeGroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004-061
; CURRENT APPLICATION NUMBER: US/10/239,103
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 09/813,333
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-239-103-61
Query Match      85.7%; Score 66; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00035;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      2 NFAGIEAAASATQG 15
      |||||
Db      1 NFAGIEAAASATQG 14
      |||||
RESULT 33
US-09-813-333-59
; Sequence 59, Application US/09813333
; Patent No. US20020119160A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004 US
; CURRENT APPLICATION NUMBER: US/09/813,333
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-239-103-59
Query Match      77.9%; Score 60; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      2 NFAGIEAAASAIQ 14
      |||||
Db      1 NFAGIEAAASAIQ 13
      |||||
RESULT 34
US-10-044-703-59
; Sequence 59, Application US/10044703
; Publication No. US20020192233A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004 US
; CURRENT APPLICATION NUMBER: US/10/044,703
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-044-703-59
Query Match      77.9%; Score 60; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      2 NFAGIEAAASAIQ 14
      |||||
Db      1 NFAGIEAAASAIQ 13
      |||||
RESULT 35
US-10-239-103-59
; Sequence 59, Application US/10239103
; Publication No. US20040057961A1
; GENERAL INFORMATION:
; APPLICANT: Brown University Research Foundation
; APPLICANT: DeGroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004-061
; CURRENT APPLICATION NUMBER: US/10/239,103
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 09/813,333
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-239-103-59
Query Match      77.9%; Score 60; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      2 NFAGIEAAASAIQ 14
      |||||
Db      1 NFAGIEAAASAIQ 13
      |||||
```

```
Db 1 NFAGIEAAASAIQ 13
|||||
RESULT 36
US-10-079-167-79
; Sequence 79, Application US/10079167
; Publication No. US20030138454A1
; GENERAL INFORMATION:
; APPLICANT: Hill, Adrian V.S.
; APPLICANT: McShane, Helen
; APPLICANT: Gilbert, Sarah C.
; APPLICANT: Reece, William
; APPLICANT: Schneider, Joerg
; TITLE OF INVENTION: Vaccination Method
; FILE REFERENCE: 2907.1000-001
; CURRENT APPLICATION NUMBER: US/10/079,167
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/454,204
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: PCT/GB98/01681
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: GB 97 11957.2
; PRIOR FILING DATE: 1997-06-09
; PRIOR APPLICATION NUMBER: PCT/GB01/04116
; PRIOR FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: GB 00 23203.3
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 79
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: T cell epitope in ESAT6
US-10-079-167-79
Query Match 70.1%; Score 54; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNPAGIEAAA 10
|||||
Db 6 WNPAGIEAAA 15

RESULT 37
US-10-345-000-1
; Sequence 1, Application US/10345000
; Publication No. US20040018177A1
; GENERAL INFORMATION:
; APPLICANT: OXON PHARMACEUTICALS LIMITED
; TITLE OF INVENTION: VACCINATION METHOD
; FILE REFERENCE: 550-409
; CURRENT APPLICATION NUMBER: US/10/345,000
; CURRENT FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-345-000-1
Query Match 70.1%; Score 54; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNPAGIEAAA 10
|||||
Db 6 WNPAGIEAAA 15

RESULT 38
US-10-520-084-1
; Sequence 1, Application US/10520084
; Publication No. US20050208594A1
; GENERAL INFORMATION:
; APPLICANT: Ajit LALVANI
; APPLICANT: Katie EWER
; APPLICANT: ISIS INNOVATION LIMITED
; TITLE OF INVENTION: DIAGNOSTICS METHOD
; FILE REFERENCE: 3772-22 / N.86130A JCT
; CURRENT APPLICATION NUMBER: US/10/520,084
; CURRENT FILING DATE: 2005-01-05
; PRIOR APPLICATION NUMBER: PCT/GB01/002936
; PRIOR FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: GB 0215710.5
; PRIOR FILING DATE: 2002-07-05
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-520-084-1
Query Match 70.1%; Score 54; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNPAGIEAAA 10
|||||
Db 6 WNPAGIEAAA 15

RESULT 39
US-10-425-115-201779
; Sequence 201779, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 201779
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_115605C.1.pep
US-10-425-115-201779
Query Match 59.7%; Score 46; DB 4; Length 122;
Best Local Similarity 64.3%; Pred. No. 6.7;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NFAGIEAAASAIQ 15
|||||
Db 47 NAAGVQAAAAYQG 60

RESULT 40
US-10-425-115-201777
; Sequence 201777, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
```

```
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 201777
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_115603C.1.pep
US-10-425-115-201777
```

```
Query Match 59.7%; Score 46; DB 4; Length 207;
Best Local Similarity 64.3%; Pred. No. 12;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 NFAGIEAASAIQ 15
DB 132 NAAGVQAAAYQG 145
```

RESULT 41

```
US-10-520-084-3
; Sequence 3, Application US/10520084
; Publication No. US20050208594A1
; GENERAL INFORMATION:
; APPLICANT: Ajit Lalwani
; APPLICANT: Katie Ewer
; APPLICANT: Isis Innovation Limited
; TITLE OF INVENTION: DIAGNOSTICS METHOD
; FILE REFERENCE: 3772-22 / N.86130A JCI
; CURRENT APPLICATION NUMBER: US/10/520,084
; CURRENT FILING DATE: 2005-01-05
; PRIOR APPLICATION NUMBER: PCT/GB03/002936
; PRIOR FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: GB 0215710.5
; PRIOR FILING DATE: 2002-07-05
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-520-084-3
```

```
Query Match 57.1%; Score 44; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 6 IEAASAIQ 15
DB 1 IEAASAIQ 10
```

RESULT 42

```
US-10-425-115-264053
; Sequence 264053, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
```

```
; SEQ ID NO 264053
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_172431C.1.pep
US-10-425-115-264053
Query Match 55.8%; Score 43; DB 4; Length 158;
Best Local Similarity 69.2%; Pred. No. 29;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 WNFAGIEAASAI 13
DB 30 WSKAGITAAAI 42
```

RESULT 43

```
US-10-767-701-40957
; Sequence 40957, Application US/10767701
; Publication No. US20040172694A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 40957
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C13324_1.pep
US-10-767-701-40957
```

```
Query Match 55.8%; Score 43; DB 4; Length 324;
Best Local Similarity 46.7%; Pred. No. 62;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
```

```
QY 1 WNFAGIEAASAIQ 15
DB 19 WNYCGRRLAGAVDG 33
```

RESULT 44

```
US-10-369-493-21850
; Sequence 21850, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Harry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 21850
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Rhodobacter capsulatus
US-10-369-493-21850
```

```
Query Match 55.8%; Score 43; DB 4; Length 400;
```

```
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 201780
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(515)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_115606C.1.pep
US-10-425-115-201780

Query Match          54.5%; Score 42; DB 4; Length 515;
Best Local Similarity 57.1%; Pred. No. 1.5e+02;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      2 NFAGIEAAASAIQG 15
DB      447 NAAGVQATAAYQG 460

RESULT 48
US-10-437-963-133273
; Sequence 133273, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Brad
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 133273
; LENGTH: 1447
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_3515C.1.pep
US-10-437-963-133273

Query Match          54.5%; Score 42; DB 4; Length 1447;
Best Local Similarity 53.8%; Pred. No. 4.5e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      1 WNPAGIEAAASAI 13
DB      1422 WQFAGIDTVHSAV 1434

RESULT 49
US-10-437-963-108079
; Sequence 108079, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
```

```
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 201780
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(515)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_115606C.1.pep
US-10-425-115-201780

Query Match          54.5%; Score 42; DB 4; Length 515;
Best Local Similarity 57.1%; Pred. No. 1.5e+02;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      2 NFAGIEAAASAIQG 15
DB      447 NAAGVQATAAYQG 460

RESULT 48
US-10-437-963-133273
; Sequence 133273, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Brad
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 133273
; LENGTH: 1447
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_3515C.1.pep
US-10-437-963-133273

Query Match          54.5%; Score 42; DB 4; Length 1447;
Best Local Similarity 53.8%; Pred. No. 4.5e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      1 WNPAGIEAAASAI 13
DB      1422 WQFAGIDTVHSAV 1434

RESULT 49
US-10-437-963-108079
; Sequence 108079, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
```

```
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 201780
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(515)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_115606C.1.pep
US-10-425-115-201780

Query Match          54.5%; Score 42; DB 4; Length 515;
Best Local Similarity 57.1%; Pred. No. 1.5e+02;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      2 NFAGIEAAASAIQG 15
DB      447 NAAGVQATAAYQG 460

RESULT 48
US-10-437-963-133273
; Sequence 133273, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Brad
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 133273
; LENGTH: 1447
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_3515C.1.pep
US-10-437-963-133273

Query Match          54.5%; Score 42; DB 4; Length 1447;
Best Local Similarity 53.8%; Pred. No. 4.5e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      1 WNPAGIEAAASAI 13
DB      1422 WQFAGIDTVHSAV 1434

RESULT 49
US-10-437-963-108079
; Sequence 108079, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
```

```
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Xihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 108079
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_12368C.1.pep
US-10-437-963-108079

Query Match      53.2%; Score 41; DB 4; Length 93;
Best Local Similarity 53.3%; Pred. NO. 36;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      1 WNFAGIEAASAIQG 15
DB      22 WIFALMAAAGSVQG 36

RESULT 50
US-10-264-213-168
; Sequence 168, Application US/10264213
; Publication No. US20040009490A1
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Havukkala, Ilkka J
; APPLICANT: Lubbers, Mark William
; APPLICANT: Dekker, James
; TITLE OF INVENTION: Polynucleotides, materials incorporating
; FILE REFERENCE: 11000.1043c3
; CURRENT APPLICATION NUMBER: US/10/264,213
; CURRENT FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 168
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Lactobacillus rhamnosus
US-10-264-213-168

Query Match      53.2%; Score 41; DB 4; Length 149;
Best Local Similarity 57.1%; Pred. NO. 60;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 NFAGIEAASAIQG 15
DB      67 NIAGVEAAAGLFG 80

Search completed: May 4, 2006, 15:38:51
Job time : 138 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 15:35:06 ; Search time 18 Seconds
(without alignments)
38.571 Million cell updates/sec

Title: US-09-830-839-6

Perfect score: 77

Sequence: 1 WNFAGIEAASAIQ 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications AA New:*
1: /SIDSS/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
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3: /SIDSS/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	77	100.0	20	11 US-11-041-893-237	Sequence 237, Appl
3	77	100.0	20	11 US-11-156-365-26	Sequence 26, Appl
4	77	100.0	95	11 US-11-041-893-214	Sequence 214, Appl
5	77	100.0	97	9 US-10-909-957-4	Sequence 4, Appl
6	77	100.0	249	9 US-10-909-957-2	Sequence 2, Appl
7	71	92.2	15	11 US-11-041-893-217	Sequence 217, Appl
8	60	77.9	15	11 US-11-156-365-8	Sequence 8, Appl
9	54	70.1	10	11 US-11-041-893-246	Sequence 246, Appl
10	54	70.1	13	11 US-11-041-893-42	Sequence 42, Appl
11	54	70.1	13	11 US-11-041-893-48	Sequence 48, Appl
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13	54	70.1	15	11 US-11-041-893-218	Sequence 218, Appl
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19	39	50.6	326	11 US-11-087-099-1226	Sequence 1226, Ap
20	39	50.6	380	11 US-11-096-568A-6971	Sequence 6971, Ap
21	39	50.6	396	11 US-11-096-568A-6970	Sequence 6970, Ap

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39	50.6	1866	8	US-10-511-937-2968	Sequence 2968, Ap
39	50.6	1866	9	US-10-511-989-186	Sequence 186, App
39	50.6	281	11	US-11-079-463-6409	Sequence 6409, Ap
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249	33	42.9	407	9	US-10-873-528-14	Sequence 14, Appl	322	746	11	US-11-074-176-314	Sequence 314, Appl
250	33	42.9	408	11	US-11-087-099-2091	Sequence 2091, Ap	323	749	11	US-11-074-176-54	Sequence 54, Appl
251	33	42.9	417	11	US-11-108-528-64	Sequence 64, Appl	324	777	9	US-10-821-234-1658	Sequence 1658, Ap
252	33	42.9	417	11	US-11-108-528-66	Sequence 66, Appl	325	777	11	US-11-124-367A-301	Sequence 301, App
253	33	42.9	423	11	US-11-087-099-8901	Sequence 8901, Ap	326	777	11	US-11-124-367A-303	Sequence 303, App
254	33	42.9	424	11	US-11-087-099-5962	Sequence 5962, Ap	327	843	11	US-11-188-298-10483	Sequence 10483, A
255	33	42.9	425	11	US-11-087-099-6684	Sequence 6684, Ap	328	869	11	US-11-072-512-2532	Sequence 2532, Ap
256	33	42.9	425	11	US-11-188-298-6103	Sequence 6103, Ap	329	900	11	US-11-045-004-890	Sequence 890, App
257	33	42.9	426	11	US-11-087-099-2781	Sequence 2781, Ap	330	901	9	US-10-793-626-342	Sequence 342, App
258	33	42.9	426	11	US-11-087-099-6894	Sequence 6894, Ap	331	908	11	US-11-077-619-90	Sequence 90, Appl
259	33	42.9	427	11	US-11-172-740-333	Sequence 333, App	332	909	11	US-11-077-619-8	Sequence 8, Appl
260	33	42.9	435	9	US-10-506-454-797	Sequence 797, App	333	1119	11	US-11-079-463-7747	Sequence 7747, Ap
261	33	42.9	436	11	US-11-087-099-7235	Sequence 7235, Ap	334	4834	8	US-10-505-928-827	Sequence 827, App
262	33	42.9	437	11	US-11-087-099-871	Sequence 871, App	335	7465	11	US-11-087-099-7521	Sequence 7521, Ap
263	33	42.9	439	11	US-11-087-099-3160	Sequence 3160, Ap	336	169	11	US-11-045-004-851	Sequence 851, App
264	33	42.9	439	11	US-11-087-099-3928	Sequence 3928, Ap	337	207	11	US-11-096-568A-174	Sequence 174, App
265	33	42.9	439	11	US-11-087-099-6119	Sequence 6119, Ap	338	207	11	US-11-096-568A-175	Sequence 175, App
266	33	42.9	439	11	US-11-087-099-8125	Sequence 8125, Ap	339	221	11	US-11-096-568A-173	Sequence 173, App
267	33	42.9	439	11	US-11-087-099-9275	Sequence 9275, Ap	340	407	11	US-11-092-140-4	Sequence 4, Appl
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269	33	42.9	455	11	US-11-087-099-2048	Sequence 2048, Ap	342	818	11	US-11-087-099-5597	Sequence 5597, Ap
270	33	42.9	466	11	US-11-087-099-2102	Sequence 2102, Ap	343	43	11	US-11-008-119-11	Sequence 11, Appl
271	33	42.9	466	11	US-11-087-099-5346	Sequence 5346, Ap	344	54	9	US-10-467-657-412	Sequence 412, App
272	33	42.9	466	11	US-11-087-099-7729	Sequence 7729, Ap	345	89	11	US-11-079-463-7353	Sequence 7353, Ap
273	33	42.9	466	11	US-11-087-099-9291	Sequence 9291, Ap	346	105	9	US-10-453-372-1178	Sequence 1178, Ap
274	33	42.9	466	11	US-11-087-099-12077	Sequence 12077, A	347	126	11	US-11-087-099-7822	Sequence 7822, Ap
275	33	42.9	466	11	US-11-188-298-4884	Sequence 4884, Ap	348	148	11	US-11-106-270-6	Sequence 6, Appl
276	33	42.9	466	11	US-11-188-298-11332	Sequence 11332, A	349	162	11	US-11-106-270-8	Sequence 8, Appl
277	33	42.9	466	11	US-11-188-298-13056	Sequence 13056, A	350	196	11	US-11-188-298-5157	Sequence 5157, Ap
278	33	42.9	466	11	US-11-188-298-18164	Sequence 18164, A	351	196	11	US-11-188-298-10225	Sequence 10225, A
279	33	42.9	466	11	US-11-188-298-19644	Sequence 19644, A	352	211	9	US-10-498-026-107	Sequence 107, App
280	33	42.9	467	11	US-11-087-099-2054	Sequence 2054, Ap	353	211	9	US-10-498-026-108	Sequence 108, App
281	33	42.9	468	11	US-11-087-099-3324	Sequence 3324, Ap	354	220	11	US-11-188-298-18421	Sequence 18421, A
282	33	42.9	468	11	US-11-087-099-3450	Sequence 3450, Ap	355	221	11	US-11-188-298-5464	Sequence 5464, Ap
283	33	42.9	468	11	US-11-087-099-9301	Sequence 9301, Ap	356	221	11	US-11-188-298-13669	Sequence 13669, A
284	33	42.9	468	11	US-11-087-099-10159	Sequence 10159, A	357	229	9	US-10-506-454-1065	Sequence 1065, Ap
285	33	42.9	468	11	US-11-087-099-12285	Sequence 12285, A	358	230	11	US-11-096-568A-17448	Sequence 17448, A
286	33	42.9	472	11	US-11-087-099-12291	Sequence 12291, A	359	239	11	US-11-096-568A-19957	Sequence 19957, A
287	33	42.9	473	9	US-10-793-626-60	Sequence 60, Appl	360	241	11	US-11-087-099-6572	Sequence 6572, Ap
288	33	42.9	473	11	US-11-087-099-3847	Sequence 3847, Ap	361	243	11	US-11-096-568A-3662	Sequence 9662, Ap
289	33	42.9	475	11	US-11-087-099-1870	Sequence 1870, Ap	362	252	11	US-11-188-298-9306	Sequence 9306, Ap
290	33	42.9	475	11	US-11-087-099-7571	Sequence 7571, Ap	363	253	9	US-10-509-691-2	Sequence 2, Appl
291	33	42.9	481	11	US-11-087-099-6086	Sequence 6086, Ap	364	255	11	US-11-096-568A-19956	Sequence 19956, A
292	33	42.9	482	11	US-11-087-099-4146	Sequence 4146, Ap	365	267	11	US-11-096-568A-9661	Sequence 9661, Ap
293	33	42.9	483	11	US-11-087-099-4117	Sequence 4117, Ap	366	276	11	US-11-188-298-11587	Sequence 11587, A
294	33	42.9	485	11	US-11-087-099-3604	Sequence 3604, Ap	367	276	11	US-11-096-568A-9660	Sequence 9660, Ap
295	33	42.9	485	11	US-11-087-099-10044	Sequence 10044, A	368	279	11	US-11-079-463-5319	Sequence 5319, Ap
296	33	42.9	486	11	US-11-087-099-6341	Sequence 6341, Ap	369	280	11	US-11-096-568A-17447	Sequence 17447, A
297	33	42.9	486	11	US-11-087-099-2642	Sequence 2642, Ap	370	294	11	US-11-188-298-18075	Sequence 18075, A
298	33	42.9	487	11	US-11-087-099-2506	Sequence 2506, Ap	371	311	11	US-11-188-298-5849	Sequence 5849, Ap
299	33	42.9	487	11	US-11-188-298-18754	Sequence 18754, A	372	319	11	US-11-079-463-5849	Sequence 334, App
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301	33	42.9	501	11	US-11-055-822-52	Sequence 52, Appl	374	325	11	US-11-188-298-5632	Sequence 5632, Ap
302	33	42.9	501	11	US-11-239-674-50	Sequence 50, Appl	375	325	11	US-11-239-674-4	Sequence 4, Appl
303	33	42.9	507	11	US-11-188-298-5321	Sequence 5321, Ap	376	334	11	US-11-188-298-1567	Sequence 1567, Ap
304	33	42.9	510	11	US-11-096-568A-17760	Sequence 17760, A	377	336	9	US-10-793-626-2278	Sequence 2278, Ap
305	33	42.9	511	11	US-11-188-298-13117	Sequence 13117, A	378	349	11	US-11-087-099-523	Sequence 523, App
306	33	42.9	517	9	US-10-485-517-310	Sequence 310, App	379	350	11	US-11-106-270-16	Sequence 14, Appl
307	33	42.9	536	11	US-11-096-568A-17759	Sequence 17759, A	380	352	11	US-11-106-270-16	Sequence 1746, Appl
308	33	42.9	538	11	US-11-188-298-4138	Sequence 4138, Ap	381	353	11	US-11-096-568A-17446	Sequence 17446, A
309	33	42.9	552	11	US-11-087-099-10983	Sequence 10983, A	382	367	9	US-11-188-298-21874	Sequence 21874, A
310	33	42.9	558	9	US-10-506-454-1531	Sequence 1531, Ap	383	368	11	US-10-858-730-217	Sequence 217, App
311	33	42.9	566	11	US-11-072-512-2407	Sequence 2407, Ap	384	370	11	US-11-188-298-16300	Sequence 16300, A
312	33	42.9	571	9	US-10-216-161A-132	Sequence 132, App	385	373	11	US-11-045-004-1588	Sequence 1588, Ap
313	33	42.9	576	11	US-11-188-298-9208	Sequence 9208, Ap	386	375	11	US-11-096-568A-10981	Sequence 10981, A

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390	32	41.6	417	11	US-11-120-422-2	Sequence 2, Appl	463	41.6	1565	9	US-10-453-372-1180	Sequence 1180, Ap
391	32	41.6	417	11	US-11-226-480-2	Sequence 2, Appl	464	41.6	1566	8	US-10-453-372-1190	Sequence 1190, Ap
392	32	41.6	417	11	US-11-228-079-2	Sequence 2, Appl	465	41.6	2026	8	US-10-505-928-831	Sequence 831, App
393	32	41.6	418	9	US-11-056-454-1438	Sequence 1438, Ap	466	41.6	2053	9	US-10-453-372-1174	Sequence 1174, Ap
394	32	41.6	420	11	US-11-096-568A-11992	Sequence 11992, A	467	41.6	2143	9	US-10-453-372-1188	Sequence 1188, Ap
395	32	41.6	424	11	US-11-232-440-23	Sequence 23, Appl	468	41.6	175	11	US-11-098-686-102	Sequence 102, App
396	32	41.6	424	11	US-11-194-991-82	Sequence 82, Appl	469	41.6	388	11	US-11-096-568A-17432	Sequence 17432, A
397	32	41.6	432	9	US-10-194-487-74	Sequence 74, Appl	470	41.6	408	11	US-11-096-568A-17431	Sequence 17431, A
398	32	41.6	432	9	US-10-195-883-74	Sequence 74, Appl	471	41.6	416	9	US-10-506-454-931	Sequence 931, App
399	32	41.6	432	9	US-10-195-888-74	Sequence 74, Appl	472	41.6	482	11	US-11-188-298-10847	Sequence 10847, A
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402	32	41.6	432	9	US-10-501-841-45	Sequence 45, Appl	475	41.6	594	11	US-11-087-099-1758	Sequence 1758, Ap
403	32	41.6	448	11	US-11-096-568A-11991	Sequence 11991, A	476	41.6	614	11	US-11-087-099-3677	Sequence 3677, Ap
404	32	41.6	450	11	US-11-096-568A-34710	Sequence 24710, A	477	41.6	2204	11	US-11-052-554A-134	Sequence 134, App
405	32	41.6	452	9	US-10-858-730-282	Sequence 282, App	478	41.6	31	8	US-10-530-061-2500	Sequence 2500, Ap
406	32	41.6	457	11	US-11-079-463-6587	Sequence 6587, Ap	479	41.6	49	11	US-11-183-567A-18	Sequence 18, Appl
407	32	41.6	459	11	US-11-087-099-8637	Sequence 8637, Ap	480	41.6	52	11	US-11-172-740-2044	Sequence 2044, Ap
408	32	41.6	467	11	US-11-087-099-3539	Sequence 3539, Ap	481	41.6	72	11	US-11-079-463-9930	Sequence 9930, Ap
409	32	41.6	469	11	US-11-087-099-4123	Sequence 4123, Ap	482	41.6	74	9	US-10-467-657-9050	Sequence 9050, Ap
410	32	41.6	475	11	US-11-087-099-7087	Sequence 7087, Ap	483	41.6	90	9	US-10-467-657-2210	Sequence 2210, Ap
411	32	41.6	476	11	US-11-087-099-1256	Sequence 1256, Ap	484	41.6	113	11	US-11-096-568A-25100	Sequence 25100, A
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413	32	41.6	476	11	US-11-087-099-8740	Sequence 8740, Ap	486	41.6	115	11	US-11-079-463-6533	Sequence 6533, Ap
414	32	41.6	478	11	US-11-087-099-9555	Sequence 9555, Ap	487	41.6	123	9	US-10-467-657-7936	Sequence 7936, A
415	32	41.6	483	11	US-11-057-012-26	Sequence 8872, Ap	488	41.6	143	11	US-11-096-568A-19073	Sequence 19073, A
416	32	41.6	483	11	US-11-057-012-26	Sequence 26, Appl	489	41.6	143	11	US-11-172-740-861	Sequence 861, App
417	32	41.6	496	11	US-11-069-642-20	Sequence 20, Appl	490	41.6	145	11	US-11-096-568A-15611	Sequence 15611, A
418	32	41.6	497	11	US-11-188-298-3253	Sequence 3253, Ap	491	41.6	151	11	US-11-096-568A-25099	Sequence 25099, A
419	32	41.6	497	11	US-11-188-298-5703	Sequence 5703, Ap	492	41.6	151	9	US-10-793-626-3164	Sequence 3164, Ap
420	32	41.6	497	11	US-11-188-298-7140	Sequence 7140, Ap	493	41.6	154	11	US-11-096-568A-16014	Sequence 16014, A
421	32	41.6	499	11	US-11-188-298-7140	Sequence 7140, Ap	494	41.6	159	11	US-11-183-664-12	Sequence 12, Appl
422	32	41.6	502	11	US-11-188-298-13575	Sequence 13575, A	495	41.6	169	11	US-11-096-568A-16013	Sequence 16013, A
423	32	41.6	508	11	US-11-188-298-9832	Sequence 9832, Ap	496	41.6	173	11	US-11-188-298-2582	Sequence 2582, A
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427	32	41.6	525	11	US-11-194-991-69	Sequence 69, Appl	500	41.6	185	11	US-11-079-463-9917	Sequence 9917, Ap
428	32	41.6	525	11	US-11-194-991-71	Sequence 71, Appl	501	41.6	185	11	US-11-045-004-64	Sequence 64, Appl
429	32	41.6	525	11	US-11-194-991-73	Sequence 73, Appl	502	41.6	196	11	US-11-188-298-7598	Sequence 7598, Ap
430	32	41.6	525	11	US-11-194-991-75	Sequence 75, Appl	503	41.6	205	11	US-11-079-463-5835	Sequence 5835, Ap
431	32	41.6	532	11	US-11-096-568A-25921	Sequence 25921, A	504	41.6	210	11	US-11-188-298-15586	Sequence 15586, A
432	32	41.6	543	11	US-11-087-099-4125	Sequence 4125, Ap	505	41.6	212	11	US-11-044-111-6	Sequence 6, Appl
433	32	41.6	544	11	US-11-188-298-9865	Sequence 9865, Ap	506	41.6	212	11	US-11-044-111-26	Sequence 26, Appl
434	32	41.6	545	11	US-11-188-298-3478	Sequence 3478, Ap	507	41.6	215	11	US-11-183-664-26	Sequence 26, Appl
435	32	41.6	549	11	US-11-201-916-13	Sequence 13, Appl	508	41.6	221	11	US-11-264-096-2096	Sequence 2096, Ap
436	32	41.6	552	11	US-11-194-991-1	Sequence 1, Appl	509	41.6	221	11	US-11-096-568A-19072	Sequence 19072, A
437	32	41.6	555	11	US-11-096-568A-25920	Sequence 25920, A	510	41.6	222	11	US-11-096-568A-19071	Sequence 19071, A
438	32	41.6	556	11	US-11-087-099-6700	Sequence 6700, Ap	511	41.6	227	9	US-10-467-657-570	Sequence 570, App
439	32	41.6	556	11	US-11-087-099-8042	Sequence 8042, Ap	512	41.6	239	11	US-11-044-111-5	Sequence 5, Appl
440	32	41.6	556	11	US-11-188-298-6539	Sequence 6539, Ap	513	41.6	239	11	US-11-044-111-25	Sequence 25, Appl
441	32	41.6	556	11	US-11-188-298-7432	Sequence 7432, Ap	514	41.6	240	11	US-11-212-443-159	Sequence 159, App
442	32	41.6	556	11	US-11-188-298-17159	Sequence 17159, A	515	41.6	240	11	US-11-087-099-4635	Sequence 4635, Ap
443	32	41.6	565	11	US-11-096-568A-25919	Sequence 25919, A	516	41.6	241	11	US-11-087-099-7424	Sequence 7424, Ap
444	32	41.6	577	11	US-11-054-381-130	Sequence 130, App	517	41.6	242	11	US-11-172-740-1484	Sequence 1484, Ap
445	32	41.6	609	9	US-10-511-538-253	Sequence 253, App	518	41.6	248	9	US-10-644-807-326	Sequence 326, App
446	32	41.6	634	11	US-11-188-298-2298	Sequence 2298, Ap	519	41.6	251	11	US-11-096-568A-22969	Sequence 22969, A
447	32	41.6	648	11	US-11-096-568A-24709	Sequence 24709, A	520	41.6	252	11	US-11-096-568A-8528	Sequence 8528, Ap
448	32	41.6	648	11	US-11-096-568A-24708	Sequence 24708, A	521	41.6	254	11	US-11-096-568A-8527	Sequence 8527, Ap
449	32	41.6	710	11	US-11-201-519-16	Sequence 16, Appl	522	41.6	256	11	US-11-096-568A-22968	Sequence 22968, A
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451	32	41.6	758	11	US-11-188-298-12555	Sequence 12555, A	524	41.6	257	11	US-11-188-298-10828	Sequence 10828, A
452	32	41.6	765	11	US-11-242-650-8	Sequence 8, Appl	525	41.6	258	11	US-11-090-439-38	Sequence 38, Appl
453	32	41.6	783	11	US-11-194-991-77	Sequence 77, Appl	526	41.6	261	11	US-11-096-568A-22967	Sequence 22967, A
454	32	41.6	785	11	US-11-194-991-79	Sequence 79, Appl	527	41.6	269	9	US-10-467-657-7278	Sequence 7278, Ap
455	32	41.6	856	11	US-11-201-519-12	Sequence 12, Appl	528	41.6	273	9	US-10-453-372-1062	Sequence 1062, Ap
456	32	41.6	856	11	US-10-858-730-208	Sequence 208, App	529	41.6	276	9	US-10-453-372-1060	Sequence 1060, Ap
457	32	41.6	1140	9	US-10-858-730-208	Sequence 30715, A	530	41.6	276	9	US-10-506-454-1125	Sequence 1125, Ap
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459	32	41.6	1216	11	US-11-096-568A-30714	Sequence 30714, A	532	41.6	286	11	US-11-188-298-13455	Sequence 13455, A
	32	41.6	1227	11	US-11-096-568A-30713	Sequence 30713, A						

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534	31	40.3	288	11	US-11-096-568A-1916	Sequence 1916, Ap	607	31	40.3	465	11	US-11-087-099-3526	Sequence 3526, Ap
535	31	40.3	291	11	US-11-087-099-3559	Sequence 3559, Ap	608	31	40.3	468	11	US-11-096-568A-6021	Sequence 6021, Ap
536	31	40.3	293	11	US-11-264-096-1755	Sequence 1755, Ap	609	31	40.3	469	11	US-11-188-298-15973	Sequence 15973, A
537	31	40.3	295	11	US-11-079-463-6219	Sequence 6219, Ap	610	31	40.3	471	11	US-11-087-099-4362	Sequence 4362, A
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ALIGNMENTS

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RESULT 1
US-11-041-893-41
; Sequence 41, Application US/11041893
; Publication No. US20060002941A1
; GENERAL INFORMATION:
; APPLICANT: Mahairas, Gregory G.
; TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
; FILE REFERENCE: 100123.401
; CURRENT FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US/11/041,893
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/616,855
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/538,713
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-11-041-893-41
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Best Local Similarity 100.0%; Pred. No. 3e-07;
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Db 6 WNPAGIEAAASAIQG 20
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US-11-041-893-237
; Sequence 237, Application US/11041893
; Publication No. US20060002941A1
; GENERAL INFORMATION:
; APPLICANT: Mahairas, Gregory G.
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Sequence 49, Appl
Sequence 50, Appl
Sequence 985, App
Sequence 4176, Ap
Sequence 47, Appl
Sequence 49, Appl
Sequence 1, Appli
Sequence 4, Appli
Sequence 46, Appl
Sequence 225, App
Sequence 18, Appl
Sequence 47, Appl
Sequence 34, Appl
Sequence 3, Appli
Sequence 9042, Ap
Sequence 12122, A
Sequence 6153, Ap
Sequence 9244, Ap
Sequence 7153, Ap
Sequence 354, App
Sequence 340, App
Sequence 150, App
Sequence 59, Appl
Sequence 12698, A
Sequence 7846, Ap
Sequence 18278, A
Sequence 2459, Ap
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Db 6 WNPAGIEAAASAIQG 20
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RESULT 3
US-11-156-365-26
; Sequence 26, Application US/11156365
; Publication No. US20060040332A1
; GENERAL INFORMATION:
; APPLICANT: BECKMAN COULTER, INC.
; APPLICANT: MAERKER, Markus
; TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS EPITOPES AND METHODS OF USE THEREOF
; FILE REFERENCE: BECK1160-2
; CURRENT APPLICATION NUMBER: US/11/156,365
; CURRENT FILING DATE: 2005-06-16
; PRIOR APPLICATION NUMBER: US 60/622,505
; PRIOR FILING DATE: 2004-10-27
; PRIOR APPLICATION NUMBER: US 60/580,559
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-11-156-365-26
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Query Match 100.0%; Score 77; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e-07;
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QY 1 WNPAGIEAAASAIQG 15
Db 6 WNPAGIEAAASAIQG 20
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RESULT 4
US-11-041-893-214
; Sequence 214, Application US/11041893
; Publication No. US20060002941A1
; GENERAL INFORMATION:
; APPLICANT: Mahairas, Gregory G.
; TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
; FILE REFERENCE: 100123.401
; CURRENT APPLICATION NUMBER: US/11/041,893
; CURRENT FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/616,855
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/538,713
; PRIOR FILING DATE: 2004-01-23
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; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 214
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Mycobacteria tuberculosis
US-11-041-893-214

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Best Local Similarity 100.0%; Pred. No. 1.6e-06; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 6 WNFAGIEAAASAIQ 20
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RESULT 5

US-10-909-957-4
; Sequence 4, Application US/10909957
; Publication No. US20060024332A1
; GENERAL INFORMATION:
; APPLICANT: Waters, Wade R
; APPLICANT: Palmer, Mitchell V
; APPLICANT: Minion, Frank C
; TITLE OF INVENTION: Recombinant ESAT-6:CFP-10 Fusion Protein Useful for
; TITLE OF INVENTION: Specific Diagnosis of Tuberculosis
; FILE REFERENCE: 0072.04 - Waters et al.
; CURRENT APPLICATION NUMBER: US/10/909,957
; CURRENT FILING DATE: 2004-08-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Mycobacterium bovis
US-10-909-957-4

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QY 1 WNFAGIEAAASAIQ 15
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DB 8 WNFAGIEAAASAIQ 22
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RESULT 6

US-10-909-957-2
; Sequence 2, Application US/10909957
; Publication No. US20060024332A1
; GENERAL INFORMATION:
; APPLICANT: Waters, Wade R
; APPLICANT: Palmer, Mitchell V
; APPLICANT: Minion, Frank C
; TITLE OF INVENTION: Recombinant ESAT-6:CFP-10 Fusion Protein Useful for
; TITLE OF INVENTION: Specific Diagnosis of Tuberculosis
; FILE REFERENCE: 0072.04 - Waters et al.
; CURRENT APPLICATION NUMBER: US/10/909,957
; CURRENT FILING DATE: 2004-08-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Mycobacterium bovis
US-10-909-957-2

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Best Local Similarity 100.0%; Pred. No. 4.7e-06; Indels 0; Gaps 0;
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QY 1 WNFAGIEAAASAIQ 15

DB 39 WNFAGIEAAASAIQ 53
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RESULT 7

US-11-041-893-217
; Sequence 217, Application US/11041893
; Publication No. US2006002941A1
; GENERAL INFORMATION:
; APPLICANT: Mahairas, Gregory G.
; TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
; TITLE OF INVENTION: ALTERING AGENTS AND METHODS OF USE
; FILE REFERENCE: 100123.401
; CURRENT APPLICATION NUMBER: US/11/041,893
; CURRENT FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/616,855
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/538,713
; PRIOR FILING DATE: 2004-01-23
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 217
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mycobacteria tuberculosis
US-11-041-893-217

Query Match 92.2%; Score 71; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.5e-06; Indels 0; Gaps 0;
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QY 1 WNFAGIEAAASAIQ 14
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DB 2 WNFAGIEAAASAIQ 15
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RESULT 8

US-11-156-365-8
; Sequence 8, Application US/11156365
; Publication No. US20060040332A1
; GENERAL INFORMATION:
; APPLICANT: BECKMAN COULTER, INC.
; APPLICANT: MAEUREN, Markus
; TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS EPITOPES AND METHODS OF USE THEREOF
; FILE REFERENCE: BECK1160-2
; CURRENT APPLICATION NUMBER: US/11/156,365
; CURRENT FILING DATE: 2005-06-16
; PRIOR APPLICATION NUMBER: US 60/622,505
; PRIOR FILING DATE: 2004-10-27
; PRIOR APPLICATION NUMBER: US 60/580,559
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-11-156-365-8

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Best Local Similarity 100.0%; Pred. No. 0.00022; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FAGIEAAASAIQ 15
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DB 1 FAGIEAAASAIQ 13
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RESULT 9

US-11-041-893-246
; Sequence 246, Application US/11041893
; Publication No. US2006002941A1
; GENERAL INFORMATION:

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; APPLICANT: Mahairas, Gregory G.
; TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
; FILE REFERENCE: 100123.401
; CURRENT APPLICATION NUMBER: US/11/041,893
; CURRENT FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/616,855
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/538,713
; PRIOR FILING DATE: 2004-01-23
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 246
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mycobacteria tuberculosis
US-11-041-893-246

Query Match          70.1%; Score 54; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAAA 10
   |||||
Db 1 WNFAGIEAAA 10

RESULT 10
US-11-041-893-42
; Sequence 42, Application US/11041893
; Publication No. US20060002941A1
; GENERAL INFORMATION:
; APPLICANT: Mahairas, Gregory G.
; TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
; FILE REFERENCE: 100123.401
; CURRENT APPLICATION NUMBER: US/11/041,893
; CURRENT FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/616,855
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/538,713
; PRIOR FILING DATE: 2004-01-23
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-11-041-893-42

Query Match          70.1%; Score 54; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAAA 10
   |||||
Db 4 WNFAGIEAAA 13

RESULT 11
US-11-041-893-48
; Sequence 48, Application US/11041893
; Publication No. US20060002941A1
; GENERAL INFORMATION:
; APPLICANT: Mahairas, Gregory G.
; TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
; FILE REFERENCE: 100123.401
; CURRENT APPLICATION NUMBER: US/11/041,893
; CURRENT FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/616,855
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/538,713
; PRIOR FILING DATE: 2004-01-23
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 218
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mycobacteria tuberculosis
US-11-041-893-218
```

```
; PRIOR FILING DATE: 2004-01-23
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-11-041-893-48

Query Match          70.1%; Score 54; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAAA 10
   |||||
Db 4 WNFAGIEAAA 13

RESULT 12
US-11-041-893-216
; Sequence 216, Application US/11041893
; Publication No. US20060002941A1
; GENERAL INFORMATION:
; APPLICANT: Mahairas, Gregory G.
; TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
; FILE REFERENCE: 100123.401
; CURRENT APPLICATION NUMBER: US/11/041,893
; CURRENT FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/616,855
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/538,713
; PRIOR FILING DATE: 2004-01-23
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 216
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mycobacteria tuberculosis
US-11-041-893-216

Query Match          70.1%; Score 54; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAAA 10
   |||||
Db 6 WNFAGIEAAA 15

RESULT 13
US-11-041-893-218
; Sequence 218, Application US/11041893
; Publication No. US20060002941A1
; GENERAL INFORMATION:
; APPLICANT: Mahairas, Gregory G.
; TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
; FILE REFERENCE: 100123.401
; CURRENT APPLICATION NUMBER: US/11/041,893
; CURRENT FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/616,855
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/538,713
; PRIOR FILING DATE: 2004-01-23
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 218
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mycobacteria tuberculosis
US-11-041-893-218
```

Query Match 70.1%; Score 54; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 12; Conservative 0; Mismatches 0; Indels

Qy 4 AGIEAAASAIQG 15
Db 1 AGIEAAASAIQG 12

```

RECORD 14
US-11-041-893-43
; Sequence 43, Application US/11041893
; Publication No. US20060002941A1
; GENERAL INFORMATION:
; APPLICANT: Mahairas, Gregory G
; TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
; ; TITLE OF INVENTION: ALTERING AGENTS AND METHODS OF USE
; FILE REFERENCE: 100123.401
; CURRENT APPLICATION NUMBER: US/11/041,893
; CURRENT FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/616,855
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/538,713
; PRIOR FILING DATE: 2004-01-23
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 9
; TYPE: PR1
; ORGANISM: Mycobacterium tuberculosis
US-11-041-893-43

```

Query Match 64.9%; Score 50; DB 11; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.9e+05;
Matches 9: Conservative 0; Mismatches 0; Indels

Qy 1 WNFAGIEAA 9
|||||

Dp 1 WNFAGIEAA 9
|||||

```

RESULT 15
US-11-041-893-247
; Sequence 247, Application US/11041893
; Publication No. US2006002941A1
; GENERAL INFORMATION:
; APPLICANT: Mahaitas, Gregory G.
; TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
; ; TITLE OF INVENTION: ALTERING AGENTS AND METHODS OF USE
; ; FILE REFERENCE: 100123.401
; ; CURRENT APPLICATION NUMBER: US/11/041,893
; ; CURRENT FILING DATE: 2005-01-24
; ; PRIOR APPLICATION NUMBER: US 60/616,855
; ; PRIOR FILING DATE: 2004-10-06
; ; PRIOR APPLICATION NUMBER: US 60/538,713
; ; PRIOR FILING DATE: 2004-01-23
; ; NUMBER OF SEQ ID NOS: 295
; ; SOFTWARE: FastSeq for Windows Version 4.0
; ; SEQ ID NO 247
; ; LENGTH: 10
; ; TYPE: prt
; ; ORGANISM: Mycobacteria tuberculosis
US-11-041-893-247

```

Query Match 57.1%; Score 44; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches 10: Conservative 0: Mismatches 0: Indels

Qy 6 IEAAASAIQG 15
|||

Dh 1 IEAAASAIQG 10

```

RESULT 16
US-11-041-893-238
; Sequence 238, Application US/11041893
; Publication No. US2006002941A1
; GENERAL INFORMATION:
; APPLICANT: Mahaitas, Gregory G.
; TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
; TITLE OF INVENTION: ALTERING AGENTS AND METHODS OF USE
; FILE REFERENCE: 100123.401
; CURRENT APPLICATION NUMBER: US/11/041,893
; CURRENT FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/616,855
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/538,713
; PRIOR FILING DATE: 2004-01-23
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 238
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mycobacteria tuberculosis
US-11-041-893-238

```

Query Match 57.1%; Score 44; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 10: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 IEAAASAIQG 15
db 1 IEAAASAIQG 10

```

RESULT 17
US-11-188-298-2826
US-11-188-298-2826, Application US/11188298
; Publication NO. US2006007522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 2826
; LENGTH: 294
; TYPE: PrT
; ORGANISM: Escherichia blattae
US-11-188-298-2826

```

```

Query Match      51.9%; Score 40; DB 11; Length 294;
Best Local Similarity 58.3%; Pred. No. 18;
Matches         7: Conservative 1: Mismatches 4: Indels 0: Gaps 0

```

Qy 1 WNFAGIEAAASA 12
|||:|
Db 70 WNEAGVEVVAEA 81

```

RESULT 18
US-11-096-568A-6972
; Sequence 6972, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-determined DN
; TITLE OF INVENTION: Thery
; FILE REFERENCES: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 6972

```

; LENGTH: 324
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)-(324)
; OTHER INFORMATION: Ceres Seq. ID no. 15169353
US-11-096-568A-6972

Query Match 50.6%; Score 39; DB 11; Length 324;
Best Local Similarity 63.6%; Pred. No. 31;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WNFAGIEAAAS 11
|||||: |||:
Db 36 WNFVFAAAAT 46

RESULT 19
US-11-087-099-1226
; Sequence 1226, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 1226
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Escherichia coli
US-11-087-099-1226

Query Match 50.6%; Score 39; DB 11; Length 326;
Best Local Similarity 50.0%; Pred. No. 31;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASA 12
||: ||: ||: ||:
Db 202 WSFIGVESASVA 213

RESULT 20
US-11-096-568A-6971
; Sequence 6971, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 6971
; LENGTH: 380
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(380)
; OTHER INFORMATION: Ceres Seq. ID no. 15169352
US-11-096-568A-6971

Query Match 50.6%; Score 39; DB 11; Length 380;
Best Local Similarity 63.6%; Pred. No. 36;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WNFAGIEAAAS 11
|||||: |||:
Db 92 WNFVFAAAAT 102

RESULT 21
US-11-096-568A-6970
; Sequence 6970, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 6970
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(396)
; OTHER INFORMATION: Ceres Seq. ID no. 15169351
US-11-096-568A-6970

Query Match 50.6%; Score 39; DB 11; Length 396;
Best Local Similarity 63.6%; Pred. No. 38;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WNFAGIEAAAS 11
|||||: |||:
Db 108 WNFVFAAAAT 118

RESULT 22
US-11-087-099-10405
; Sequence 10405, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 10405
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Salmonella enterica subsp. enterica serovar Typhi
US-11-087-099-10405

Query Match 50.6%; Score 39; DB 11; Length 445;
Best Local Similarity 50.0%; Pred. No. 43;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASA 12
||: ||: ||: ||:
Db 202 WSFIGVESASVA 213

RESULT 23
US-11-087-099-12374
; Sequence 12374, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 12374
; LENGTH: 445
; TYPE: PRT

; ORGANISM: Escherichia coli O157:H7 EDL933
US-11-087-099-12374

Query Match 50.6%; Score 39; DB 11; Length 445;
Best Local Similarity 50.0%; Pred. No. 43;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASA 12
|:|:|:|:|
Db 202 WFIGVESASVA 213

RESULT 24

US-11-188-298-11360
; Sequence 11360, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 11360
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Escherichia coli O157:H7 EDL933
US-11-188-298-11360

Query Match 50.6%; Score 39; DB 11; Length 445;
Best Local Similarity 50.0%; Pred. No. 43;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASA 12
|:|:|:|:|
Db 202 WFIGVESASVA 213

RESULT 25

US-10-511-989-24
; Sequence 24, Application US/10511989
; Publication No. US20060053496A1
; GENERAL INFORMATION:
; APPLICANT: University of North Carolina-Chapel Hill
; APPLICANT: Ting, Jenny
; APPLICANT: Linhoff, Michael
; APPLICANT: Harton, Johnathan
; APPLICANT: Williams, Kristi
; APPLICANT: Lich, John
; APPLICANT: O'Connor, William
; APPLICANT: Moore, Christopher
; APPLICANT: Davis, Beckley
; APPLICANT: Brickey, W. Jane
; APPLICANT: Conti, Brian
; APPLICANT: Zhang, Jinghua
; APPLICANT: Zhu, Xin-Sheng
; TITLE OF INVENTION: CATERPILLER GENE FAMILY
; FILE REFERENCE: 5470.368WO
; CURRENT APPLICATION NUMBER: US/10/511,989
; CURRENT FILING DATE: 2004-10-21
; PRIOR APPLICATION NUMBER: US 60/376,626
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 1487
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-989-24

Query Match 50.6%; Score 39; DB 9; Length 1487;

Best Local Similarity 57.1%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASA 14
|||:|:|:|:|
Db 1398 WNLGDEAAAEAAQ 1411

RESULT 26

US-10-511-937-2968
; Sequence 2968, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: Expression Diagnostics, Inc.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2968
; LENGTH: 1866
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2968

Query Match 50.8%; Score 39; DB 8; Length 1866;
Best Local Similarity 57.1%; Pred. No. 2e+02;
Matches 8; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASA 14
|||:|:|:|:|
Db 1777 WNLGDEAAAEAAQ 1790

RESULT 27

US-10-511-989-186
; Sequence 186, Application US/10511989
; Publication No. US20060053496A1
; GENERAL INFORMATION:
; APPLICANT: University of North Carolina-Chapel Hill
; APPLICANT: Ting, Jenny
; APPLICANT: Linhoff, Michael
; APPLICANT: Harton, Johnathan
; APPLICANT: Williams, Kristi
; APPLICANT: Lich, John
; APPLICANT: O'Connor, William
; APPLICANT: Moore, Christopher
; APPLICANT: Davis, Beckley
; APPLICANT: Brickey, W. Jane
; APPLICANT: Conti, Brian
; APPLICANT: Zhang, Jinghua
; APPLICANT: Zhu, Xin-Sheng
; TITLE OF INVENTION: CATERPILLER GENE FAMILY
; FILE REFERENCE: 5470.368WO
; CURRENT APPLICATION NUMBER: US/10/511,989
; CURRENT FILING DATE: 2004-10-21
; PRIOR APPLICATION NUMBER: US 60/376,626
; PRIOR FILING DATE: 2002-04-30

```
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 186
; LENGTH: 1866
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-989-186

Query Match          50.6%; Score 39; DB 9; Length 1866;
Best Local Similarity 57.1%; Pred. No. 2e+02;
Matches 8; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAIQ 14
   ||| |||||
Db 1777 WNLGDEAAAEAAQ 1790

RESULT 28
US-11-079-463-6409
; Sequence 6409, Application US/11079463
; Publication No. US20060073161A1
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FR
; FILE REFERENCES: PATH00-03DIV2
; CURRENT APPLICATION NUMBER: US/11/079,463
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/128,705
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/540,209
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 6409
; LENGTH: 281
; TYPE: PRT
; ORGANISM: B.fragilis
US-11-079-463-6409

Query Match          49.4%; Score 38; DB 11; Length 281;
Best Local Similarity 40.0%; Pred. No. 39;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASAIQ 15
   | : || : |||
Db 33 WGYAGADTLPAADIG 47

RESULT 29
US-11-188-298-7795
; Sequence 7795, Application US/11188298
; Publication No. US2006007522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCES: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 7795
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Oryza sativa
US-11-188-298-7795

Query Match          49.4%; Score 38; DB 11; Length 341;
Best Local Similarity 72.7%; Pred. No. 48;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 GIEAAASAIQ 15
   | ||||| : |||
```

```
Db 62 GGERAAAVQ 72

RESULT 30
US-11-188-298-12202
; Sequence 12202, Application US/11188298
; Publication No. US2006007522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCES: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 12202
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Oryza sativa
US-11-188-298-12202

Query Match          49.4%; Score 38; DB 11; Length 341;
Best Local Similarity 72.7%; Pred. No. 48;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 GIERAAASAIQ 15
   ||||| : |||
Db 62 GGERAAAVQ 72

RESULT 31
US-11-087-099-4027
; Sequence 4027, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCES: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 4027
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Yersinia pestis CO92
US-11-087-099-4027

Query Match          49.4%; Score 38; DB 11; Length 444;
Best Local Similarity 50.0%; Pred. No. 64;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 WNFAGIEAAASA 12
   | : || : |||
Db 200 WSFIGVETASVA 211

RESULT 32
US-11-087-099-8366
; Sequence 8366, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCES: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 8366
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Escherichia coli
US-11-087-099-8366
```

Query Match 49.4%; Score 38; DB 11; Length 454;
Best Local Similarity 60.0%; Pred. No. 66;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WNFAGIEAAA 10
DB 217 WAFVGVESAA 226

RESULT 33

US-11-294-997-9
; Sequence 9, Application US/11294997
; Publication No. US20060067926A1
; GENERAL INFORMATION:
; APPLICANT: Bowers, John
; APPLICANT: Bowers, Alex
; TITLE OF INVENTION: Novel Serine Threonine Kinase Member, h2520-59
; FILE REFERENCE: 01017/36524C
; CURRENT APPLICATION NUMBER: US/11/294,997
; CURRENT FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: US 09/909,474
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,204
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (136)
; OTHER INFORMATION: Xaa = unknown or other
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (138)
; OTHER INFORMATION: Xaa = unknown or other
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (141)
; OTHER INFORMATION: Xaa = unknown or other
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (142)
; OTHER INFORMATION: Xaa = unknown or other
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (143)
; OTHER INFORMATION: Xaa = unknown or other
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (152)
; OTHER INFORMATION: Xaa = unknown or other
US-11-294-997-9

Query Match 48.1%; Score 37; DB 11; Length 153;
Best Local Similarity 50.0%; Pred. No. 30;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 WNFAGIEAAA 12
DB 35 WSWAGIPSSAA 46

RESULT 34

US-11-087-099-7801
; Sequence 7801, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement

; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 7801
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(198)
; OTHER INFORMATION: unsure at all Xaa locations
US-11-087-099-7801

Query Match 48.1%; Score 37; DB 11; Length 198;
Best Local Similarity 50.0%; Pred. No. 40;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 WNFAGIEAAA 14
DB 4 FGFVGIEXAASDVE 17

RESULT 35

US-11-087-099-1149
; Sequence 1149, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 1149
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Shigella flexneri 2a str. 2457T
US-11-087-099-1149

Query Match 48.1%; Score 37; DB 11; Length 338;
Best Local Similarity 46.2%; Pred. No. 72;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 NFAGIEAAA 14
DB 79 HFAGLKAAVESQ 91

RESULT 36

US-11-188-298-19423
; Sequence 19423, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 19423
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Bifidobacterium longum DJO10A
US-11-188-298-19423

Query Match 48.1%; Score 37; DB 11; Length 339;
Best Local Similarity 66.7%; Pred. No. 72;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 AGIEAAA 15

```
Db      116 AGLSGAAIAIQ 127
      ||: || |||||
Query Match      48.1%; Score 37; DB 11; Length 356;
Best Local Similarity 66.7%; Pred. No. 75;
Matches 8; Conservative 1; Mismatches 3; Indels 3; Gaps 0;

RESULT 37
US-11-087-099-3823
; Sequence 3823, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 3823
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Shigella flexneri 2a str. 301
US-11-087-099-3823

Query Match      48.1%; Score 37; DB 11; Length 342;
Best Local Similarity 46.2%; Pred. No. 73;
Matches 6; Conservative 5; Mismatches 2; Indels 2; Gaps 0;

QY      2 NFAGIEAAASAIQ 14
      :|||:|:|:|:|:|
Db      83 HFAGLKAAVSVQ 95

RESULT 38
US-11-188-298-11353
; Sequence 11353, Application US/11188298
; Publication No. US2006007522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 11353
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Bifidobacterium longum NCC2705
US-11-188-298-11353

Query Match      48.1%; Score 37; DB 11; Length 350;
Best Local Similarity 66.7%; Pred. No. 75;
Matches 8; Conservative 1; Mismatches 1; Indels 3; Gaps 0;

QY      4 AGIEAAASAIQ 15
      ||: || |||||
Db      127 AGLSGAAIAIQ 138

RESULT 39
US-11-087-099-3095
; Sequence 3095, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 3095
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Vibrio parahaemolyticus RIMD 2210633
```

```
US-11-087-099-3095
Query Match      48.1%; Score 37; DB 11; Length 356;
Best Local Similarity 66.7%; Pred. No. 76;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      3 FAGIEAAASAIQ 14
      |||:|:|:|:|
Db      244 FAGLESAASQ 255

RESULT 40
US-11-294-997-11
; Sequence 11, Application US/11294997
; Publication No. US20060067926A1
; GENERAL INFORMATION:
; APPLICANT: Boylan, John
; APPLICANT: Bowers, Alex
; TITLE OF INVENTION: Novel Serine Threonine Kinase Member, h2520-59
; FILE REFERENCE: 01017/36524C
; CURRENT APPLICATION NUMBER: US/11/294,997
; CURRENT FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: US 09/909,474
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,204
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-294-997-11

Query Match      48.1%; Score 37; DB 11; Length 360;
Best Local Similarity 50.0%; Pred. No. 77;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY      1 WNFAGIEAAASA 12
      |::|||:|:|:|
Db      4 WSWAGIPSSAAA 15

RESULT 41
US-11-045-004-1762
; Sequence 1762, Application US/11045004
; Publication No. US20060078901A1
; GENERAL INFORMATION:
; APPLICANT: BUCHRIESER, CARMEN
; APPLICANT: FRANGEUL, LIONEL
; APPLICANT: COUVE, ELISABETH
; APPLICANT: RUSNIOK, CHRISTOPHE
; APPLICANT: FSIHI, HAFIDA
; APPLICANT: DEHOUX, PIERRE
; APPLICANT: DUSSURGET, OLIVIER
; APPLICANT: CHETODANI, FARID
; APPLICANT: NEDJARI, HAFED
; APPLICANT: GLASER, PHILIPPE
; APPLICANT: KUNST, FRANCK
; APPLICANT: COSSART, PASCALE
; APPLICANT: DANIELS, JUSTIN
; APPLICANT: GOEBEL, WERNER
; APPLICANT: KREFT, JURGEN
; APPLICANT: KUHN, MICHAEL
; APPLICANT: NG, EVA
; APPLICANT: VAZQUEZ-BOLAND, ANTONIO
; APPLICANT: DOMINGUEZ-BERNAL, GUSTAVO
; APPLICANT: GARRIDO-GARCIA, PATRICIA
; APPLICANT: TIERREZ-MARTINEZ, ALBERTO
; APPLICANT: AMEND, ALEXANDRA
; APPLICANT: CHAKRABORTY, TRINAD
; APPLICANT: DOMANN, EUGEN
; APPLICANT: HAIN, THORSTEN
```

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; APPLICANT: BERCHE, PATRICK
; APPLICANT: CHARBIT, ALAIN
; APPLICANT: DURANT, LIONEL
; APPLICANT: PEREZ-DIAZ, JOSE-CLAUDIO
; APPLICANT: BAQUERO, FERNANDO
; APPLICANT: GARCIA DEL PORTILLO, FRANCISCO
; APPLICANT: GOMEZ-LOPEZ, NURIA
; APPLICANT: MADUENIO, ENCARN
; APPLICANT: PABLOS, BETRIZ DE
; APPLICANT: WEHLAND, JURGEN
; APPLICANT: KARST, UWE
; APPLICANT: ENTIAN, KARL-DIETER
; APPLICANT: HAUF, JORG
; APPLICANT: ROSE, MATTHIAS
; APPLICANT: VOSS, HAMUT
; TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
; FILE REFERENCE: 05394.0018-02
; CURRENT APPLICATION NUMBER: US/11/045,004
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: 10/637,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: 10/257,023
; PRIOR FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: PCT/FR01/01118
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: FR 00/04,629
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 2854
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1762
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-11-045-004-1762

Query Match 48.1%; Score 37; DB 11; Length 553;
Best Local Similarity 72.7%; Pred. No. 1.2e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 GIEAASAIQ 15
|||:|||||
Db 72 GIDATASITG 82

RESULT 42
US-10-525-907-40
; Sequence 40, Application US/10525907
; Publication No. US2006068476A1
; GENERAL INFORMATION:
; APPLICANT: Kroger, Burkhard
; APPLICANT: Zelder, Oskar
; APPLICANT: Kolpprogge, Corinna
; APPLICANT: Schroder, Hartwig
; APPLICANT: Hafner, Stefan
; TITLE OF INVENTION: Method for Production by Fermentation of Sulphur-Containing Fine
; FILE REFERENCE: 13111-00005-US
; CURRENT APPLICATION NUMBER: US/10/525,907
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: PCT/EP 2003/009451
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: DE 102 39 308.7
; PRIOR FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 40
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Caulobacter crescentus
US-10-525-907-40

Query Match 46.8%; Score 36; DB 9; Length 314;
Best Local Similarity 53.8%; Pred. No. 1e+02;
```

```
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 NFAGIEAAASAIQ 14
||||:|:|
Db 226 NFAGLKKMAAACQ 238

RESULT 43
US-11-188-298-18412
; Sequence 18412, Application US/11188298
; Publication No. US2006007552A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 18412
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Caulobacter crescentus CB15
US-11-188-298-18412

Query Match 46.8%; Score 36; DB 11; Length 314;
Best Local Similarity 53.8%; Pred. No. 1e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 NFAGIEAAASAIQ 14
||||:|:|
Db 226 NFAGLKKMAAACQ 238

RESULT 44
US-11-096-568A-23460
; Sequence 23460, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 23460
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(374)
; OTHER INFORMATION: Ceres Seq. ID no. 12412587
US-11-096-568A-23460

Query Match 46.8%; Score 36; DB 11; Length 374;
Best Local Similarity 46.7%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 WNPAGIEAAASAIQ 15
||||:|:|
Db 173 WNPAGIAHRAVDLEG 187

RESULT 45
US-11-096-568A-23459
; Sequence 23459, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
```

```
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 23459
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(376)
; OTHER INFORMATION: Ceres Seq. ID no. 12412586
US-11-096-568A-23459
```

```
Query Match 46.8%; Score 36; DB 11; Length 376;
Best Local Similarity 46.7%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
```

```
QY 1 WNFAGIEAASAIQ 15
   |||||
Db 175 WNVAGIAHRAVDLEG 189
```

```
RESULT 46
US-11-087-099-1278
; Sequence 1278, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 1278
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Shewanella oneidensis MR-1
US-11-087-099-1278
```

```
Query Match 46.8%; Score 36; DB 11; Length 406;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 WNFAGIEA 8
   |||||
Db 180 WSLFIEA 187
```

```
RESULT 47
US-11-096-568A-23458
; Sequence 23458, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 23458
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(412)
; OTHER INFORMATION: Ceres Seq. ID no. 12412585
US-11-096-568A-23458
```

```
Query Match 46.8%; Score 36; DB 11; Length 412;
```

```
Best Local Similarity 46.7%; Pred. No. 1.3e+02;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 WNFAGIEAASAIQ 15
   |||||
Db 211 WNVAGIAHRAVDLEG 225
```

```
RESULT 48
US-11-188-298-7493
; Sequence 7493, Application US/11188298
; Publication No. US2006007522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 7493
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Rickettsia sibirica
US-11-188-298-7493
```

```
Query Match 46.8%; Score 36; DB 11; Length 427;
Best Local Similarity 54.5%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 WNFAGIEAAS 11
   |||||
Db 195 WGFIEGICATT 205
```

```
RESULT 49
US-11-087-099-3085
; Sequence 3085, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 3085
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Coccidia burnetii RSA 493
US-11-087-099-3085
```

```
Query Match 46.8%; Score 36; DB 11; Length 448;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 WNFAGI 6
   |||||
Db 278 WNFAGV 283
```

```
RESULT 50
US-11-087-099-11164
; Sequence 11164, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
```

```
; SEQ ID NO 11164
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Pasteurella multocida
US-11-087-099-11164

Query Match      46.8% Score 36; DB 11; Length 470;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      1 WNFAGIEAAA 10
      |||:||||
Db      210 WFFVGVGAA 219

Search completed: May 4, 2006, 15:39:30
Job time : 29 secs
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